

Mon Nov 1 10:45:58 2004

us-10-044-692-1.rni

VP 6,261,836 (various 3-10-10)
signature 324-10070
on 6,261,836
Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 29, 2004, 16:25:00 : Search time 310 Seconds
(without alignments)
9205.862 Million cell updates/sec

Title: US-10-044-692-1

Perfect score: 4015

Sequence: 1 GCAGGCGTGGCTGCTGC.....TTTTCAGTTTGAAAAA 4015

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

1649014

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4015	100.0	US-08-851-843A-224	Sequence 224, App
2	4015	100.0	US-08-974-549A-1	Sequence 1, App1
3	4015	100.0	US-08-854-050-224	Sequence 224, App
4	4015	100.0	US-09-430-323-224	Sequence 224, App
5	4015	100.0	US-09-572-423B-3	Sequence 3, App1
6	4015	100.0	US-09-128-354-1	Sequence 1, App1
7	4015	100.0	US-09-675-321-1	Sequence 1, App1
8	4015	100.0	US-09-052-919-1	Sequence 1, App1
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17	4008.6	99.8	US-09-721-456-343	Sequence 343, App
18	3849.2	95.9	US-08-851-843A-173	Sequence 173, App
19	3849.2	95.9	US-08-974-549A-292	Sequence 292, App
20	3849.2	95.9	US-08-854-050-173	Sequence 173, App
21	3849.2	95.9	US-09-430-323-173	Sequence 173, App
22	3849.2	95.9	US-09-402-181B-292	Sequence 292, App
23	3849.2	95.9	US-09-721-456-292	Sequence 292, App
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29	2205.2	54.9	3451	3	US-09-721-456-721	Sequence 721, App
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31	2200.8	54.8	3396	4	US-09-721-456-639	Sequence 639, App
32	2196.6	54.7	3396	3	US-08-974-549A-638	Sequence 638, App
33	2196.6	54.7	3396	4	US-09-721-456-638	Sequence 638, App
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40	1877.2	46.8	2171	3	US-08-854-050-100	Sequence 100, App
41	1877.2	46.8	2171	3	US-09-430-323-100	Sequence 100, App
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43	1877.2	46.8	2171	4	US-09-721-456-266	Sequence 266, App
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ALIGNMENTS

RESULT 1
US-08-851-843A-224
Sequence 224, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 224:

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RESULT 2
US-08-974-549A-1
; Sequence 1, Application US/08974549A
; Patent No. 6166178

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
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LOCATION: 56..3454

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GENERAL INFORMATION:
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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017


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QY 1681 CAAGTTCTGCACTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
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Db 1741 TGTTCACGAGACCAAGCTTTCAAAAAGAACAGGCTCTTTTCTTACCGAAGATGTCTGAG 1800
QY 1801 CAAGTTGCAAGAGCTTGGATGATGACAGCACTTGAAGAGGATGACGTGGGAGCTGTGTC 1860
Db 1801 CAAGTTGCAAGAGCTTGGATGATGACAGCACTTGAAGAGGATGACGTGGGAGCTGTGTC 1860
QY 1861 GGAAGCAGAGATCAGGAGCATCGGAGCCAGAGCCGCTCTGACGTCCAGATCTCGG 1920
Db 1861 GGAAGCAGAGATCAGGAGCATCGGAGCCAGAGCCGCTCTGACGTCCAGATCTCGG 1920
QY 1921 CTTTCATCCCGAAGCTTGAAGCTGTGCGCGCTGATTTGTAACATGACATGATGATGATGATGAT 1980
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DB 3541 CACACCCAGGCGCCGAGCCGCTGGAGTCTGAGGCTTGAAGTGTGTTGGCCGAGGCTTG 3600
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DB 3901 CCCTGTACACAGGAGGAGCCCTGACCTGATGGGGGTCCCTGTGGGTCAATTGGGGG 3960
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DB 3961 GAGGTCTGTGGAGAGTAAATCTGAATATATGATTTTTCAGTTTGAAGAAAA 4015

RESULT 7
US-09-675-321-1
Sequence 1, Application US/09675321
Patent No. 6440735
GENERAL INFORMATION:
APPLICANT: Gaeta, Federico C.A.
APPLICANT: Gaeta Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
FILE REFERENCE: Response to a Telomerase Antigen
CURRENT APPLICATION NUMBER: US/09/675,321
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/112,006
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: WO PCT/US99/06898
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56) .. (3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-09-675-321-1

Query Match 100.0%; Score 4015; DB 4; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GCGGCTCCCGCTGCGACGAGCGTGCCTCTGTGCGACACCTACCGGAGGTGT 120
QY 121 GCGGCTGCGACGTTGTGTCGCGCGCTTGGAGGCTCCAGAGGCTGTGTGACGCGG 180
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DB 181 GGAACCGGCGGCTTTCGCGCGCTGTGCGCGACAGTGTGCTGTGCGCGGAGCGC 240
QY 241 AGGCG 300
DB 241 AGGCG 300
QY 301 CCGAGTGTGACAGAGGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 301 CCGAGTGTGACAGAGGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 GGTGTGAGCGGCG 420
DB 361 GGTGTGAGCGGCG 420
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QY 601 TCAGGCG 660
DB 601 TCAGGCG 660
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DB 841 GCGTGGACCGAGTGAACGTTGTTCTGTGTGTGTCACTGTGCAAGCCCGGAGAGC 900
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QY	181	GGACCCGGGGGCTTTCCGGCGCTGGTGGGCCAGTACCTTGATGTGGTGGCCCTGGAGCG	240
Db	181	GGACCCGGGGGCTTTCCGGCGCTGGTGGGCCAGTACCTTGATGTGGTGGCCCTGGAGCG	240
QY	241	ACGGCCGGCCCCCGCGGCCCTCTTCCGCCAGGTGTCCTGTGATAGAGAGCTGTGGC	300
Db	241	ACGGCCGGCCCCCGCGGCCCTCTTCCGCCAGGTGTCCTGTGATAGAGAGCTGTGGC	300
QY	301	CCGAGTGTGACAGAGGCTGTGCCAGGCGCGCGAGAAAGTGTGAGCTTCGCTTCGC	360
Db	301	CCGAGTGTGACAGAGGCTGTGCCAGGCGCGCGAGAAAGTGTGAGCTTCGCTTCGC	360
QY	361	GCTGCTGAGCGGGGCCCGGGGGGCCCTCCAGAGCTTTCACCAACGAGGTGGCAGCTA	420
Db	361	GCTGCTGAGCGGGGCCCGGGGGGCCCTCCAGAGCTTTCACCAACGAGGTGGCAGCTA	420
QY	421	CCGAGCCAAACAGGTGACCGAAGCACTGGGGGGGACCGGGGCTGGGGGCTGTGCTGG	480
Db	421	CCGAGCCAAACAGGTGACCGAAGCACTGGGGGGGACCGGGGCTGGGGGCTGTGCTGG	480
QY	481	CCGCGTGGGCGACAGAGTGTGATCCTGTGATGCTGGACGCTGGCCTCTTTGTGCTGT	540
Db	481	CCGCGTGGGCGACAGAGTGTGATCCTGTGATGCTGGACGCTGGCCTCTTTGTGCTGT	540
QY	541	GGCTCCCACTGTGCGCTTACAGAGTGTGGGGGCGCGCTGTATACAGTGGCGCTGGCAC	600
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QY	601	TCAGGCGCGGCCCGCGCCACACGTATGTGAGCCCGCAAGGCTGTGGATGTGAAACGAGC	660
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QY	661	CTGGAAACCATTAACGTGTAGGGAGGCGGGGGTCCCTCTGGGCTGTGCAGCCCGGGTGGAG	720
Db	661	CTGGAAACCATTAACGTGTAGGGAGGCGGGGGTCCCTCTGGGCTGTGCAGCCCGGGTGGAG	720
QY	721	GAGGCGCGGGGCGACGTGCAGCGAAGTGTGCGCTTGCGCCAAAGAGGCCAGGCGTGGCG	780
Db	721	GAGGCGCGGGGCGACGTGCAGCGAAGTGTGCGCTTGCGCCAAAGAGGCCAGGCGTGGCG	780
QY	781	TGCCCCCTGAGCCGGAGCGGACCGCTGTGGGCAAGGAGTCTGTGGCCACCCGGGCGAGAC	840
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QY	841	GGGTGAGCCGAGTGAACCGGTGTTCTGTGTGGTGTACCTGTGCACACCCGCGGAAGAAC	900
Db	841	GGGTGAGCCGAGTGAACCGGTGTTCTGTGTGGTGTACCTGTGTGCACACCCGCGGAAGAAC	900
QY	901	CACGCTTTTGAAGGGTGGCTCTGTGACAGCGGCACTTCCACCCATCGTGGGGCGGCA	960
Db	901	CACCTCTTTGAGGGTGGCTCTGTGACAGCGGCACTTCCACCCATCGTGGGGCGGCA	960
QY	961	GGACCAAGGGGGCCCCCATTCACATCGGGGACACAGTCTCTGTGGACACCGCTTGTTC	1020
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QY	1021	CCGGGTGTACGCGGAGCCAAACACTTCTCTACTCTCAGGCGCAAGAGACACTTGG	1080
Db	1021	CCGGGTGTACGCGGAGCCAAACACTTCTCTACTCTCAGGCGCAAGAGACACTTGG	1080
QY	1081	GGCTCTCTTCTACTACGTCTCTGTAGGGCCAGCTGACTGGGCTTCGAGGCTGTGGA	1140
Db	1081	GGCTCTCTTCTACTACGTCTCTGTAGGGCCAGCTGACTGGGCTTCGAGGCTGTGGA	1140
QY	1141	GACCATCTTTCTGGGCTTCAGGCGCTGTGATGTGCAGAGACTCCCGCAGGTTGCCCGCT	1200
Db	1141	GACCATCTTTCTGGGCTTCAGGCGCTGTGATGTGCAGAGACTCCCGCAGGTTGCCCGCT	1200
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[illegible]

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US-08-912-951-1
Sequence 1, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0200
 INFORMATION FOR SEQ ID NO: 1:
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 STRANDEDNESS: single
 TOPOLOGY: linear
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 LOCATION: 56..3454
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 transcriptase (hTrr) catalytic protein
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 US-08-912-951-1

Query Match 100.0%; Score 4015; DB 4; Length 4015;
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 Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 3421 ACTGCTCTGAGCTTCAAGACATCTGAGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3480
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Db 2881 GCAGAGCACTACTCCAGCTATGCGCCGACCTTCATCAGAGCCAGTCTCACTTCAACCG 2940
Qy 2941 CGGCTTCAAGGCTGGAGAGAAATGCGTCCGAAATCTTTGGGGTCTTGGCGGTGAAGT 3000
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Db 3001 TCACAGCGCTGTTTGTGATTTGGAGGTGAACAGCTTCACAGCGGTGACACCAATCTA 3060
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Db 3901 CCTGTACACAGGCGAGAGACCTTGACCTGATGAGGAGTCCCTGTGGATCAAAATGGGG 3960
Qy 3961 GAGGTCTGTGGAGTAAATCTGAATATATGAGTTTTCAGTTTGAAGAAAA 4015
Db 3961 GAGGTCTGTGGAGTAAATCTGAATATATGAGTTTTCAGTTTGAAGAAAA 4015

RESULT 12
US-09-721-456-1
Sequence 1, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721.456
FILING DATE: 22-NOV-6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974.549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724.643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844.419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846.017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851.843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854.050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911.312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912.951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915.503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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QY 1921 CTTCAATCCCAAGCTGAGGGGCTGGGGCCGATTTGAAATGAGACTAGCTGTGGAGC 1980
DB 1921 CTTCAATCCCAAGCTGAGGGGCTGGGGCCGATTTGAAATGAGACTAGCTGTGGAGC 1980
QY 1981 CAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACTGTT 2040
DB 1981 CAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACTGTT 2040
QY 2041 CAGCGGTCTCAATTAAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2100
DB 2041 CAGCGGTCTCAATTAAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2100
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DB 2221 GGAAGAGCTCAGAGAGGTATCGCCAGCATCATCAAACTCCAGAAACGTAATGCGTGG 2280
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DB 2521 CAAATCTCAAGTCAAGTCCAGAGGAGTCCCGAGGGCTCCATCTCTCAAGCTGCTG 2580
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DB 2821 GCGGGCCCAAGGCTTATCCCTGTGTGGGGCTGTGTGTGATACCGGAGCCTTGAAGGT 2880
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DB 2941 CCGCTTCAAGAGCTGAGAGAGAACATGCGTGCAGAACTTTTGGGGTCTTGGGGCTGAAGTG 3000

QY 3001 TCACAGCCGTGTTCTGATTTTGCAGTGAACAGCTCCAGAGGTTGACCAACATCTA 3060
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DB 3121 TCAGCAAGTTGAGAGAACCCCAATTTTCTGGGGGCTGATCTGACAGGGGCTCCCT 3180
QY 3181 CTGCTACTCCATCTGAAAGCCCAAGAACGAGAGATGTGCTGAGGGGGCCCAAGGGCGCG 3240
DB 3181 CTGCTACTCCATCTGAAAGCCCAAGAACGAGAGATGTGCTGAGGGGGCCCAAGGGCGCG 3240
QY 3241 CCGGCTCTGCTGCTCCGAGGGCGTGAAGTGTGTGTCACAGAGATTTCTGCTCAAGCT 3300
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QY 3301 GACTGAGACCGGTGACCTTACAGTGCACCTCTGGGGGTGACTCAGAGACGCCAGCGCA 3360
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DB 3601 CATGTCCGCTGAAAGCTGAGTGTGAGTGTGAGGCTGAGGAGTGTGAGGAGTGTGAGGAGT 3660
QY 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGCGCTGCGCTTCAACCCA 3720
DB 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGCGCTGCGCTTCAACCCA 3720
QY 3721 GGGCCAGCTTTTCTTACAGGAGCCCGGCTTCACTCCCAATGAGTAATGTCATCC 3780
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RESULT 13
US-09-953-052-1
; Sequence 1, Application US/09953052
; Patent No. 6627619

Db	3181	TTGCTACTCCATCTCTGAAAGCCAAAGAACGACGGAGTATGCTGTGGGGGCGCAAGGGGGCCGC	3248
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Db	3241	CGGGCCCTCTGCGCTTCCGAGGGCCGGACATGTGCTGTGCCACCAAGCATTTCTGCTCAAGCT	3300
QY	3301	GACTCGACACCGGTGCACTCACTGTGGCCACTCTGTGGGGGTCACTCAAGGAACAGCCCAAGACGA	3360
Db	3301	GACTCGACACCGGTGTCACTCACTGTGGCCACTCTGTGGGGGTCACTCAAGGAACAGCCCAAGACGA	3360
QY	3361	GCTGAGTGGAAAGCTCCCGGGGAGCGACGCTGACTGCGCTGTGAGGCGCGAGCCAAACCCGGC	3420
Db	3361	GCTGAGTGGAAAGCTCCCGGGGAGCGACGCTGACTGCGCTGTGAGGCGCGAGCCAAACCCGGC	3420
QY	3421	ACTGCGCCCTCAAGACTTTCAAGAACCATCTCTGTGACTGATGATGACACCCGCCCAACAGCAGCGCGA	3480
Db	3421	ACTGCGCCCTCAAGACTTTCAAGAACCATCTCTGTGACTGATGATGACACCCGCCCAACAGCAGCGCGA	3480
QY	3481	GAGCAGACACACGAGCGCCCTGTCAACGCCGGGCTCTACGTCCCAAGGAGAGAGGGGGCGGC	3540
Db	3481	GAGCAGACACACGAGCGCCCTGTCAACGCCGGGCTCTACGTCCCAAGGAGAGAGGGGGCGGC	3540
QY	3541	CACACCCAGGCGCGCACCGCTGGAGTGTGAGGCGCTGAGTGAATTTTGGCCGAGCGCTG	3600
Db	3541	CACACCCAGGCGCGCACCGCTGGAGTGTGAGGCGCTGAGTGAATTTTGGCCGAGCGCTG	3600
QY	3601	CATGTCCGGCTGGAAGGCTGAGTGTTCGGCTGAAGGCTTAAGCGAGTGTCCACCCAAAGGCT	3660
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QY	3661	GAGTGTCCAGACACACTGCGCTTCACTTCCCAACAGGCTGAGCGCTGGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGACACACTGCGCTTCACTTCCCAACAGGCTGAGCGCTGGCTCCACCCCA	3720
QY	3721	GGGCGCAGCTTTTCTCACACAGGAGCGCGGCTTTCACCTCCCAATAGGAATATGTCATCC	3780
Db	3721	GGGCGCAGCTTTTCTCACACAGGAGCGCGGCTTTCACCTCCCAATAGGAATATGTCATCC	3780
QY	3781	CCAAATTCGCAATTTGTCAACCCCTCGCCCTGCGCCCTTTCGCTTCCACCCCAACATCC	3840
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QY	3841	AGTGTGAGAACCTTGAGAAAGAACCTGTGAGAGCTTGTGGAAATTTTGGAGTGAACAAAGTGTG	3900
Db	3841	AGTGTGAGAACCTTGAGAAAGAACCTGTGAGAGCTTGTGGAAATTTTGGAGTGAACAAAGTGTG	3900
QY	3901	CCCTGTACACAGGCGAGGACCTTGCACTGTGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
Db	3901	CCCTGTACACAGGCGAGGACCTTGCACTGTGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
QY	3961	GAGGTGCTGTGGAGTAAATAATCTGAATATATGATTTTTCAGTTTGGAAAAAAA 4015	
Db	3961	GAGGTGCTGTGGAGTAAATAATCTGAATATATGATTTTTCAGTTTGGAAAAAAA 4015	

RESULT 14
US-09-465-491-1

Sequence 1, Application US/09465491
Patent No. 6664046
GENERAL INFORMATION:
APPLICANT: Chang, Sheng-Yung P.
APPLICANT: Santini, Christopher D.
TITLE OF INVENTION: Quantitation of hTERT mRNA Expression
FILE REFERENCE: RRA1002
CURRENT APPLICATION NUMBER: US/09/465,491
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-465-491-1

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Query Match	100.0%	Score 4015;	DB 4;	Length 4015;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 4015; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	GCAGCGCTGCGTCTTGCTGCGCAGTGGAGAAACCTTGACCCCGGACACCCCGCGATATCC	60
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QY	61	GCGCGCTTCCCGCTGCGGAGCGGCTCCCTCTGCGCAGCACACTACCGAGAGTGTCT	120
Db	61	GCGCGCTTCCCGCTGCGGAGCGGCTCCCTCTGCGCAGCACACTACCGAGAGTGTCT	120
QY	121	GCGCGTGGCCACGTTGCTGTGGCGGCGCTGGGGGCCCAAGGCTGGGCGCTGTGTGCAGCCGCG	180
Db	121	GCGCGTGGCCACGTTGCTGTGGCGGCGCTGGGGGCCCAAGGCTGGGCGCTGTGTGCAGCCGCG	180
QY	181	GAACCCGAGCGGCTTTCCGCGCGCTGTGTGAGCCCAATGCTGTGTGACGTCCTTGAGACGC	240
Db	181	GAACCCGAGCGGCTTTCCGCGCGCTGTGTGAGCCCAATGCTGTGTGACGTCCTTGAGACGC	240
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Db	301	CCGAGTGTCTGAGAGGCTGTGTCCAGCGCGCGCGCAAGACGTGTGTGCGCTTCGCTTGGC	360
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Db	361	GCTGTCTGAGACGAGGCGCGGAGGCGCCCGCGAGGCTTTCACCAACAGCGTGTGCGACTA	420
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Db	481	CCGCGTGGGCGACGCTGTGTGTTCACCTGTGTGGACGCGTGGCGCGCTTGTGTGTGGT	540
QY	541	GCGTCCCAAGCTGCGCTACCAAGGTGTACGGGCGCGCTGTGACCAAGCTCGGCGCTGCAC	600
Db	541	GCGTCCCAAGCTGCGCTACCAAGGTGTACGGGCGCGCTGTGACCAAGCTCGGCGCTGCAC	600
QY	601	TCAAGCGCGCGCCCGCGCCAACGCTAAGTGACCCCGAAGGCGCTTGTGGATGTCCAACCGGCG	660
Db	601	TCAAGCGCGCGCCCGCGCCAACGCTAAGTGACCCCGAAGGCGCTTGTGGATGTCCAACCGGCG	660
QY	661	CTGGAACAATAGCGGTCAAGAGAGCGGGGTTCCCTGTGGCGCTGTGCACGCGCGGGGTGCAG	720
Db	661	CTGGAACAATAGCGGTCAAGAGAGCGGGGTTCCCTGTGGCGCTGTGCACGCGCGGGGTGCAG	720
QY	721	GAGCGCGGGGGCGAGTGCACAGCCCAAGTCTGCGCTTGTCCCAAGAGGCGCCAGCGCTGTGCGC	780
Db	721	GAGCGCGGGGGCGAGTGCACAGCCCAAGTCTGCGCTTGTCCCAAGAGGCGCCAGCGCTGTGCGC	780
QY	781	TGCGCCCTTAGCGCGGAGCGAGCGCCGTTTGGGCAAGGGGTCTGTGGGCCACCCGGGCGAGAC	840
Db	781	TGCGCCCTTAGCGCGGAGCGAGCGCCGTTTGGGCAAGGGGTCTGTGGGCCACCCGGGCGAGAC	840
QY	841	GCGTGAACAACGAGTACCGTGTGTTCTGTGTGTGTTCACCTGTGCACACACCGCGCAAGAAAGC	900
Db	841	GCGTGAACAACGAGTACCGTGTGTTCTGTGTGTGTTCACCTGTGCACACACCGCGCAAGAAAGC	900
QY	901	CACCTCTTTGGAGGGTGCCTCTCTGTGCAAGCGGCCACTTCCCAACCCATTCGTGTGGCGCGCA	960
Db	901	CACCTCTTTGGAGGGTGCCTCTCTGTGCAAGCGGCCACTTCCCAACCCATTCGTGTGGCGCGCA	960
QY	961	GCACCAACGCGGGCCCCCATTCACATGCGGGCACCAATGCCCTTGGGACAGGCTTGTGC	1020
Db	961	GCACCAACGCGGGCCCCCATTCACATGCGGGCACCAATGCCCTTGGGACAGGCTTGTGC	1020

QY	1021	CCCGGTGAAGCCGAGACCAAGACATTCCTCTCACTCCCTCAGGCGACAAAGAGCAGCTGGC	1080
Db	1021	CCGGGTGAAGCCGAGACCAAGACATTCCTCTCACTCCCTCAGGCGACAAAGAGCAGCTGGC	1080
QY	1081	GCCCTCTTCTCACTCAAGCTCTCTGAGGCCAGGCTGACTGAGCGCTCGAGAGCTGCTGGA	1140
Db	1081	GCCCTCTTCTCACTCAAGCTCTCTGAGGCCAGGCTGACTGAGCGCTCGAGAGCTGCTGGA	1140
QY	1141	GACCACTTTTCTGGGTTCCAGGCTCTGGAATGCCAGGGACTCCCGCAGAGTTGCCCCGCT	1200
Db	1141	GACCACTTTTCTGGGTTCCAGGCTCTGGAATGCCAGGGACTCCCGCAGAGTTGCCCCGCT	1200
QY	1201	GCCCCAGCGCTACTGGCAAAATGCGGCCCTCTTTTCTGGAGCTGCTGTGGAAAACAAGCGCA	1260
Db	1201	GCCCCAGCGCTACTGGCAAAATGCGGCCCTCTTTTCTGGAGCTGCTGTGGAAAACAAGCGCA	1260
QY	1261	GTGCCCCCTAAGGGGGTGTCTCTGAAGCGCATCTGCCCGCTGCACTGGCGCTCAACCCAGC	1320
Db	1261	GTGCCCCCTAAGGGGGTGTCTCTGAAGCGCATCTGCCCGCTGCACTGGCGCTCAACCCAGC	1320
QY	1321	AGCCGGTCTCTGTGCGCCGGAGAAAGCCCAAGGGCTGTGGCGCGCCCCAGAGAGAGGA	1380
Db	1321	AGCCGGTCTCTGTGCGCCGGAGAAAGCCCAAGGGCTGTGGCGCGCCCCAGAGAGAGGA	1380
QY	1381	CACAGACCCCGCTGCGCTGTGTCAGCTGCTCCGACAGACAGCAAGCCCTGTGGCAGTGTA	1440
Db	1381	CACAGACCCCGCTGCGCTGTGTCAGCTGCTCCGACAGACAGCAAGCCCTGTGGCAGTGTA	1440
QY	1441	CGGCTGTGTGGGGGCTGGCCGCTGGCTGGTGGTCCCAAGCCTCTGGGGCTTCAAGCA	1500
Db	1441	CGGCTGTGTGGGGGCTGGCCGCTGGCTGGTGGTCCCAAGCCTCTGGGGCTTCAAGCA	1500
QY	1501	CAACGAACGCGCTCTCTCCTCAGAGAACCAACAAGATTATCTCCCTGGGGAAAGCTGACAA	1560
Db	1501	CAACGAACGCGCTCTCTCCTCAGAGAACCAACAAGATTATCTCCCTGGGGAAAGCTGACAA	1560
QY	1561	GCTCTCTGTGAGAGAGCTGACGTGGAAGATGAGCGTGCAGGACCTGCGCTTGGCTGGCAG	1620
Db	1561	GCTCTCTGTGAGAGAGCTGACGTGGAAGATGAGCGTGCAGGACCTGCGCTTGGCTGGCAG	1620
QY	1621	GAGCCCAAGGGGTTTGGCTGTGTTCCGGCCGACAGACACACGTGTGCTGATAGAGATCTGGC	1680
Db	1621	GAGCCCAAGGGGTTTGGCTGTGTTCCGGCCGACAGACACACGTGTGCTGATAGAGATCTGGC	1680
QY	1681	CAAGTTCTCTGACATGAGCTGATGAGTGTGTACGTGCTGAGAGCTGTCAAGTCTTCTTTTA	1740
Db	1681	CAAGTTCTCTGACATGAGCTGATGAGTGTGTACGTGCTGAGAGCTGTCAAGTCTTCTTTTA	1740
QY	1741	TGTACCGAGAGACAGTTTCAAAAGAAACAGGCTCTTTTCTACCGGAAAGTGTCTGGAG	1800
Db	1741	TGTACCGAGAGACAGTTTCAAAAGAAACAGGCTCTTTTCTACCGGAAAGTGTCTGGAG	1800
QY	1801	CAAGTTGCAAAAGCATTTGGAAATCAGACAGCACTTTGAAGAGGGTGCAGCTGCGGAGCTGTC	1860
Db	1801	CAAGTTGCAAAAGCATTTGGAAATCAGACAGCACTTTGAAGAGGGTGCAGCTGCGGAGCTGTC	1860
QY	1861	GGAAGCAGAGGTCAGGAGCATTCGGAAAGCTCAGGCCCGCTCTGTGAACGTTCAGACTCCG	1920
Db	1861	GGAAGCAGAGGTCAGGAGCATTCGGAAAGCTCAGGCCCGCTCTGTGAACGTTCAGACTCCG	1920
QY	1921	CTTTCATCCCCCAAGGCTGACGGGCTGCGGCCGATTTGTGAATGGAATCTACGTCTGGGAGC	1980
Db	1921	CTTTCATCCCCCAAGGCTGACGGGCTGCGGCCGATTTGTGAATGGAATCTACGTCTGGGAGC	1980
QY	1981	CAGAACGTTTCCGAGAGAAAAGAGGSCCGAGCGCTTCACTTCAGAGGTTGAAGGCACTGTT	2040
Db	1981	CAGAACGTTTCCGAGAGAAAAGAGGSCCGAGCGCTTCACTTCAGAGGTTGAAGGCACTGTT	2040
QY	2041	CAGCGTGTCTCAACTACGAGCGGGGCGCGCGCCCGGCTCTCTGTGGCCCTCTGTGGCTGGG	2100
Db	2041	CAGCGTGTCTCAACTACGAGCGGGGCGCGCGCCCGGCTCTCTGTGGCCCTCTGTGGCTGGG	2100
QY	2101	CTTGAGCGATATCCACAGGGCTTGGCGCACCTTGCTGCTGCTGCTGTGGGCGCAGAGACC	2160

Dp	2101	CTGTGACGATATCCACAGGGGCTGGGGCACTTTCGTGTCGTGTGCGGGGCCCAAGAACCC	2160
Qy	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGGTACGACCCATCCCCA	2220
Dp	2161	GGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGGTACGACCCATCCCCA	2220
Qy	2221	GGACAGGCTACCGGAGGTCAATCCGCAAGCATCATMAAACCAGAAACGTAATCGGTGCG	2280
Dp	2221	GGACAGGCTACCGGAGGTCAATCCGCAAGCATCATMAAACCAGAAACGTAATCGGTGCG	2280
Qy	2281	TCGGTATGCGGTGTCAGAAAGGCCGCCCATGGGCGACGTCCCAAGGCGTTCAAGAGCA	2340
Dp	2281	TCGGTATGCGGTGTCAGAAAGGCCGCCCATGGGCGACGTCCCAAGGCGTTCAAGAGCA	2340
Qy	2341	CGTCTTAACCTTGAACAGACTCCAGCCGTACATGCGACAGTTGTTGCTCACTTGCAGA	2400
Dp	2341	CGTCTTAACCTTGAACAGACTCCAGCCGTACATGCGACAGTTGTTGCTCACTTGCAGA	2400
Qy	2401	GACCAAGCCGCTGAGGGATGCCGTGTCATGCGACAGACCTCCCTGAATGAAGGCGAG	2460
Dp	2401	GACCAAGCCGCTGAGGGATGCCGTGTCATGCGACAGACCTCCCTGAATGAAGGCGAG	2460
Qy	2461	CAGTGGGCTCTTCGACGCTCTTCTTACGCTCAATGTGCCACAGCGCGTGGCATAGGGG	2520
Dp	2461	CAGTGGGCTCTTCGACGCTCTTCTTACGCTCAATGTGCCACAGCGCGTGGCATAGGGG	2520
Qy	2521	CAATCTTAAGTCCAGTGGCCAGGGGATCCCGAGGGGCTCAATCTCTCAAGCTGCTTG	2580
Dp	2521	CAATCTCTTAAGTCCAGTGGCCAGGGGATCCCGAGGGGCTCAATCTCTCAAGCTGCTTG	2580
Qy	2581	CAGGCTGTGCTACGGGCGACATGAGAGAAAGGCTTTGGGGGATTTGGCGGGAAGGGCT	2640
Dp	2581	CAGGCTGTGCTACGGGCGACATGAGAGAAAGGCTTTGGGGGATTTGGCGGGAAGGGCT	2640
Qy	2641	GCTCTTCGCTTTGGTGTGATATTTCTTTTGTGTGACCTCACTCACTCAACGCGAATAC	2700
Dp	2641	GCTCTTCGCTTTGGTGTGATATTTCTTTTGTGTGACCTCACTCACTCAACGCGAATAC	2700
Qy	2701	CTTCTCTCAGAGACCTCGGTCGAGAGTGTCCCTGAGATGAGTACGTCGTCGTGTGAATTCG	2760
Dp	2701	CTTCTCTCAGAGACCTCGGTCGAGAGTGTCCCTGAGATGAGTGTCCCTGAGATGAGTACG	2760
Qy	2761	GACAGTGTGAACCTTCCCTGTAGAGAGAGAGGCGCTGGGTGGACGAGCTTTTGTTCAGAT	2820
Dp	2761	GACAGTGTGAACCTTCCCTGTAGAGAGAGAGGCGCTGGGTGGACGAGCTTTTGTTCAGAT	2820
Qy	2821	GGCGGGCCACAGGCGTATTCGCCGTGTGGGGCGGCGTGTGAGTATACCAGAACCTGGAGAGT	2880
Dp	2821	GGCGGGCCACAGGCGTATTCGCCGTGTGGGGCGGCGTGTGAGTATACCAGAACCTGGAGAGT	2880
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Dp	2881	GCAGAGGACTTACTCCAGCTATGCCCGGACCTTCATCAAGAGCAAGTCTCACTTCAACCG	2940
Qy	2941	CGGTTTAAAGGCTGGGAGGAAATGTGTGCAAACTCTTTGGGGGCTTGGCGGCTGAAGTG	3000
Dp	2941	CGGTTTAAAGGCTGGGAGGAAATGTGTGCAAACTCTTTGGGGGCTTGGCGGCTGAAGTG	3000
Qy	3001	TCACAGGCTGTTCTCTGATTTGAGAGGTGAAGAGCCCTCAAGAGCGGTGTGACCAACATTA	3060
Dp	3001	TCACAGGCTGTTCTCTGATTTGAGAGGTGAAGAGCCCTCAAGAGCGGTGTGACCAACATTA	3060
Qy	3061	CAAGATCTCTCTGTCAGAGCGTACAGGTTTCAAGGATGTGTGTCAGAGCTCCCATTTCA	3120
Dp	3061	CAAGATCTCTCTGTCAGAGCGTACAGGTTTCAAGGATGTGTGTCAGAGCTCCCATTTCA	3120
Qy	3121	TCAGCAAGTTTGAAGAAACCCACATTTTCTGTGGCGGTCACTCTGACAGGCGCTCCCT	3180
Dp	3121	TCAGCAAGTTTGAAGAAACCCACATTTTCTGTGGCGGTCACTCTGACAGGCGCTCCCT	3180
Qy	3181	CTGTATCTCCATCTGAAAGCCAGAGACGACAGGATGTGTGCTGGGGGCGCAAGGCGCGCGC	3240

Db	3181	CTGTACTCCATCTCTGAAAGCCAGAAACGACGGGATGTCGTGTGGGGGCGAAGGGCGCGC	3240
QY	3241	CGGCGCTTCTGCGCTTCCGAGGCGCTGTCAGTGGCTGTGCCACCAAGCATTTCTGTCCAGCT	3300
Db	3241	CGGCGCTTCTGCGCTTCCGAGGCGCTGTCAGTGGCTGTGCCACCAAGCATTTCTGTCCAGCT	3300
QY	3301	GACTCGACACCGGTGTCACCTACGTGCGCCTCTGTGGGGGTCACTCAGAGACGCGCCAGACGA	3360
Db	3301	GACTCGACACCGGTGTCACCTACGTGCGCCTCTGTGGGGGTCACTCAGAGACGCGCCAGACGA	3360
QY	3361	GCTGAGTCGGAAGCTCCCGGGGAGCGACTGACTGCTCTGGAGGCGCGACCAACCCGGC	3420
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QY	3421	ACTGCGCTCAGACTTTCAGAACCATTCCTTGAGATGTATATGCGACCCCGCCACACCGCGCGA	3480
Db	3421	ACTGCGCTCAGACTTTCAGAACCATTCCTTGAGATGTATATGCGACCCCGCCACACCGCGCGA	3480
QY	3481	GAGCAGACACACGAGACGCCCTGTCAAGCGCGGCTCTACGTCCACGAGGAGGAGGGGCGGC	3540
Db	3481	GAGCAGACACACGAGACGCCCTGTCAAGCGCGGCTCTACGTCCACGAGGAGGAGGGGCGGC	3540
QY	3541	CACACCCAGGCGCGCACCGGCTGGAGATCTGAGGCGCTGAGTGTGTTGGCTCGAGGCGCTG	3600
Db	3541	CACACCCAGGCGCGCACCGGCTGGAGATCTGAGGCGCTGAGTGTGTTGGCTCGAGGCGCTG	3600
QY	3601	CATGTCCGGCTGGAAGGCTGAGTGTCCCGGCTGAGGCGCTGAGGAGTGTCCACCCAAAGGCT	3660
Db	3601	CATGTCCGGCTGGAAGGCTGAGTGTCCCGGCTGAGGCGCTGAGGAGTGTCCACCCAAAGGCT	3660
QY	3661	GAGTGTCCAGACACACTGCGCTTTCATTCCCAAGGCTGTGGGCTTCGCTCCACCCCA	3720
Db	3661	GAGTGTCCAGACACACTGCGCTTTCATTCCCAAGGCTGTGGGCTTCGCTCCACCCCA	3720
QY	3721	GGGCGAGCTTTTCTCTCACACGAGAGCGCGGCTTTCACCTCCCAATAGGAATAGTCATCC	3780
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QY	3781	CCAATTTGCCATTGTATTACCCCTCCGCTGCGCTCTTTGGCTTTCCACCCCAACCAATCC	3840
Db	3781	CCAATTTGCCATTGTATTACCCCTCCGCTGCGCTCTTTGGCTTTCCACCCCAACCAATCC	3840
QY	3841	AGGTGAGAGACCTGTGAGAGAACCTGTGGAGCTCTGGGAATTTGGAGTACCAAAAGGTGTG	3900
Db	3841	AGGTGAGAGACCTGTGAGAGAACCTGTGGAGCTCTGGGAATTTGGAGTACCAAAAGGTGTG	3900
QY	3901	CCCTGTACACAGGCGGAGACCCCTGCACTGTGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
Db	3901	CCCTGTACACAGGCGGAGACCCCTGCACTGTGATGGGGGTCCCTGTGGGTCAAAATTTGGGGG	3960
QY	3961	GAGGTGCTGTGGGAGTAATAATACGAATATATGATTTTTCAGTTTGAATAAAAAA 4015	
Db	3961	GAGGTGCTGTGGGAGTAATAATACGAATATATGATTTTTCAGTTTGAATAAAAAA 4015	

RESULT 15
US-08-974-549A-343
; Sequence 343, Application US/08974549A

GENERAL INFORMATION:
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APPLICANT: Lingner, Joachim
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APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco

```

1 STATE: California
2 COUNTRY: USA
3 ZIP: 94111-3834
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: PatentIn Release #1.0, Version #1.30
10
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/974,549A
13 FILING DATE: 19-NOV-1997
14 CLASSIFICATION: 536
15
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 08/724,643
18 FILING DATE: 01-OCT-1996
19
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 08/844,419
22 FILING DATE: 18-APR-1997
23
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/846,017
26 FILING DATE: 25-APR-1997
27
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/851,843
30 FILING DATE: 06-MAY-1997
31
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US 08/854,050
34 FILING DATE: 09-MAY-1997
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36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: US 08/911,312
38 FILING DATE: 14-AUG-1997
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40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 08/912,951
42 FILING DATE: 14-AUG-1997
43
44 PRIOR APPLICATION DATA:
45 APPLICATION NUMBER: US 08/915,503
46 FILING DATE: 14-AUG-1997
47
48 PRIOR APPLICATION DATA:
49 APPLICATION NUMBER: WO PCT/US97/17618
50 FILING DATE: 01-OCT-1997
51
52 PRIOR APPLICATION DATA:
53 APPLICATION NUMBER: WO PCT/US97/17885
54 FILING DATE: 01-OCT-1997
55
56 ATTORNEY/AGENT INFORMATION:
57 NAME: Apple, Randolph Ted
58 REGISTRATION NUMBER: 36,429
59 REFERENCE/DOCKET NUMBER: 015389-002610US
60
61 TELECOMMUNICATION INFORMATION:
62 TELEPHONE: (415) 576-0200
63 TELEFAX: (415) 576-0300
64
65 INFORMATION FOR SEQ ID NO: 343:
66 SEQUENCE CHARACTERISTICS:
67 LENGTH: 4037 base pairs
68 TYPE: nucleic acid
69 STRANDEDNESS: single
70 TOPOLOGY: linear
71
72 MOLECULE TYPE: cDNA
73
74 FEATURE:
75 NAME/KEY: CDS
76 LOCATION: 56..3454
77 OTHER INFORMATION: /note= "refined sequence of hprt cDNA"
78
79 US-08-974-549A-343

```

[illegible]

QY	121	GCCTGCTGACACGTTCTGTGTGTCGAGCCCTGTGAGCCCAAGAGCTGAGCGAGCTGTGACGCCG	180
Db	121	GCCTGCTGAGCACAAGTTCTGTGTGAGCGCTGTGAGGCCCAAGAGCTGTGAGCGAGCTGTGAGCGCG	180
QY	181	GGACCCGAGGAGGCTTTCCGAGCGCTGTGTGAGCCCAAGTGCCTGTGTGTGTGTGTCCTCTGGAGACGC	240
Db	181	GGACCCGAGGAGGCTTTCCGAGCGCTGTGTGAGCCCAAGTGCCTGTGTGTGTGTGTCCTCTGGAGACGC	240
QY	241	ACGGCCGCCCCCGCCGCCCTCTCTTCCGCAAGTGTCTGTCTTAAGAGAGCTGTGTGAC	300
Db	241	ACGGCCGCCCCCGCCGCCCTCTCTTCCGCAAGTGTCTGTCTTAAGAGAGCTGTGTGAC	300
QY	301	CCGAGTGTCTGACAGAGGCTGTGTGAGGCGCGCGCAAGAACGTGTGTGCTTTGTGCTTGC	360
Db	301	CCGAGTGTCTGACAGAGGCTGTGTGAGGCGCGCGCAAGAACGTGTGTGCTTTGTGCTTGC	360
QY	361	GCTGCTGGAACGAGGCGCCGCGAGGAGCCCGCCCAAGGCTTCAACAACAAGCTGTGCAACTA	420
Db	361	GCTGCTGGAACGAGGCGCCGCGAGGAGCCCGCCCAAGGCTTCAACAACAAGCTGTGCAACTA	420
QY	421	CCTGCCCAACACGCTGACCGACGCACTGTGAGGAGACGAGGAGCGTGTGAGGCTGTGTGCG	480
Db	421	CCTGCCCAACACGCTGACCGACGCACTGTGAGGAGAGCGAGGAGCGTGTGAGGCTGTGTGCG	480
QY	481	CCGCGTGGGCGACACGACGTGTGTGCTTCACTGTGTGACGCTGTGTGCTTGTGTGTGTGT	540
Db	481	CCGCGTGGGCGACACGACGTGTGTGCTTCACTGTGTGACGCTGTGTGCTTGTGTGTGTGT	540
QY	541	GAGCTCCACAGCTGTGTGCTGTACAGTGTGTGAGGAGCGCGCTGTGTACAGTGTGTGAGCTGTG	600
Db	541	GAGCTCCACAGCTGTGTGCTGTACAGTGTGTGAGGAGCGCGCTGTGTACAGTGTGTGAGCTGTG	600
QY	601	TCAGGCCCGGCCCCCGGCAACACGCTAATGTGACCCCAAGAGCGTCTGTGAGATGTGAAACGAGC	660
Db	601	TCAGGCCCGGCCCCCGGCAACACGCTAATGTGACCCCAAGAGCGTCTGTGAGATGTGAAACGAGC	660
QY	661	CTGGAACCATATAGCGTACAGAGGAGCGCGAGGCTCCCGTGGGCGTGGCAAGCCCGAGGTGTGAC	720
Db	661	CTGGAACCATATAGCGTACAGAGGAGCGCGAGGCTCCCGTGGGCGTGGCAAGCCCGAGGTGTGAC	720
QY	721	GAGGCGCGAGGAGCAATGTGCACGCAAGTCTGCCCTTGTGCCAAGAGGCGCAGGCTGTGAGCGC	780
Db	721	GAGGCGCGAGGAGCAATGTGCACGCAAGTCTGCCCTTGTGCCAAGAGGCGCAGGCTGTGAGCGC	780
QY	781	TGCCCTTATAGCGCGAGCGGAGCGCCCGTGTGGAGAGGAGTCTGTGAGGCCAACCCGAGGACGAC	840
Db	781	TGCCCTTATAGCGCGAGCGGAGCGCCCGTGTGGAGAGGAGTCTGTGAGGCCAACCCGAGGACGAC	840
QY	841	GCGTGTGACCGAGTGTGACCGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
Db	841	GCGTGTGACCGAGTGTGACCGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
QY	901	CACCTCTTTTGGAGAGGAGT	960
Db	901	CACCTCTTTTGGAGAGGAGT	960
QY	961	GCACCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1020
Db	961	GCACCAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1020
QY	1021	CCGAGTGTGAGCGCGAGACCAAGCACTTCTGTACTCTTCAAGGCGACAAAGAGAGCACTGTG	1080
Db	1021	CCGAGTGTGAGCGCGAGACCAAGCACTTCTGTACTCTTCAAGGCGACAAAGAGAGCACTGTG	1080
QY	1081	GCCTCTCTCTTCTACTACTACTCTTGTGAGGCGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT	1140
Db	1081	GCCTCTCTCTTCTACTACTACTCTTGTGAGGCGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT	1140
QY	1141	GACCATCTTTCTGTGGTTTCAAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1200
Db	1141	GACCATCTTTCTGTGGTTTCAAGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1200

QY	1201	GGCCCCAGGCGTACTGCGCAAAATGCGGCCCTCTGTTTCTTGAAGCTGCTTGGGAAACACGCGCA	126
Db	1201	GGCCCCAGGCGTACTGCGCAAAATGCGGCCCTCTGTTTCTTGAAGCTGCTTGGGAAACACGCGCA	126
QY	1261	GTGCCCCCTAACGGGAGTGTCTCTCAAGACGCACTGCGCCGCTGCGAGCTGCGAGTCAACCCAGC	132
Db	1261	GTGCCCCCTAACGGGAGTGTCTCTCAAGACGCACTGCGCCGCTGCGAGCTGCGAGTCAACCCAGC	132
QY	1321	AACCGGTGTCTGTGCTGCCGAGAGAGCCCAAGGCTCTGTGCGCGCTCCGAGAGAGAGA	138
Db	1321	AACCGGTGTCTGTGCTGCCGAGAGAGCCCAAGGCTCTGTGCGCGCTCCGAGAGAGAGA	138
QY	1381	CACAGACCCCGCTGCTGTGTGAGACTGTCCGACAGACAGCAGGCCCTGAGAGGTGTA	144
Db	1381	CACAGACCCCGCTGCTGTGTGAGACTGTCCGACAGACAGCAGGCCCTGAGAGGTGTA	144
QY	1441	CGGCTTTCGTGCGGAGCTTGCTTGCGCGGAGTGTGTCCAGGCGCTTGTGGGCTCTCAGGCA	150
Db	1441	CGGCTTTCGTGCGGAGCTTGCTTGCGCGGAGTGTGTCCAGGCGCTTGTGGGCTCTCAGGCA	150
QY	1501	CAAGCAAGCGCGCTTCCCTCAGAGAACCAACAAGTCACTCCCTGGGAGAACGATGCGCA	156
Db	1501	CAAGCAAGCGCGCTTCCCTCAGAGAACCAACAAGTCACTCCCTGGGAGAACGATGCGCA	156
QY	1561	GCTCTGCTGAGAGAGCTGACGTGGAAGATGAGGTGCGGAGCTGCGCTTGTGCTGCGCAG	162
Db	1561	GCTCTGCTGAGAGAGCTGACGTGGAAGATGAGGTGCGGAGCTGCGCTTGTGCTGCGCAG	162
QY	1621	GAGCCCAAGGGGTGTGGCTGTGTTCCGGCCGACAGACACCGTGTGCTGAGAGATCTTGGC	168
Db	1621	GAGCCCAAGGGGTGTGGCTGTGTTCCGGCCGACAGACACCGTGTGCTGAGAGATCTTGGC	168
QY	1681	CAAGTCTCTGACTGAGCTGATGAGTGTGTGATGCTGTGAGCTGTCTCAGGCTTCTTCTT	174
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QY	1741	TGTCACTGAGAACCAACGTTTCAAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAG	180
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QY	1801	CAAGTGTGAAGCAATGTGGAATCAACAAGCACTTGAABAAGGTTGAGTGTGCGGAGCTGTG	186
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QY	1861	GGAAGCAGAGGTCAAGCAGACATTCGAGAAACCAAGGCCCGCTGTGTCAGCTCAACTCCG	192
Db	1861	GGAAGCAGAGGTCAAGCAGACATTCGAGAAACCAAGGCCCGCTGTGTCAGCTCAACTCCG	192
QY	1921	CTTCAATCCCAAGCTACAAGGCTGACGGGCTGTGGCCGATTTGTGAACATGGACTACGTCGTGGAGC	198
Db	1921	CTTCAATCCCAAGGCTACAAGGCTGACGGGCTGTGGCCGATTTGTGAACATGGACTACGTCGTGGAGC	198
QY	1981	CAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGCTCACTCGAGGCTGAAAGCACTGTT	204
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QY	2041	CAGGCTGTCACTACATCAAGAGCGGCGCGCGCCCTCTGTGGCGCTCTGTGTCTGGG	210
Db	2041	CAGGCTGTCACTACATCAAGAGCGGCGCGCGCCCTCTGTGGCGCTCTGTGTCTGGG	210
QY	2101	CCTGGAAGATTCACAGAGGCTGTGAGCAGCTTGATGTCAGTGTGTGGGCGCAGAGACCC	216
Db	2101	CCTGGAAGATTCACAGAGGCTGTGAGCAGCTTGATGTCAGTGTGTGGGCGCAGAGACCC	216
QY	2161	GCGGCTGAGCTGTACTTTTGTCAAGGTGATGTGAAGCGGCGCTGACGACCACTATCCCCA	222
Db	2161	GCGGCTGAGCTGTACTTTTGTCAAGGTGATGTGAAGCGGCGCTGACGACCACTATCCCCA	222
QY	2221	GGAAGGCTCAACGGAAGTCACTGCGCAGACTCATCAAAACCCAGAACACGTATCTGCTGGC	228
Db	2221	GGAAGGCTCAACGGAAGTCACTGCGCAGACTCATCAAAACCCAGAACACGTATCTGCTGGC	228
QY	2281	TGCGTATGCGGTGTCAGAAAGCGCGCCATGTGGGCAAGTGTCCGACAGGCTTCTCAAGAGCCA	234

Db	2281	TCGGTATGSCGGTGGTCCAGAAAGCCGCCCAATGGGCAACTCCGCAAGAGCTTTCAAGAGCA	2340
QY	2341	CGTCTTACCTTTGACAGACTTCCAGCCGTCATGCGACAGTTGCTGCTCACTTCAGAGA	2400
Db	2341	CGTCTTACCTTTGACAGACTTCCAGCCGTCATGCGACAGTTGCTGCTCACTTCAGAGA	2400
QY	2401	GACCAAGCCCGGTGAGGGATGCGCGTCATGACAGAGCTTCCTCCGAATGAGGCCAG	2460
Db	2401	GACCAAGCCCGGTGAGGGATGCGCGTCATGACAGAGCTTCCTCCGAATGAGGCCAG	2460
QY	2461	CAGTGGCCCTTTCGACGCTTCTCAACGTTTATGAGCCACAGCCGCGSCATCAAGGGG	2520
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QY	2881	GCAGAGCAGTACTTCAGACTATGCCCCGAGACCTCCATCAGAGCCAGTCTCACTTTCAACG	2940
Db	2881	GCAGAGCAGTACTTCAGACTATGCCCCGAGACCTCCATCAGAGCCAGTCTCACTTTCAACG	2940
QY	2941	CGGCTTCAAGGCTGGGAGAAATGTCGTGCAAACTTTTGGGGTCTTGGCGCTGAAGTG	3000
Db	2941	CGGCTTCAAGGCTGGGAGAAATGTCGTGCAAACTTTTGGGGTCTTGGCGCTGAAGTG	3000
QY	3001	TCACAGCCTGTTTCTGGAATTTGACAGGTAAACAAGCTTCCAGACGGGTGSCAACATCTA	3060
Db	3001	TCACAGCCTGTTTCTGGAATTTGACAGGTAAACAAGCTTCCAGACGGGTGSCAACATCTA	3060
QY	3061	CAAGATCTCTCGTGCAGAGCGTACAGGTTTCAACGATGTGTGCTGACGCTCCATTTC	3120
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QY	3121	TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGTCAATCTTCGACAGGCTCCCT	3180
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QY	3181	CTGCTACTTCATCTCGAAGGCCAAMAGCAGAGGATGTGCTGGGGGCAAGGGGCGCGC	3240
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QY	3241	CGGCGCTCTGCGCTCGAGAGCCGTGACAGTGGCTGAGCCACCAAGATTCCTGCTCAAGCT	3300
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Search completed: October 30, 2004, 03:18:16
Job time : 321 secs

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OM protein - nucleic search, using frame_plus.p2n model

Run on: October 28, 2004, 09:37:02 ; Search time 209 Seconds
(without alignments)
3849.823 Million cell updates/sec

Title: US-10-044-692-2

Perfect score: 5961
Sequence: 1 MPRAFCRAVSLRLSHYRE.....TALFANANPALPSDEKTLID 1132

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Fgapop 10.0, Fgapext 0.5
Delop 6.0, Delext 7.0

Searched: 824507 segs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	3396	3	US-08-974-549A-638 Sequence 638, App
2	5961	100.0	3396	3	US-08-974-549A-639 Sequence 639, App
3	5961	100.0	3396	3	US-08-974-549A-640 Sequence 640, App
4	5961	100.0	3396	3	US-08-974-549A-641 Sequence 641, App
5	5961	100.0	3396	3	US-08-974-549A-642 Sequence 642, App
6	5961	100.0	3396	4	US-09-721-456-638 Sequence 638, App
7	5961	100.0	3396	4	US-09-721-456-639 Sequence 639, App
8	5961	100.0	3396	4	US-09-721-456-640 Sequence 640, App
9	5961	100.0	3396	4	US-09-721-456-641 Sequence 641, App
10	5961	100.0	3396	4	US-09-721-456-642 Sequence 642, App
11	5961	100.0	3451	3	US-08-974-549A-721 Sequence 721, App
12	5961	100.0	3451	4	US-09-721-456-721 Sequence 721, App

13	5961	100.0	4015	3	US-08-851-843A-224 Sequence 224, App
14	5961	100.0	4015	3	US-08-974-549A-1 Sequence 1, Appl
15	5961	100.0	4015	3	US-08-854-050-224 Sequence 224, App
16	5961	100.0	4015	3	US-09-430-323-224 Sequence 224, App
17	5961	100.0	4015	3	US-09-572-423B-3 Sequence 3, Appl
18	5961	100.0	4015	3	US-09-128-354-1 Sequence 1, Appl
19	5961	100.0	4015	4	US-09-675-321-1 Sequence 1, Appl
20	5961	100.0	4015	4	US-09-052-919-1 Sequence 1, Appl
21	5961	100.0	4015	4	US-08-912-951-1 Sequence 1, Appl
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26	5961	100.0	4015	4	US-09-465-491-1 Sequence 1, Appl
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28	5952	99.8	4037	4	US-09-402-181B-343 Sequence 343, App
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30	5593.5	93.8	3855	3	US-08-974-549A-4 Sequence 4, Appl
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34	5579	93.6	4029	3	US-08-851-843A-173 Sequence 173, App
35	5579	93.6	4029	3	US-08-974-549A-292 Sequence 292, App
36	5579	93.6	4029	3	US-08-854-050-173 Sequence 173, App
37	5579	93.6	4029	3	US-09-430-323-173 Sequence 173, App
38	5579	93.6	4029	4	US-09-402-181B-292 Sequence 292, App
39	5579	93.6	4029	4	US-09-721-456-292 Sequence 292, App
40	3505	58.8	3496	4	US-09-042-460-1 Sequence 1, Appl
41	3134	52.6	1866	4	US-09-582-924B-11 Sequence 11, Appl
42	2789	46.8	51552	4	US-09-733-294A-30 Sequence 30, Appl
43	2782	46.7	4200	4	US-08-912-951-6 Sequence 6, Appl
44	2782	46.7	4321	4	US-09-402-181B-6 Sequence 6, Appl
45	2782	46.7	4335	3	US-08-974-549A-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-974-549A-638
Sequence 638, Application US/08/974549A
Patent No. 616178
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Langer, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 638:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396 /note= "hTERT-encoding sequence employing
OTHER INFORMATION: alternative codon distributions for
OTHER INFORMATION: E. coli (all genes)"
US-08-974-549A-638
Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPheLeuValGln 40
Db 61 GTCCTCCGCTGGCGACCTTGTGCGCGCTGCGCGCCGCGAGGCTGGCGCTGGTGCAG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 121 CGCGGGGATCCGCGCGGCTTCCGCGCTGCTGCGCGAGTGCCTGGTGTGCTGCGCTG 180
QY AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
Db 181 GATGCGCGCGCGCGCGCGCGCGCGAGCTTTCGCGAGGTGAGTGCCTGAAAGAACTG 240
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QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTyrGlyLeu 140
Db 361 AGCTATCTGCGAACAACCTGACCATGCGCTGCGCGAGCGCGCGCGGAGCTGCTG 420
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Db 421 CTGGCGCGCGTGGGAGATGATGTGCTGGTGATCTGCTGCGCGCTGCGCGCTGTTGG 480
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Db 481 CTGGTGGCGCGCGAGCTGCGCGTATCAGGTGCGCGCGCGCGCTGTATCAGCTGGCGCG 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db 541 GCGACCCAGCGCGCGCGCGCGCGCGCGCGAGCGCGCGCGCGCTGCGCGTGGCGA 600
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QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProAlaArgProArg 240
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QY 241 GlyAlaAlaProGlyProGlyProGlyThrProValGlyGlnGlySerTyrAlaHisProGly 260
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QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
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 Db 1381 GGTGTGGCTTTGTGGCGCGCTGCGCCGCTGCGCTGCGCGCTGCGCGCTGCGCGCAC 1440
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 QY 501 AAlaLySLeuSerLeuGlnGluLeuThrTrpLySMeSerValArgAspCyAla1rPleu 520
 Db 1501 GCGAAACCTAGCCTGAGGAACTGACCTGAAATAGAGCGTGGCATTTGGCGGTGGCTG 1560
 QY 521 ArgAArgSerProGlyValGlyCySValProAlaAlaGlnHisAArgLeuArgGlnGlu 540
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 QY 781 GlnGluThrSerProLeuAArgAspAlaVal11eGlnGlnSerSerSerLeuAaGln 800
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 Db 2641 AAAACCTTTCTGCGCAACCTGTGGCGCGCGCGCGCGCAATATGCTGGCTGTGAACCTG 2700
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 Db 2941 AAATGCCATAGCCTGTTCTGATCTGACAGTGAAACAGCTGCAGACCGTGTGCACCAAC 3000
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 QY 1021 PheHisGlnGlnValTrpLySAsnProThrPhePheLeuAArgVal11eSerAspThrAla 1040
 Db 3061 TTTTATGACAGAGTGTGAAAAAACCGACCTTTTTCGCGGTATGACATACCGCG 3120
 QY 1041 SerLeuCysTrpSer11eLeuLySAlaLySAsnAlaGlyMetSerLeuGlyAlaLySgly 1060
 Db 3121 ACCCTGTCTATAGCATTTCTGAAACGAAAAACGCGGCGATGAGCTGGCGCGCAAGGC 3180
 QY 1061 AlaAlaGlyProLeuProSerGluAlaValAlaGlnTrpLeuCysHisGlnAlaPheLeuLeu 1080
 Db 3181 GCGGCGGCGCGCTGCGAGCAAGGAGTGAGTGAGTGTGCAATCAGCGCTTTCTGCTG 3240
 QY 1081 LysLeuThrAArgHisAArgValThrTrpValProLeuLeuGlySerLeuAArgThrAlaGln 1100
 Db 3241 AAATGACCGCGCATGCGGTGACATATGCGCGCTGCGGAGCGCTGGCGACCGCGCAG 3300
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 Db 3361 CCGGCGCTGCGAGCATTTTAAACCATTTCTGAT 3396

RESULT 2

US-08-974-549A-639

; Sequence 639, Application US/08974549A

; Patent No. 616178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
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 REFERENCE/DOCKET NUMBER: 015389-002610US
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 INFORMATION FOR SEQ ID NO: 639:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3396 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY:
 LOCATION: 1..3396 /note="hTERT-encoding sequence employing
 OTHER INFORMATION: alternative codon distributions for
 OTHER INFORMATION: enteric bacteria (high expressing
 OTHER INFORMATION: genes)"

US-08-974-549A-639
 Alignment Scores:
 Pred. No.: 0
 Score: 5961.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 3
 Gaps: 0
 US-10-044-692-2 (1-1132) x US-08-974-549A-639 (1-3396)

QY	1	MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgInu	20
DB	1	ATGGCGCGTCCGCGGTTGGCGGTCTGCTTCCCTGCTCCGTTCCACACGCTGA	60
QY	21	ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln	40
DB	61	GTTCTGCGCGCTGACCTTCGTTGCTGCGGTCCGACAGGTTGGCGTCTGCTCAG	120
QY	41	ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr	60
DB	121	CGTGTGACCGCGCGTCTTCCGTCCTGCTGCTGCTCAGTGCCTGCTTGGCGTCTG	180
QY	61	AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGlnLeu	80
DB	181	GACGCTCGTCCGCGCGCGCTGCTCGTCTTCCGTCAGGTTTCTGCTGAAAGACTG	240
QY	81	ValAlaArgValLeuGlnArgLeuGlyGlnArgGlyAlaGlyAsnValLeuAlaPheGly	100
DB	241	GTTGCTCGTCTCAGCGCTGCGCAACGTCGTCTGCTGCTGCTGCTGCTGCTGCTG	300
QY	101	PheAlaLeuLeuAspGlyValAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg	120
DB	301	TTCGCTCTGCTGAGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
QY	121	SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTTPGlyLeuLeu	140
DB	361	TCTTACTGCGCAGACACCGTTACGACGCTGCGTGGTCCGCGTCTGCGGTCTGCTG	420
QY	141	LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
DB	421	CTGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	480
QY	161	LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlyLeuGlyAla	180
DB	481	CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	540
QY	181	AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgGlyCysGln	200
DB	541	GCTACCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	600
QY	201	ArgAlaTTPAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly	220
DB	601	CGTGTGTAACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660
QY	221	AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
DB	661	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720
QY	241	GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTTPAlaHisProGly	260
DB	721	GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	780
QY	261	ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu	280
DB	781	CGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840
QY	281	GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
DB	841	GAGGTACTCTCCCTGGAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
QY	301	ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTTPAspThrPro	320

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Db 901 CCGTCAGCACACGCTGGTCGGCGCTCCACCTCCCGCGCGCTCGTGGGACACCCG 960
Qy 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyValAspLysGln 340
Db 961 TCGCCGCGCGGTTTACCGCTAAACCAACCTTCTCTACTCTCCGCTGACCAAGAACAG 1020
Qy 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1021 CTGGCGTCGCTCTCTCTGCTGCTCTCTGCGCGCTGCTGACCGGTGCTGCTGCTG 1080
Qy 361 ValGlnThrLysPheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
Db 1081 GTTGAACACATCTCTCCGGGTTCCCGCTCGGTGATCCCGGTACCCCGGCTGCTCGCG 1140
Qy 381 ArgLeuProGlnArgTyrLTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
Db 1141 CGCTGCGCGAGGTTACTGGCAGATGCGCTCGCTCTCTGAACTGCTGGGTAAACCAAC 1200
Qy 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
Db 1201 GCTCAGTGCCTGACCGGTGTTCTGCTGAACCACTGCGCGCTGCTGCTGCTGTTAC 1260
Qy 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGln 440
Db 1261 CCGGCTGCTGTTGTTGCGCTCGTGAACCAACCGCAGGGTTCGTTGCTGCTCGGAAAGAA 1320
Qy 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db 1321 GAAGAACCGACCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
Db 1381 GTTTCAGGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
Qy 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheLeuLeuSerLeuGlyLysHis 500
Db 1441 CCGTCACACGAAAGTGTGTTCCGCTGAACACCAACCAAAATTCATCTCCCTGGGTAAACAC 1500
Qy 501 AlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
Db 1501 GCTAAACCTGCTGAGGAACCTGACCTGAAATATCCGTTGCTGCTGCTGCTGCTGCTG 1560
Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGln 540
Db 1561 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Qy 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db 1621 CTGGCTAAATTCCTGCACTGGCTGATGCTCGTTTACGTTGAACTGCTGCTGCTCTTC 1680
Qy 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db 1681 TTCTACGTTACCGAAACCACTTCGCAAAACCGCTGTTCTTCAACCGTAAATCCGTT 1740
Qy 581 TrpSerLysLeuGlnSerLysLeuGlnHisArgGlnHisLeuLysArgValGlnLeuArgLys 600
Db 1741 TGGTCCAACTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
Qy 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 CTGTCCGAAGCTGAAGTTCGTGACGACCGTGAAGCTGCTGCTGCTGCTGCTGCTGCT 1860
Qy 621 LeuArgPheLeuProLysProAspGlyLeuArgProLysValAsnMetAspTyrValVal 640
Db 1861 CTGCGTTTATCCCGAAACCGACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Qy 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGlnArgLeuThrSerArgValLysAla 660
Db 1921 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Qy 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 1981 CTGTTCTCCGTTCTGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Qy 681 LeuGlyLeuAspAspAlaLeuHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
Db 2041 CTGGGCTGAGACATCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Qy 701 AspProProProGlnLeuTyrPheValLysValAspValThrGlyValAlaTyrAspThrLys 720
Db 2101 GACCCGCGCGCGAAGCTGATCTGTTAAAGTTGACGTTACCGGTGCTTACCAACACATC 2160
Qy 721 ProGlnAspArgLeuThrGlnValLysSerLysLeuLysProGlnAsnThrTyrCys 740
Db 2161 CCGCAGAACCGTGTACCGAAGTTATCGCTTCAATCAATCAACCGCAGAACCACTTACTGC 2220
Qy 741 ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db 2221 GTTTCGCTTACGCTGTTTTCAGAAAGCTGCTACAGGCTGACGTTCTGTTAACTTTCAAA 2280
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db 2281 TCCACGTTTCCACCTGACCGACCTGACCGCTGACCGCTGACCTGCTGCTGCTGCTGCTG 2340
Qy 781 GlnGlnThrSerProLeuArgAspAlaValValLysGlnSerSerSerLeuLeuGln 800
Db 2341 CAGGAACCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgLys 820
Db 2401 GCTTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Qy 821 ArgGlyLysSerTyrValGlnCysGlnGlyLysProGlnGlySerLysLeuSerThrLeu 840
Db 2461 CCGTGAATTCCTACGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
Qy 841 LeuCysSerLeuCysTyrGlyAspMetGlyLysLeuPheAlaGlyLysArgArgArg 860
Db 2521 CTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGlyTyrGlyCysValValAsnLeu 900
Db 2641 AAACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
Qy 901 ArgLysThrValValAsnPheProValGlnAspGlnAlaLeuGlyGlyThrAlaPheVal 920
Db 2701 CCGTAAACCGTTGTTAACTTCCCGGTGGAAGCAGAAAGCTGCTGCTGCTGCTGCTGCT 2760
Qy 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAGATGCGGCTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2800
Qy 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerLysArgAlaSerLeuThrPhe 960
Db 2821 GAAGTTACGCTGCACTACCTCCCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
Qy 961 AsnArgGlyPheLeuAlaGlyValArgAsnMetArgLysLeuPheGlyValLeuArgLeu 980
Db 2881 AACCGTGTTCGTTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValLysThrArg 1000
Db 2941 AATGCTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Qy 1001 IleTyrLysLysLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATCTCAAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Qy 1021 PheHisGlnGlnValTrpLysAsnProThrPheLeuArgValLysSerAspThrAla 1040
Db 3061 TTCCACACGACGTTTGGAAAAACCGACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
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Db 481 TTGGTGTCTCATCTTGTGCTTATCAAGTTGTGGTCCACCATGTATCAATGGGTCT 540
Qy 181 AAlaThrGlnAlaArgProProHISAlaSerGlyProAlaArgArgLeuGlyCys61u 200
Db 541 GCTCTCAAGCTAGACCCACCAACATGCTTGTGTCCAGAAAGAAATGGGTGTAA 600
Qy 201 ArgAlaTTPanHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 601 AGAGCTTGAATCATCTTGTTRAGAAAGCTGTGTTCCATTGGGTTGCCAGCTCAAGT 660
Qy 221 AAlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProGlyArgProArgArg 240
Db 661 GCTAGAAAGAGGGGTGTCTGCTCTAGATCTTGGCATTTGCCAAAAAGACCAAGAGA 720
Qy 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTTPAlaHisProGly 260
Db 721 GGTGTCTGTCCAGAACCAAGAAAGAACTCAGTTGGTCAAGGTTCTTGGGCTCATCCAGGT 780
Qy 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
Db 781 AGAAGTAAAGGTCACTGTATAGAGGTTTTGTGTGTTCTCCAGCTAGACCAAGCTGAA 840
Qy 281 GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 841 GAAGTCACTTCTTTGGAAGGTGCTTGTCTGCTGTATAGACATTCATCCATCTGTGGT 900
Qy 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProArgProTTPAspThrPro 320
Db 901 AGACAAACATCATGCTGCTGCCACCATCTCTTAAACCAACCAAGACATGGGATCTCCA 960
Qy 321 CysProProValTyrAlaGluThrIleHisPheLeuTyrSerSerGlyAspIleGluGln 340
Db 961 TGTCCACAGTTTATGCTGAACCTAAACATTTTGTATCTTCTGGTGATTAAGAACAA 1020
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Db 1021 TTGAGACCATCTTTTGTGTCTTGTGAGACCATCTTTGACGTGGTCAAGAAATGG 1080
Qy 361 ValGluThrIlePheLeuGlySerArgProTTPMetProGlyThrProArgArgLeuPro 380
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Qy 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuGlyAsnHis 400
Db 1141 AGATTGCCAACAAAGATATTTGGCAATGAGACCATGTTTGGAAATGTTGGGTATACAT 1200
Qy 401 AAlaGlnCysProTyrGlyValLeuLeuLeuYsThrHisCysProLeuArgAlaAlaValThr 420
Db 1201 GCTCAATGTCATATGATGTGTTTGTGAAAACTCATTTGCCATTGAGAGCTGCTTACT 1260
Qy 421 ProAlaAlaGlyValCysAlaArgGluLeuYsProGlnGlySerValAlaAlaProGluGlu 440
Db 1261 CCAGTGTCTGGGTGTTGTGCTTGAAGAAAAACCAAGGTTCTGTGCTGCCAAGAAA 1320
Qy 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln 460
Db 1321 GAAGTACTGATCAAGAAAGATTTGATCAATGTGAGACCAACATTTCTTCCATGGCAA 1380
Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrPglySer 480
Db 1381 GTTTRTGTGTTTGTTRAGAGCTTGTGTAAGATGCTTCCACAGGTTTGTGGGGTCT 1440
Qy 481 ArgHisaGlnGluArgArgPheLeuArgAsnThrIleYsPhePheIleSerLeuGlyIleYsHis 500
Db 1441 AGACATAATGAAGAAAGATTTTGTGAAGAAATATAAAAAATTTATTTCTTGGGTAAACAT 1500
Qy 501 AlaIleYsLeuSerLeuGlnGluLeuThrTTPIleYsMetSerValArgAspCysAlaThrLeu 520
Db 1501 GCTAAATGTCTTTCCAAGAAATGACTTGAAGAAAGTCTGTGTAAGATTTGCTGGGTG 1560
Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGluIle 540
Db 1561 AGAAGATCTCCAGGTGTGGTGTGTTCCAGCTGCAACATAGATTGAGAGAAATTT 1620
Qy 541 LeuAlaYsPheLeuHisTTPLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
Db 1621 TTGGCTAAATTTTGTCAATGGTGTATGTCTGTATATGTGTGAATTTGTAGATCTTTT 1680
Qy 561 PheTyrValThrGluThrThrPheGlnYsAsnArgLeuPhePheTyrArgYsSerVal 580
Db 1681 TTTTATGTATCAAGAACTACTTTTCAAAAAATAGATTTGTTTATTAAGAAATCTGTT 1740
Qy 581 TTPSerYsLeuGlnSerIleGlyIleArgGlnHisIleuYsAlaGlyGlnLeuArgGlu 600
Db 1741 TGTCTAAATTTGCAATCATATTGTATTAAGACAAATTTGAAAGAAAGTTCAATTAGAGAA 1800
Qy 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 TTGTCTGAAGCTGAAGTTTGAACATAGAACACTAGACCAAGCTTTGTTCATCTTGA 1860
Qy 621 LeuArgPheIleProYsProAspGlyLeuArgProIleValaAsnMetAspTyrValVal 640
Db 1861 TTGAGATTTATCCAAAAACAGATGGTTTGAACCAATTTGTAATATGATATGTTGTT 1920
Qy 641 GlyAlaArgThrPheArgArgGluLeuArgAlaGluArgLeuThrSerArgValYsAla 660
Db 1921 GGTCTAGAACTTTTGAAGAAAGAAAAAGAGCTGAAAGATTTGACTTCTAGAGATTAAAGCT 1980
Qy 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 1981 TTGTTTCTGTTTGAATATATGAAGAGCTGAAGACCAAGGTTTGGGTGCTTGTT 2040
Qy 681 LeuGlyLeuAspAspIleHisArgAlaTTPArgThrPheValLeuArgValArgAlaGln 700
Db 2041 TTGGGTTTGAATATATTCATAGAGCTTGGAGAACTTTTGTGTTGAGAGTTAGAGCTCA 2100
Qy 701 AspProProGluLeuTyrPheValYsAlaAspValThrGlyAlaTyrAspThrIle 720
Db 2101 GATCCACACACAGAAATGTATTTTGTAAAGTTATGTACTGTGGTCTTAATGATATCATTT 2160
Qy 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleYsProGlnAsnThrTyrCys 740
Db 2161 CCACAAAGTATAGACTGAAGATTATGCTCTATATTAACCAACCAAAATATCATTTATGT 2220
Qy 741 ValArgArgTyrAlaValAlaGlnYsAlaHisArgIleHisValArgYsAlaPheYs 760
Db 2221 GTTGAAGATATGCTGTTGTTCAAAAAGCTGCTCATGTGTCATTTGAGAAAAGCTTTTAA 2280
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
Db 2281 TCTCATGTTTCTACTTTGACATGATTTGCAACATATATGAGACAAATTTGTGCTCATTTGG 2340
Qy 781 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGlu 800
Db 2341 CAAGAACTTCTCATTAAGAGATGCTGTTGTATGAACAATCTTCTTCTTGAATAA 2400
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2401 GCTTCTTGTGTTGTTGATGCTTTTGTGAGATTTATAGTGTCAATGCTGTTAGAAAT 2460
Qy 821 ArgGlyYsSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2461 AGAGGTAAATCTTATGTTCAATGTCAAGGTATTCACAAAGGTTCTAATTTGTCTTACTTTG 2520
Qy 841 LeuYsSerLeuCysTyrGlyAspMetGlnAsnYsLeuPheAlaGlyIleArgArgAsp 860
Db 2521 TTGTGTTCTTGTGTATGATATGAGAAATAAATTTGTTGCTGATTAAGAGAAAT 2580
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGTTTGTTGTTGAGATTTGTTGATGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2640
Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValaAsnLeu 900
Db 2641 AAAACTTTTGAAGAACTTTGTTAGAGTGTTCAGAAATATGTTGTGTGTTAATTTGG 2700
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Qy	901	ArchylsThrValValAsnPhProValGlnuSpGlnAlaLeuGlyValThrAlaPheVal	920
Db	2701	AGAAAACTGTTGTTAATTTCACATTAAGAATGAGCTTGGGGTGACTGCTTTGTT	2760
Qy	921	GlnMetProAlaHisGlyLeuPheProTrrPcysGlyLeuLeuLeuAspThrArgThrLeu	940
Db	2761	CAAAATGCCAGCTCAGTGTGTTTTCATGAGTGCTGGTTGTTGGATACATGAACCTTG	2820
Qy	941	GluValGlnSerAspTyrSerSerTyrValAlaArgThrSerIleArgAlaSerLeuThrPhe	960
Db	2821	GAACTTCATCTGATTAATTCCTTATCTTATGCTGAACCTCTATTAAGCTCTCTTACATCTT	2880
Qy	961	AsnArgGlyPheLeuSalAGlyArgAsnMetArgArgGlyLeuPheGlyValLeuArgLeu	980
Db	2881	AATAGAGCTTTTAAAGCTGCTGTAAGAAATATGAGAGAAATATGTTGGCTGTTTGAAGATTG	2940
Qy	981	LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
Db	2941	AAATGTCATCTCTTGTTTGGATTGGCAAGTTATCTTTGGCAACCTGTTGTATCAAT	3000
Qy	1001	IleTyrIleValIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
Db	3001	ATTATATAAAATTTTGTTGTTCCAAAGCTTAAGATTTCAATGCTTGTTGGTTTGCAATTGCA	3060
Qy	1021	PheHisGlnGlnValATrrPlyAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
Db	3061	TTTATCATCAACAAGTTTGGAAAAATCCAACTTTTTTTGGAGAGTTATTTCTGATCACTGCT	3120
Qy	1041	SerLeuCysTyrSerIleLeuValAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	1060
Db	3121	TCTTTGTGTATTCATATTTTGTAAGCTTAATAATGCTGTATGCTTTGGGGGTAAAGGT	3180
Qy	1061	AlaAlaGlyProLeuProSerGlnAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
Db	3181	GCTGCTGTCATTCATGTCATCGAAGCTGTTCAAGTGTCATCAACCTTTTGTG	3240
Qy	1081	LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
Db	3241	AAATGACTAGACATAGAGTACTTATGTTCCATTTGGTGTCTTTGGAGAACCTGCTCA	3300
Qy	1101	ThrGlnLeuSerArgGlyLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn	1120
Db	3301	ACTCAATTTGTGTAGAAAATTCACAGGTACTACTTTGACTGCTTTGGAAAGCTGCTAAT	3360
Qy	1121	ProAlaLeuProSerAspPheLeuThrIleLeuAsp	1132
Db	3361	CCAGCTTGGCATCTGATTTTAAAACTATTTTGGAT	3396
RESULT 4			
US-08-974-549A-641			
Sequence 641, Application US/08974549A			
Patent No. 6166178			
GENERAL INFORMATION:			
APPLICANT: Cecn, Thomas R.			
APPLICANT: Lingner, Joachim			
APPLICANT: Nakamura, Toru			
APPLICANT: Chapman, Karen B.			
APPLICANT: Morin, Gregg B.			
APPLICANT: Harley, Calvin B.			
APPLICANT: Andrews, William H.			
TITLE OF INVENTION: Human Telomerase Catalytic Subunit			
NUMBER OF SEQUENCES: 727			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Townsend and Townsend and Crew LLP			
STREET: Two Embarcadero Center, Eighth Floor			
CITY: San Francisco			
STATE: California			
COUNTRY: USA			
ZIP: 94111-3834			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			


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Db      61 GTTTGGCACTGGTACTTGGTGTAGAGATTGGGCTCCAGAGTTGGAGATTGGTCAA 120
Qy      41 ArgGlyAAspProAlaIlePheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
Db      121 AGAGGTGACCCAGCTGCTTTCAGAGCTTGGTGCATATGTTGGTGTGGTTCATGG 180
Qy      61 AspAlaAspProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80
Db      181 GACGCTAGACCAACCAACGCTGCTCATCTTTCAGACAAAGTTCTTGTGTAAGAATTG 240
Qy      81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlnAlaLysAsnValLeuAlaPheGly 100
Db      241 GTTGTAGAGTTTTCAAAGATTGTGTGAAGAAGGCTAAGAACGTTTGGCTTCGGT 300
Qy      101 PheAlaLeuLeuAspGlnAlaArgGlyValProProGlnAlaPheThrSerValArg 120
Db      301 TTCGCTTGTGTGACGCGTCTAGAGGTGGTCCACGAAGCTTTCATCTTCTGTAGA 360
Qy      121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTrpGlyLeuLeu 140
Db      361 TCTTACTTCCAAACACTGTCTTACTGACGCTTGGAGAGTTCTGGTCTTGGGGTTTGTG 420
Qy      141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db      421 TTGAGAAAGAGTTGGTGAACGCTTTGGTCACTTGTGGCTAGAGTGTCTTGTTCGTT 480
Qy      161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db      481 TTGGTGTCCCATCTTGTGCTTACCAAGTTTGTGGTCCACATGTGACCAATTTGGTGTCT 540
Qy      181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
Db      541 GCTACTCAAGCTTAGACCAACCAACGCTTCTGGTCCAGAAAGATTGGGTTGTGA 600
Qy      201 ArgAlaIleProAsnHisSerValAlaArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
Db      601 AGAGCTTGGAAACCATCTGTAGAGAGCTGGTGTCCATTTGGGTTTGCACGCTCCAGGT 660
Qy      221 AlaArgArgArgGlyValSerAlaSerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
Db      661 GCTAAGAAAGAGGTGGTCTCTCTCTAGACTTGTGCCATTTGCCAAAGAACCAAGAA 720
Qy      241 GlyAlaAlaProGlnProGlnArgThrProValGlnGlnSerThrAlaHisProGly 260
Db      721 GGTGCTGCTCCAGAACCAAGAAAGACTCCAGTTGGTCAAGGTTCTTGGGCTCAACCGGT 780
Qy      261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGln 280
Db      781 AGAACTAGAGGTTCATCTGACAGAGGTTCTGTGTGTTTCTCCAGCTAGACCAAGCTGA 840
Qy      281 GlnAlaIleThrSerLeuGlnGlnAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db      841 GAAGCTACTCTTCTTGGAAAGGTCTTGTCTGTGACTAGACACTTCAACCATCTGTGTGGT 900
Qy      301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
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Qy      321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyLysAspGlnGln 340
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Qy      341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
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Db      1141 AGATTGCCAAGAAATACTGGCAATGAGACCATTTGTTCTTGGAAATTGGGTAAACAC 1200
Qy      401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
Db      1201 GCTCAATGTCATAGCGGTTTGTGTAAGACTGCTGTCATTTAGAGACTGCTGTACT 1260
Qy      421 ProAlaAlaGlyValCysAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGln 440
Db      1261 CCAGCTGCTGGTGTGTGCTAGAGAAAGACCAAGGTTGTTGTTGCTGCTCCAAAGAA 1320
Qy      441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db      1321 GAAGACCTGACCCCAAGAAAGATTGGTTCATTTGTGAACAACACTCTTCTCCAAAGCAA 1380
Qy      461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
Db      1381 GTTACGGTTTCTGTAAGACTTGTGTGAAGATTGGTTCCACAGGTTTGTGGGTTCT 1440
Qy      481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
Db      1441 AGACACAAAGAAAGAAAGATTCTTGAGAAACCTAAGAAATTCTTCTTGGGTAAAGAC 1500
Qy      501 AlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
Db      1501 GCTAAGTTGTCTTTCCAAGAAATTGACTTGAAAGATGCTGTTTAGAGACTGTGCTGGTGG 1560
Qy      521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlnIle 540
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QY 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
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QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
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RESULT 5
US-08-974-549A-642
Sequence 642, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cecchi, Thomas R.
APPLICANT: Ingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
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COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/117618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/117885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,429
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 642:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 3396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..3396
; OTHER INFORMATION: /note="generic" hTBT protein encoding
; OTHER INFORMATION: sequence"
US-08-974-549A-642

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Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

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US-10-044-692-2 (1-1132) x US-08-974-549A-642 (1-3396)

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QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTThrArgLeuValGln 40
DB 61 GTTTGGCCATTGGCCCACTTCGTCGTTGGGTCACAAAGTTGGCGTTGGTTCAA 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CGTGGTGAATCCAGCCGCCCTTCGTCGTTGGTTCGCCCATGTTGGTTGTGTTCATGG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeu 80
DB 181 GATGCCCGGTCACACACCGCCCATCTTCCGCAAGTTCTTGTGGAAGAAATTG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGlyArgGlyValAlaLysAsnValLeuAlaPheGly 100
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QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTrrpGlyLeuLeu 140
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QY 141 LeuAlaArgValAlaAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
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DB 901 CGTCAACACACGCGCGGTCCACCATCTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyValAspLysGlnGln 340
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QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1021 TTGCGTCCATCTTCTTGTGTCTTCTTGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGT 1080
QY 361 ValGlnThrThrLeuPheLeuGlySerArgProTrrpMetProGlyTThrProArgArgLeuPro 380
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QY 381 ArgLeuProGlnArgTyrTrrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
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QY 401 AlaGlnCysProTrrpGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB 1201 GCCCATGTCCATACGATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
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DB 1261 CCAGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrrpGln 460
DB 1321 GAAGATCCGATCCACGTCGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrrpGlySer 480
DB 1381 GTTTACGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysPheLeuSerLeuGlyLysHis 500
DB 1441 CGTCAACAAAGACGTCGTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTrrpLysMetSerValArgAspCysAlaTrrpLeu 520
DB 1501 GCCAAATTTCTTGTCAAAATTAACCTGTGAATAATGTCGTGTGTGTGTGTGTGTGTGTGT 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluLe 540
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DB 1621 TTGGCCAAATTTCTGTGACATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
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QY 661 LeuPheSerValLeuAsnTyrGluValAlaArgArgProGlyLeuLeuGluValAspVal 680
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RESULT 6

US-09-721-456-638
Sequence 638, Application US/09721456
Patent No. 6617110

GENERAL INFORMATION:

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Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.

Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:

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STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-6617110-2000

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-Nov-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996

APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 638:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396 /note="NRT-encoding sequence employing
OTHER INFORMATION: alternative codon distributions for
E. coli (all genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 638:
US-09-721-456-638

Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-044-692-2 (1-1132) x US-09-721-456-638 (1-3396)
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QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPheValGln 40
DB 61 GTGCTGCG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CGCGGCGGATCCG 180
QY 61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuValGln 80
DB 181 GATGCGAACTG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGlyArgGlyAlaValSerValLeuAlaPheGly 100
DB 241 GTGGCGTTGGC 300
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGGCG 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrPheGlyLeu 140
DB 361 ACCTATCTCCGCGAAACCG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160

DB 421 CTGCGTTGG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
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QY 201 ArgAlaTyrPheHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGCGGCGGAAACCATAGCG 660
QY 221 AlaArgArgArgGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCG 720
QY 241 GlyAlaAlaProGlyProGlyLysArgThrProValGlyGlnGlySerTyrPheAlaHisProGly 260
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DB 781 CGCACCG 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAAGGCGACCG 900
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QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
DB 961 TCG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgGlyLeu 360
DB 1021 CTGCG 1080
QY 361 ValGluThrIlePheLeuGlySerArgProTyrPheProLeuArgAlaAlaValThr 420
DB 1081 GTGGAAACATTTTCTGGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB 1141 CGCGTGGCG 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB 1201 GCGCGTGGCG 1260
QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGlu 440
DB 1261 CG 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
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QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
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 Db 1981 CTGTTTATGAGGTGTGAACATGAAACCGCGCGCGCGCGCTGCTGGCGCGGAGCGTG 2040
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 Db 2101 GATCCCGCGCGGAACTGATATTTGTGAAAGTGATGTGACCGGGCGCGATGATACATT 2160
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 QY GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisIleuThrHisAla 880
 Db 2581 GGGCTGTGCTGTGGCTGTGATTAATTTCTGTGTGTGATCCCGCATCTGACCCATGCG 2640

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 QY SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
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 Db 3301 ACCGAGCTGAGCGGCAAACTGCCGGGCAACACCTTGACCGGCTGGAAAGCGGCGGAAC 3360
 QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
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RESULT 7

US-09-721-456-639

; Sequence 639, Application US/09721456

; Patent No. 6617110

GENERAL INFORMATION:

APPLICANT:

Cech, Thomas R.

Linsinger, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 639:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION: /note="NRT-encoding sequence employing
alternative codon distributions for
enteric bacteria (high expressing
genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 639:
US-09-721-456-639
Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Gaps: 0
DB: 4
US-10-044-692-2 (1-1132) x US-09-721-456-639 (1-3396)
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QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPargLeuValGln 40

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QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysValProTyr 60
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QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
DB 181 GACGCTCGTCCGCGCGCGCTGCTCCGCTTCCTCCGACGGTTTCCGCTGAAAGAAC 240
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QY 101 PheAlaLeuLeuAspGlyValaArgGlyGlyProProGlnAlaPheThrSerValArg 120
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QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValaTyrGlyLeuLeu 140
DB 361 TCTTACCTCCGACACCGCTTACCGACGCTGCGGTTCGCGGTCTGGGGTCTGCTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGCGCTCGGTGGTGAACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
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QY 181 AlaThrGlnAlaArgProProProAlaAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 541 GCTACCCAGCTCTGCTCCGCGCGCGACGCTTCGCGCTGCTGCTGCTGCTGCTGCTG 600
QY 201 ArgAlaTyrAsnHisSerValaArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CCGTCTGGAAACACCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
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QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
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DB 781 CGTACCCGCTGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyTyrArgHisSerHisProSerValGly 300
DB 841 GAAGTACCTCCCTGGAAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
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QY 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
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QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
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DB 1261 CCGGCTGCTGGTGTGTGGCTGTGTAAGAAACCAAGGGTTCCTGTCTGTCCGGAAGAA 1320
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DB 1321 GAAGAACCGAACCCGGGCTGTGTGTTCAAGCTGTGCTGTCAGCACTCTCCCGTGGCAG 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
DB 1381 GTTACGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheHisSerLeuGlyLysHis 500
DB 1441 CGTCAACAGAACGTCGTCTCTGCTTCAACCAAAATTCAATCTCTGGGTAAACAC 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTyrLysMetSerValArgAspCysAlaTyrPleu 520
DB 1501 GCTAACTGTCTCTGAGAACTGACCTGGAATATCGTGTGTGTGTGTGTGTGTGTGTGT 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluLe 540
DB 1561 CGTGGTCTCCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
QY 541 LeuAlaLysPheLeuHisStrLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
DB 1621 CTGGCTAAATCTCTGACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
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QY 621 LeuArgPheIleProLysProAspGlyLysArgProIleValAsnMetAspTyrValVal 640
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DB 1981 CTGTGTCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
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DB 2041 CTGGGTCTGAGACATCAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2100
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DB 2941 AAATGCCACTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3000
QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
DB 3001 ATCTACAAATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3060
QY 1021 PheHisGlnGlnValThrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
DB 3061 TTCCACACGACAGTTGTGAAAAACCGACCTTCTCTGCGTGTGTGTGTGTGTGTGTGT 3120
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaLysGly 1060
DB 3121 TCCCTGTGTACTCCATCTGTAAGACCTTAAGAACCTGTGTGTGTGTGTGTGTGTGTGT 3180
QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrPleuCysHisGlnAlaPheLeuLeu 1080
DB 3181 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlnLysSerLeuArgThrAlaGln 1100
DB 3241 AAACGACCCGTCACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3300
QY 1101 ThrGlnLysSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
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QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
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Db 3361 CCGGCTGCGCTCCGACTTCAAAACCATCTCGAC 3396

RESULT 8

US-09-721-456-640
Sequence 640, Application US/09721456
Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov. 6617110-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 640:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..3396

OTHER INFORMATION: /note="HYRT-encoding sequence employing
alternative codon distributions for
yeast (all genes)"

SEQUENCE DESCRIPTION: SEQ ID NO: 640:
US-09-721-456-640

Alignment Scores:

Pred. No.:	0	Length:	3396
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-044-692-2 (1-1132) x US-09-721-456-640 (1-3396)

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QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
Db 61 GTTTGCCATTGGCTACTTTTGTAGAGATTGGTCCAGAGTTGGAGATTGGTTCA 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
Db 121 AAGAGTGATCCAGCTGCTTTAGAGCTTTGGTGCATAGTTGGTTGTGTTCCATGG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80
Db 181 GATGCTAGACCAACCAAGCTCTCCATCTTTTAAACAAGTTCTTGTGAAGAATTG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaValAlaValAsnValLeuAlaPheGly 100
Db 241 GTTGCTAGAGTTTGCAGAAAGATTGTGTGAAGAAGTGCTAAAGATTTTGGCTTTGGT 300
QY 101 PheAlaLeuLeuAspGlyValAlaArgGlyGlyProGlnGlnAlaPheThrSerValArg 120
Db 301 TTGGCTTTGTTGGATGTGTCTAGAGTGTCCACCAAGAGCTTTTACTTCTGTTTAA 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 140
Db 361 TCTTATTTGCCAAATACGTCTTCTGATGCTTGAGAGGTTCTGCTGGGCTTTGGTTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 421 TTGAGAAAGATTGGATGATGTTTGTGTTCAATTTGTGGCTAGAGTGTCTTGTGTT 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
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QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db 541 GCTACTCAAGCTAGACCAACCAACCACTGCTTGGGCCAAGAAGATTGGGTGTGAA 600
QY 201 ArgAlaTTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
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QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProAlaArg 240
Db 661 GCTAAGAAAGAGGTGCTTCTGCTTCTAGATCTTTGCCATTTGCCAAAAGACCAAGAGA 720
QY 241 GlyAlaAlaProGlnProGlnArgTrpProValGlyGlnGlySerTrpAlaHisProGly 260
Db 721 GGTGCTGCTCCAGAACCAAGAAAGAACTCAGTTGGTCAAGTTCTTGGGCTCATCAGGT 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
Db 781 AGAAGCTAGAGGTCCATGTGATAGAGGTTTGTGTGTTTCTCCAGCTAGACCAAGCTGAA 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
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Db      841 GAAGTACTCTTTGGAAAGGCTTTGTCTGTACTAGACATTCTCATCATCTGTTGGT 900
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Db      901 AGAACATCATGCTGTGCCACATCTACTCTTAGACACACAGACCATGGGATCTCCCA 960
Qy      321 CysProProValIyIaIaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGln 340
Db      961 TGCCACCACTTATGCTGAACATACTTTTGTGATCTCTGTGTATTAAGAACAA 1020
Qy      341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyIaArgArgLeu 360
Db      1021 TTGAGACCATCTTTTGTGTCTCTTGTAGACCATCTTGACTGGTGTAGAAAGATTG 1080
Qy      361 ValGlnThrIlePheLeuGlySerArgProTyrMetProGlyIyhrProArgArgLeuPro 380
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Qy      381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
Db      1141 AGATTGCCACAAAGATATTGGCAAAATGAGACCATTTGTTTGGAAATTTGGGTATCAT 1200
Qy      401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaValThr 420
Db      1201 GCTCAATGTCATATGCTGTTTGTGAAAACTCATTTGCTCATTTGAGAGCTGCTTACT 1260
Qy      421 ProAlaAlaGlyValCysAlaArgLysProGlnGlySerValAlaAlaProGlnGln 440
Db      1261 CCAGCTCGTGTCTTTGTCTAGAGAAACCAAGATCTGTCTGTCTCCAGAGAA 1320
Qy      441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
Db      1321 GAAGATACGATCCAGAAAGATTGTTCAATTTGTGACAAACATCTCTTCATGGCAA 1380
Qy      461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
Db      1381 GTTATGTTGTGTAGAGCTGTTGAGAAAGATTGTTCCACAGATTGTGGGGTTC 1440
Qy      481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysPheIleSerLeuGlyLysHis 500
Db      1441 AGCATAAAGAAAGAAAGATTTTGGAAATATCTAAATAATTTTCTTTGGGTAAACAT 1500
Qy      501 AlaLysLeuSerLeuGlnGlnLeuThrTyrPlyMetSerValArgAspCysAlaTyrLeu 520
Db      1501 GCTAAATTTCTTTCAGAAATATGACTTGAAATATGCTGTAGAGATTGCTGTGGTGG 1560
Qy      521 ArgArgSerProGlyValGlyCysValProAlaIaGlnHisArgLeuArgGlnGlnIle 540
Db      1561 AGAAGATCTCCAGAGTGTGTGTGTGTCCAGCTGGAACATAGATTGAGAGAAAGAAAT 1620
Qy      541 LeuAlaLysPheLeuHisIleTyrLeuMetSerValIyValIaGlnLeuLeuArgSerPhe 560
Db      1621 TTGGCTAAATTTTGGATTTGGTTGATGCTGTGTTATGTTGATTTGATTTGATTTT 1680
Qy      561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
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Qy      601 LeuSerGlyAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
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Qy      621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetCaspTyrValVal 640
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Qy      701 AspProProGlnLeuLysPheValLysValAspValThrGlyValaTyrAspThrIle 720
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Qy      721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
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RESULT 9
US-09-721-456-641
; Sequence 641, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-Nov-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 641:
SEQUENCE CHARACTERISTICS:
LENGTH: 3396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3396
OTHER INFORMATION: /note="hTERT-encoding sequence employing
alternative codon distributions for
yeast (high expressing genes)"
SEQUENCE DESCRIPTION: SEQ ID NO: 641:
US-09-721-456-641
Alignment Scores:
Pred. No.: 0 Length: 3396
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 4
US-10-044-692-2 (1-1132) x US-09-721-456-641 (1-3396)
QY 1 MetProAlaGAlaProArgCySerArgAlaValArgSerLeuLeuArgSerHisTYrArgGlu 20
DB 1 ATGCCAAGAGCTCCCAAGATGTAAGAGCTGTAGATCTTTGTAGAGTCTCAGAGAGAA 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGInGlyTYrPArgLeuValGIn 40
DB 61 GTTTGGCATTTGGCTACTTCTTCTTGAAGATTGGGTCCACAAAGTTGAGATTGGTCAA 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValaGInCysLeuValCysValProTrp 60
DB 121 AGAGGTAGCCCAAGCTGCTTTCAGAGCTTGGTGTCTCAATGTTGGTTCATGG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGInValSerCysLeuLYsGluLeu 80
DB 181 GACGTAGACCAACACAGCTGCTCCATCTTTCACAAAGTTCTGTTGAAGAAATTG 240
QY 81 ValAlaArgValLeuGInArgLeuCySGluArgGlyAlaLYsAsnValLeuAlaPheGly 100
DB 241 GTTGTCAAGTTTTCANAGATTGTGTGAAGAGTGTCAAGAACTTTGGCTTTCGCT 300
QY 101 PheAlaLeuLeuAspGlyValaArgGlyGlyProProGluAlaPheThrThSerValArg 120
DB 301 TTGGCTTGTGTGAGCGGTCTAGAGGTGGTCCACCAGAAAGCTTTCACACTTCTGTAGA 360
QY 121 SerTYrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValaITrPGLyLeuLeu 140
DB 361 TCTTACTTCCCAACAACCTGTACTACCGTTGAAGAGTTCTGGGCTTGGGTTGTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHISLeuValaArgCysAlaLeuPheVal 160
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QY 161 LeuValAlaProSerCysAlaTYrGInValCysGlyProProLeuTYrGInLeuGlyAla 180
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QY 181 AlaThrGlnAlaArgProProHISAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db 541 GCTACTCAAGCTGACCAACCAACCAAGCTTCTGCTCCAAAGAAAGATTGGGTTGTGAA 600
QY 201 ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
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QY 221 AlaArgArgArgGlySerAlaSerArgSerLeuProLeuProLysArgProAlaArg 240
Db 661 GCTGAAAGAAAGAGTGTCTGCTCTAGATCTTTGCAATGGCAAGACAAAGAAAGA 720
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Db 781 AGAAGTAAGAGTCCATCTGACAGAGGTTCTGTGTGTCTCCAGCTAGACAGCTGAA 840
QY 281 GylAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
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QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
Db 901 AGACAACACACCGCTGGTCCACCATCTACTTAGACCAACCAAGGACATCCCA 960
QY 321 CysProProValIYrAlaGluThrIYrHisPheLeuTyIYrSerSerGlyIYrAspIYrGluGln 340
Db 961 TGTCCACCAAGTATTCGTGAACTTAAGCACTTCTTACTCTGTGTAACAAGAAACAA 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1021 TTGAGACCAATCTTCTTGTGTCTTCTTGGACCAATCTTGACTGTGCTGTAAGATTG 1080
QY 361 ValGluThrIYrPheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
Db 1081 GTTGAACATATTTCTTGGGTCTTACAGCAATGATCCAGTACTCCAGAAAGATTGCCA 1140
QY 381 ArgLeuProGlnArgIYrTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
Db 1141 AGATTCCCAAGAAAGATCTGGCAAAAGAACCACTGTCTTGAATGTGTGGTAAACCA 1200
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Db 1201 GCTCATATGTCATACGGTGTGTGTAAGACTCACTGTCCATTTGAGACTGTCTGTACT 1260
QY 421 ProAlaAlaGlyValCysAlaArgGlyIYrProGlnGlySerValAlaAlaProGluGlu 440
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QY 441 GluAspTrpAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
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Db 1381 GTTTACGGTGTCTGAGACTGTGTTGAGAAGTTGGTTCCACCAAGTTTGTGGGGTTCT 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnTrpIYrLysPheHisSerLeuGlyIYrHis 500
Db 1441 AAGACAAAGAAAGAAAGATTCTTGAAACACTTAAGAGTTCAATTTCTTTGGGTAAAGAC 1500
QY 501 AlaIYrLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
Db 1501 GCTAAGTCTCTTGGAAAGATTGACTTGAAGAGTCTGTTAGAGACTGTCTGTGGTTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLe 540
Db 1561 AGAAGATCTCCAGGTGTGTGTGTGTCCAGCTGTCAACACAGATTGAGAGAAAGAAATTT 1620

QY 541 LeuAlaIYrPheLeuHisTrpLeuMetSerValIYrValValGluLeuLeuArgSerPhe 560
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Db 1801 TTGTCTGAAGCTGAAGTTAGACACACAGAAAGCTTAACCACTTGTGTGACTTCTTGA 1860
QY 621 LeuArgPheIYrProLysProAspGlyLeuArgProIYrValAsnMetAspTyIYrVal 640
Db 1861 TTGAGATTCAATCCAAAGCCAGACGGTTTGAGACCAATTTGATGACATGACATGCTGTT 1920
QY 641 GylAlaArgTrpPheArgArgGluIYrAsnArgAlaGluArgLeuThrSerArgValIYrAla 660
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Db 361 TCTTACTTGCACAAACCGCTTACCGATGCTTGCCTGCGTTCGTGGTCCGCGGTGGTGG 420
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Db 601 CGTGCTGGAAACACTCTTGTGTGAAGCCGCTTCCATTGGGTTTGGCAGCCCAAGT 660
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QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaTrpProAlaGln 280
Db 781 CGTACCCGCTGTCATCTGATCGTGTCTGTGTGTCTTCTCCAGCCCGTCCAGCCGA 840
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QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGlu 440
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RESULT 12
US-09-721-456-721
Sequence 721, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997.

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RESULT 13
US-08-851-843A-224
Sequence 224, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ. ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
OTHER INFORMATION: /note= "human telomerase reverse
OTHER INFORMATION: transcriptase (hTERT) catalytic protein
component"
US-08-851-843A-224

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-044-692-2 (1-1132) x US-08-851-843A-224 (1-4015)

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RESULT 14
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 Sequence 1, Application US/08974549A
 Patent No. 6166178
 GENERAL INFORMATION:
 APPLICANT: Cecch, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4015 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 56..3454
 OTHER INFORMATION: /product= "hTERT"
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 OTHER INFORMATION: transcriptase (hTERT) catalytic protein
 OTHER INFORMATION: component"
 US-08-974-549A-1
 Alignment Scores:
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 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.008 Conservative: 0
 Best Local Similarity: 100.008 Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-10-044-692-2 (1-1132) x US-08-974-549A-1 (1-4015)

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 ; Patent No. 6261836
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Hatley, Calvin
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: No. 6261836el Telomerase
 ; NUMBER OF SEQUENCES: 225
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
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 ; FILING DATE: 09-MAY-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
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 ; FILING DATE: 25-APR-1997
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 ; PRIOR APPLICATION DATA:
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 ; FILING DATE: 18-APR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002930US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 224:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4015 base pairs
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 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

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 Query Match: 100.00% Indels: 0
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 638 from patent US 6617110.
ACCESSION AR393358
VERSION AR393358.1 GI:40118784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3396)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
drug screening
JOURNAL Patent: US 6617110-A 638 09-SEP-2003;
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source Location/Qualifiers
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ORIGIN

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 DEFINITION Sequence 639 from patent US 6617110.
 ACCESSION AR393359
 VERSION AR393359.1 GI:40118786
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3396)
 AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B., Harley,C.B. and Andrews,W.H.
 TITLE Cells immortalized with telomerase reverse transcriptase for use in drug screening
 JOURNAL Patent: US 6617110-A 639 09-SEP-2003;
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 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuIlyGluLeu 80
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 QY 101 PheAlaLeuLeuAspIlyAlaArgGlyIlyProProGluAlaPheThrThrSerValArg 120
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 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTyrGlyLeuLeu 140
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QY	161	LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
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QY	181	AlaThrGlnAlaArgProProProhniSalASerGlyProArgArgArgLeuGlyCysGlu	200
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QY	201	ArgAlaTTPAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly	220
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QY	221	AlaArgArgArgGlyGlySerAlaSerASerASerLeuProLeuProLysArgProArgArg	240
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QY	281	GluAlaTTPSerLeuGlnGlyValaLeuSerGlyThrArgHisSerHisProSerValGly	300
Db	841	GAACTTACTCTCTGAAAGTGTCTGTGCCGTACCGGTACCTCCACCCGTCCTGTGT	900
QY	301	ArgGlnHisSalAGlyProProSerThrSerArgProProArgProTTPAspThrPro	320
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QY	321	CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln	340
Db	961	TGCCCGCGGTTTAAAGCTGAACCAACAACTTCGTACTCTCCGCTGACAAAGAACAG	1020
QY	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
Db	1021	CTGGCTCCGCTCTCTGCTGTCTCTGCTGCTCCGCTCCGTCCCTGACCGAGTCTGTCTG	1080
QY	361	ValGluThrLysPheLeuGlySerArgProTTPMetProGlyThrProArgArgLeuPro	380
Db	1081	GTTGAAACCATCTTCTCGGTTCCGCTCCGTGAGGAGCCGGGATCCCGCGTGTGCG	1140
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QY	401	AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaValThr	420
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QY	421	ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
Db	1261	CCGGCTGGTGGTGTTCGCTCGTGAAGAAACCGCAGGTTCCGTTGCTGCCGAAGAA	1320
QY	441	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln	460
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QY	461	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTTPGlySer	480
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Qy	601	LeuSerGluValaGluValaArgGlnhisArgGluLilaArgProalaLeuLeuThrSerArg	620
Db	1801	CTGTCCGAAGCTGAAGTTTCGTACGACCGCTGAAGCTGTCCTCGGCTCTGTACCTCCCGT	1866
Qy	621	LeuArgPheLileProLysProAspGlyLeuArgProLileValaAsnMetAspTyrValVal	640
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Db	2221	GTTCTGTCGTTCACGCTGTTGTCAAGAAAGCTGCTCACGGTCACTGTTCTTAAAGCTTTCAA	2280
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Qy	801	AlaSerSerGlyLeuPheAspValaPheLeuArgPheMetCysHisHisalaValaArgile	820
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Db	2461	CGTGGAATATCTTACGTTCACGTTCACAGAGATATCCCGAGAGGATTCACCTGTCCACCTG	2520
Qy	841	LeuCysSerLeuCySTyrGlyAspMetGluAsnLysLeuPhealaglyLileArgArgAsp	860
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SOURCE	Unknown.		
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AUTHORS	Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,		
TITLE	Harley,C.B. and Andrews,W.H.		
JOURNAL	Cells immortalized with telomerase reverse transcriptase for use in		
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QY 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisIleLysArgValGlnLeuArgGlu 600
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LOCUS AR393361
DEFINITION Sequence 641 from patent US 6617110.
ACCESSION AR393361
VERSION AR393361.1 GI:40118790
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3396)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Cells immortalized with telomerase reverse transcriptase for use in
drug screening
JOURNAL Patent: US 6617110-A 641 09-SEP-2003;
FEATURES
LOCATION/Qualifiers
source 1..3396
ORIGIN /organism="unknown"
/mol_type="genomic DNA"
Alignment Scores:
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Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTTP 60
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Qy	521	ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLe	540
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Qy	541	LeuAlaLysPheLeuHisTrpPheMetSerValTyrValValGluLeuLeuArgSerPhe	560
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Db	1681	TTTCACCTTACTGAACTACTTTCACAAAGAAACAGATTGTTCTTACAGAAAGCTGTT	1740
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Qy	701	AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	720
Db	2101	GACCCACCAACCAAAATTTGACTTCGTTAAGGTTGAGGTTACTGTCTTAACGACACTATT	2160
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Qy	1081	LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
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DEFINITION Sequence 642 from patent US 6617110.			
ACCESSION AR393362			
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KEYWORDS			
SOURCE Unknown.			
ORGANISM Unclassified.			


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RESULT 6
LOCUS AX957656 3396 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 3 from Patent WO03095605.
ACCESSION AX957656
VERSION AX957656.1 GI:40785528
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Moll,J., Schuchel,A. and Stouten,P.
TITLE A chimeric reverse transcriptase and methods for identifying
JOURNAL Patent: WO 03095605-A 3 20-NOV-2003;
Pharmacia Italia S.p.A. (IT)
FEATURES
source 1. 3396
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Score: 5961.00 Matches: 1132
Best Local Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Db 61 GTGCTGCGCGCTGCGCACGTTGCTGCGCGCTTGCGGCGCCCAAGGCTGCGGCTGCTGCGAG 120

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Db	1321	GAGGACACAGACCCCGCTGGCTGGTGCAGTGTCTGGCAGCACACAGCCCTTGCGAG	1380
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DEFINITION Adult bone marrow-origin cell capable of differentiating into
myocardial cell.
ACCESSION BD091553
VERSION BD091553.1 GI:22637164
KEYWORDS MO 0148149-A/16.
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3396)
AUTHORS Umezawa,A., Hata,J., Fukuda,K., Satoshi, Ogawa and Sakurada,K.
TITLE Adult bone marrow-origin cell capable of differentiating into
myocardial cell.
JOURNAL Patent: WO 0148149-A 16 05--JUL-2001;
KYOMA HAKKO KOGYO CO LTD,AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI
FUKUDA, SATOSHI OGAWA, KAZUHIRO SAKURADA
COMMENT OS Homo sapiens (human)
PN MO 0148149-A/16
PD 05-JUL-2001
PE 28-FEB-2000 WO 2000JP001148
PR 28-DEC-1999 JP 99P 372826
PI AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI FUKUDA, SATOSHI PI
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PC C12N5/06,C12N5/00,A61K35/28,A61P41/00,A61K48/00,C07K16/18 CC
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Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Dp	1141	CGCTGGCCCAAGCGCTACTGGCAATAGGGGCCCCGTCTTCTGGAGCTGTTGGGAACAC	1200
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Dp	1381	GTTGTACGGCTTCTGTGCGGGCGCTGCTGGCGCGGCTGTGGCCCGCAGGCTCTGGGGCTCC	1440
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OY	581	TrpSerLysLeuGlnSerIleGlyIleArgGlnHisIleLysAsnArgValGlnLeuArgGlu	600
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OY	601	LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
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 LOCUS BD094749
 DEFINITION The cell having the potentiality of differentiation into
 cardiomycocytes.
 ACCESSION BD094749
 VERSION BD094749.1 GI:22640337
 KEYWORDS WO 0148150-A/16.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 3396)
 Umezawa,A., Hata,A., Fukuda,K., Ogawa,S., Sakurada,K., Gojo,S. and
 Yamada,Y.
 TITLE The cell having the potentiality of differentiation into
 JOURNAL Patent: WO 0148150-A 16 05-JUL-2001;

COMMENT KYOWA HAKKO KOGYO CO LTD, AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI
 FUKUDA, SATOSHI OGAWA, KAZUHIRO SAKURADA, SATOSHI GOJO, YOJI YAMADA
 OS Homo sapiens (human)
 PN WO 0148150-A/16
 PD 02-JUL-2001
 PF 02-NOV-2000 WO 2000JP007741
 PR 28-DEC-1999 JP 99P 372826, 28-FEB-2000 WO PCTJP0001448 PI
 AKIHIRO UMEZAWA, JUNICHI HATA, KEIICHI FUKUDA, SATOSHI OGAWA, PI
 KAZUHIRO SAKURADA, SATOSHI GOJO, YOJI YAMADA
 PC C12N5/06, C12N5/10, C12N15/09, A61K31/203, A61K35/28, A61K38/19, PC
 A61K38/39,
 PC A61K38/45, A61K48/00, A61P9/10, A61P41/00, C07K16/28, C12P21/08, PC
 C12O1/02,
 PC C12O1/48, G01N33/577
 CC The cell having the potentiality of differentiation into CC
 FH Key cardiomycocytes Location/Qualifiers
 CDS (1) . (3399).
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 Best Local Similarity: 100.00% Mismatches: 0
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DEFINITION
ACCESSION BD096291 GI:22641879
VERSION WO 0148151-A/16.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Umezawa,A., Hata,D., Fukuda,K., Ogawa,S., Sakurada,K., Gojo,S. and
Yamada,Y.
TITLE Cells capable of differentiating into myocardial cells
JOURNAL Patent: WO 0148151-A 16 05-JUL-2001;
COMMENT
OS Homo sapiens (human)
PN WO 0148151-A/16
PD 05-JUL-2001
PF 27-DEC-2000 WO 2000JP009323
PR 28-DEC-1999 JP 99P 372826,28-FEB-2000 WO PCTJP0001148 PR
02-NOV-2000 WO PCTJP0007741
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Qy	621	LeuArgPheIleProIySProArgGIyLeuArgProIleValAsnMetAspTrIyValVal	640

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VERSION AX481414.1 GI:22316328
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AUTHORS Kreutzer, R., Jimmer, S., Post, S. and Haidwiger, P.
TITLE Method for inhibiting the expression of a target gene
JOURNAL Patent: WO 02055693-A 28 18-JUN-2002;
Ridopharma AG (DB)
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 21 ValLeuProLeuAlaThrPheValArGArGLeuGlyProGlnGlyTrrpArGLeuValGln 40
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ACCESSION ARI04587
VERSION ARI04587.1 GI:12817295
KEYWORDS
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ORGANISM
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech,T.R. and Lingner,J.
TITLES Telomerase
JOURNAL Patent: US 6093809-A 224 25-JUL-2000;
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US-10-044-692-2 (1-1132) x ARI04587 (1-4015)

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Calvin, B.H. and William, H.A.
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Db 1681 CAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
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OY 2581 CAGGCTGCTACGCGGAGCATGAGAGCAAGGCTTTGCGGGGATTCGCGGGGAGCGGGCT 2640
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DEFINITION Sequence 224 from patent US 6309867.
ACCESSION AR175848
VERSION AR175848.1 GI:17917147
KEYWORDS
SOURCE
ORGANISM
REFERENCE
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  Telomerase
  Patent: US 6309867-A 224 30-OCT-2001;
  Location/Qualifiers
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ORIGIN

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Query Match 100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAGAGGCTGCGCTCTGCTGCGAGAGGAGAGCCCTGGGCGGAGACCCCGGAGTGC 60
OY 61 GCGCGTCCCGCTGCGGAGCGGTGCGCTCCCTGTGCTGCGAGACCACTACCGGAGTGT 120
Db 61 GCGCGTCCCGCTGCGGAGCGGTGCGCTCCCTGTGCTGCGAGCACTACCGGAGTGT 120
OY 121 GCGCGTGGCCAGTTCGTGTCGGGCGCTTGGGGCCCAAGGCTGCGGCTGTGAGGCGG 180
Db 121 GCGCGTGGCCAGTTCGTGTCGGGCGCTTGGGGCCCAAGGCTGCGGCTGTGAGGCGG 180
OY 181 GGAACCGGAGGCTTTCCGGGCGCTGGTGGCCAGTGTGCTGTGTGCTGCTTGGAGCGC 240
Db 181 GGAACCGGAGGCTTTCCGGGCGCTGGTGGCCAGTGTGCTGTGTGCTGCTTGGAGCGC 240
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Db 421 CCGTCCCAACACGCGTGAACGACGCTGTGCGGAGACGCGGCGGTGTGTGTGTGCG 480
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Db 601 TCAAGCCCGGCG 660
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Db 661 CTGGAACCATAGAGT 720
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Db 721 GAGGCGCGGCGGCGAGT 780
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Db	2461	CAGTGGCTCTTTCAGACGTCTTTCACGCTTATGAGCCACACAGCCGGGATCAAGGG	252.0
QY	2521	CAAGTCCCTACCTCCAGTGGCCAGGGGATCCCGCAGGGCTCATCTCTTCCAGCTCTCTG	258.0
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QY	2581	CAGCCTGTGTACGAGCCGACATGAGAGAACAGCTGTTTGCGGGATTTCCGGCGGAGCGGCT	264.0
Db	2581	CAGCCTGTGTACGAGCCGACATGAGAGAACAGCTGTTTGCGGGATTTCCGGCGGAGCGGCT	264.0
QY	2641	GCTCCTGGCTTTGGTGGATGATTTTCTTTGTGTGATCAGCTCAACTCAACCCACGGGAAAC	270.0
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QY	2701	CTTCTCTCAGAGCCCTGGTCCGAGGAGTCCCTGAGATGGCTGCGTGGGAACTTGGCGAA	276.0
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QY	3061	CAAGATCTCTCTGCTGAGGGGTACAGGTTTCAAGCATGTGCTGAGCTCCATTCA	312.0
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QY	3121	TCAGCAATTTTGGAAAGAACCCCACTTTTTCCTGGGCTCATCTGTGACAGGCTCCCT	318.0
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Db	3181	CTGCTACTCCATCTCTGAAGGCCAAGAACGACAGGAGTGTGCTGGGGGCAAGGGGCGCGC	324.0
QY	3241	CGGCTCTTGGCTTCGAGGCCGTGTGAGTGTGTGTCACCAAGCATTTCTGTCAAGCT	330.0
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QY	3361	GCTGAGTGTGGAAGCTCCCGGGGAGGAGCGCTGATGCTGCTGGAGGCGGAGCCAACTCGGGC	342.0
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QY	3481	GAGCAGAACACAGAGGCCCTGTGACGCGGGGCTTACGTCCACGGGAGGAGGGGCGGCG	354.0
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QY	3541	AAACCCAGGCGCCGACCGGCTGGAGAGCTAGAGGCTTAGTGAGTTTGGCCAGGCGCTG	3600
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QY	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
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QY	3661	GAGTGTCCAGACACACCTGCGCGCTTTCACCTTCCCAAGGCGTGGGCGTCCGCTCCACCCCA	3720
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LOCUS	BD218834
DEFINITION	BD218834 4015 bp DNA linear PAT 17-JUL-2003 Method and composition for inducing immune response to telomerase antigen.
ACCESSION	BD218834
VERSION	BD218834.1 GI:33028604
KEYWORDS	JF 2002509716-A/1. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 4015)
SOURCE	Gaeeta,F.C.A. Method and composition for inducing immune response to telomerase antigen
REFERENCE	Patent: JP 2002509716-A 1 02-APR-2002;
AUTHORS	UNIVERSITY TECHNOLOGY CORP
TITLE	OS Homo sapiens (human) PN JP 2002509716-A/1 PD 02-APR-2002 PF 30-MAR-1999 JP 2000541280 PR 31-MAR-1998 US 60/112006 PI FEDERICO C A GAETTA PC CI2N5/06,A6IKJ5/I4,A6IKJ8/43,A6IKJ9/00,A6IP35/00,A6IP37/00, CI2N5/I0, PC CI2NI5/09,CI2N5/00,A6IKJ7/48,CI2N5/00,CI2NI5/00 CC human telomerase reverse transcriptase (hTERT) FH Key Location/Qualifiers (56)..(3454). FT CDS Location/Qualifiers
FEATURES	location/Qualifiers source 1..4015 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
ORIGIN	Query Match 100.0%; Score 4015; DB 6; Length 4015; Best Local Similarity 100.0%; Pred. NO. 0; Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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QY 1141 GACATCTTCTGTGGTTCAGAGCCCTGAGTGTGCGAGGATCTCCCGAGGTTGCCCCGCT 1200
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DB 3721 GGGGCGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAG 3780
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DB 3781 CCAGATTCAGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAG 3840
QY 3841 AGGTGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAG 3900
DB 3841 AGGTGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAG 3900
QY 3901 CCTGTACAGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAGTCTCTGATGAGAGAG 3960
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RESULT 4
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DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36793
VERSION E36793.1 GI:13022756
KEYWORDS JP:199253177-A/1.
SOURCE JP:199253177-A/1.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 199253177-A 1 21-SEP-1999;
JERON CORP. UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 199253177-A/1
PD 21-SEP-1999
PF 15-OCT-1998 JP 199320169
PR 01-OCT-1996 US 08/724,643,18-A
25-APR-1997 US 08/846 017,06-MAY-01

ORIGIN

Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GGCGCTTCCCGCTGACGAGCCGTGGCGCTCTCTGTGCGACGCCACTACCGGAGTGT	120
Db	61	GGCGCTTCCCGCTGACGAGCCGTGGCGCTCTCTGTGCGACGCCACTACCGGAGTGT	120
QY	121	GGCGCTGGCCACGTTCTGATGGGGCGCTGAGGGCCCGAGGGCTGAGGGCTGTGTCAACCGG	180
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Db	181	GGACCCGAGCGGCTTTCCGCGCGCTGTGGCCAGTGCCTGGATGTGCTGAGCCCTGGAGCG	240
QY	241	ACGGCGCGCCCCCGCGCGCCCTCTCTTCCGCAAGTGTCTGTCTGAAGAGACTGTGGC	300
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QY	301	CCGAGTCTGTGACAGAGCTGTGTCGAGACGGCGCGCGAGAAACGTGCTGCCTTCGAGTTGAC	360
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QY	361	GCTGTGTGACGAGGCGCTGTGTGTCGAGACGGCGCGCGAGAAACGTGCTGCCTTCGAGTTGAC	420
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QY	481	CCGCGTGGGCGACGACGATGTGTGTTCACCTTGTCTGGACGCTGCGCGCTCTTTGTGTGTGT	540
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QY	541	GGCTTCCAGCTGTGCGCTTACCAAGTGTGTGGGGCGCGCGCTGTACCAAGCTGTGGCGTGTGCAC	600
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Qy	841	GCGTGAACCAAGTACCGTGGTTTC		
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Qy	901	CACCTCTTTGAGGGGTGCGTCTCT		
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Qy	961	GCACCAAGCGGGGCCCCCATCCACA		
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Qy	1021	CCCGGTGATGCGCGAGACCAAGCAT		
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Qy	1081	GCCCTCTCTTCTACTCAAGCTCTTG		
Db	1081	GCCCTCTCTTCTACTCAAGCTCTTG		
Qy	1141	GACCATCTTTCTGSGTTTCAGAGCC		
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Qy	1201	GCCCCAGCGCTACTGGCAATGCGGC		
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Qy	2281	TCGGTATGCGCTGTGTCAGAAAGCGCGCCATGGGACATCTGCGCAAGGCTTCAAGAGCCA	2340
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Qy	2341	CGTCTTACCTTGAACAGACTTCAGACCGGTACATGCGACAGTTGTGTGCTCACCTGACGA	2400
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Qy	2701	CTTCCTCAGAGACCTGTGTCAGAGGTGTCTCAGATATGTGCTGCTGTGAACTTGCAGAA	2760
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Dd	2941	CGGCTTAAGGCTGGGAGAACATGCCTCGCAACTCTTTGGGGTCTTGCGGCTGAAGTG	3000
OY	3001	TCAAGCCTGTCTTGATTGTGACGTTGAACAGCTTCCAAGCGGTGACCAAATCTTA	3060
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Dd	3181	CTGCTACTCCATCTTGAAAAGCCAAAGAACGACGGATGTGCTGGGGGCAAGGGCGCGC	3240
OY	3241	CGGCGCTTGTGCTCCGAGGCGGTGAGTGTGTGCAACCAAGATTTCTGCTCAAGCT	3300
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Dd	3421	ACTGCGCTCAGACTTCAAGACCATCTTGGACTGATGAGCACCCGCCACAGCCAGGCCGA	3480
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Dd	3541	CACACCCAGGCGCCSACCGCTGGGAGTGTGAGGCTGAGTGAAGTCTTTGGCCAGGCGTG	3600
OY	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGTGAAGGAGTGTCCAGCCAAAGGCT	3660
Dd	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGTGAAGGAGTGTCCAGCCAAAGGCT	3660
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Dd	3661	GAGTGTCCAGACACCTGCGCTTTCATCTTCCCACAGGCTGGGGCTTCGGCTCCAG	3720
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Dd	3721	GGGCGAGCTTTTCTTCAACAGAGGCCGGGCTTCCACTCCCCACATAAGAAAT	3780
OY	3781	CCAGATTCCGCAATTGTTCACCCCTCGGCTGCGCTCTCTTGTGCG	3840
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us-10-044-692-1.rge

[illegible]

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VERSION	AR182221.1
	GI:20225137

SOURCE	Unknown.
ORGANISM	Unknown.

REFERENCE 1 (bases 1 to 4015)
AUTHORS Morin,G.B.

JOURNAL Patent: US 6337200-A 1 08-JAN-2002;
FEATURES Location/Qualifiers

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best local similarity 100.00; freq. no. 0;
Matches 4015; Conservative 0; Mismatches 0;

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61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCCGCT

DB 61 GCGCGCTACCCCGCTGCGGAGCCCGTCCGCTCCCTGCTGCGCGA

OV 121 GCGCGTGGCCACGTTTCGTGCGCGCGCCCTGGGCGCCACGGGCTT

Db 121 GCCGCTGGCCACGTTCTGTGCGCGCCCTGGGGCCCAAGGCT

[illegible]

241 ACGGCCGCCCGCCGCCCTCTCTCCGCCAGTGTCT

Db 241 ACGGCGGCCCCCGCGCGCCCCCTCTTCCGCCAGGTGTCT

D_b 301 CCGAGTGTGCAGAGGCTGTGCGAGCGGGCGGCGGAAGACCC

QY 361 GCTGCTGACGGGGCCCGGGGGCCCCCGAGGCTTCA

421 CCTGCCAACACGGTGACCGACGCACTGCGGGGAGCGGGC

✓

QY	661	CTGGAACCAT
QY <td>661</td> <td>CTGGAACCAT</td>	661	CTGGAACCAT
Db <td>661</td> <td>CTGGAACCAT</td>	661	CTGGAACCAT
QY <td>721</td> <td>GAGGCGCGGGGCG</td>	721	GAGGCGCGGGGCG
QY <td>721</td> <td>GAGGCGCGGGGCG</td>	721	GAGGCGCGGGGCG
Db <td>721</td> <td>GAGGCGCGGGGCG</td>	721	GAGGCGCGGGGCG
QY <td>781</td> <td>TGCCCCTGAGCCGG</td>	781	TGCCCCTGAGCCGG
QY <td>781</td> <td>TGCCCCTGAGCCGG</td>	781	TGCCCCTGAGCCGG
Db <td>781</td> <td>TGCCCCTGAGCCGG</td>	781	TGCCCCTGAGCCGG
QY <td>841</td> <td>GCGTGACCGAGTGAC</td>	841	GCGTGACCGAGTGAC
QY <td>841</td> <td>GCGTGACCGAGTGAC</td>	841	GCGTGACCGAGTGAC
Db <td>841</td> <td>GCGTGACCGAGTGAC</td>	841	GCGTGACCGAGTGAC
QY <td>901</td> <td>CACCTCTTTGAGGGTG</td>	901	CACCTCTTTGAGGGTG
QY <td>901</td> <td>CACCTCTTTGAGGGTG</td>	901	CACCTCTTTGAGGGTG
Db <td>901</td> <td>CACCTCTTTGAGGGTG</td>	901	CACCTCTTTGAGGGTG
QY <td>961</td> <td>GCACCAACGCGGCCCCCAT</td>	961	GCACCAACGCGGCCCCCAT
QY <td>961</td> <td>GCACCAACGCGGCCCCCAT</td>	961	GCACCAACGCGGCCCCCAT
Db <td>961</td> <td>GCACCAACGCGGCCCCCAT</td>	961	GCACCAACGCGGCCCCCAT

Dh 1021 CCGGCTGTACGCCAGACCACAG
1021 CCGGCTGTACGCCAGACCACAG

Dh 1021 CCGGCTGTACGCCAGACCACAG
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1081 GCCCTCCCTTCTCACTACACTCTCT
1140 .GGCTCGAGGCTCTGTGCA

[illegible]

Db 1141 GACCATCTTCTGGGTTCCAGGCGCTGATGCCAGGAACTCCCGCAGGTTGCCCCGCT 1200

Q7 1201 GCCCCAGGCTACTGGCAATAGGGCCCCCTGTTCTGAGAGCTCTTGGGAACCAAGCGGA 1260

1261 GTGCCCTTACGGGGTCTCTCTCAAGACGACATGCCGCTGCGAGCTGCGGTCAACCCCAAGC 1320

Db 1261 GTGCCCCACGGGGTGTCTCTCAAGACGCACTGGCCCGCTGCCAGCTGCGGTACACCCACG 1320

Dbb 1321 AGCCGCTCTGTGCCCCGGAGAACCCCAAGGCTCTGTGCGGGCCCCCGAGAGAGAGGA 1380

1381 CACAGACCCCGTCGCTGGTGAAGCTGTCGCCGACAGACAGACGCCCTTGGAGAGGTGA 1440

1441 CGGCTTCGTCGGGGCTGECTGCGCCGGGCTGATTGCCCCCAGGCGCTCTGGGGCTCCAGGCA 1500

Db 1441 CGGCTTCGTGGCGGCCTGCTGGCCCGGGTGGTGCCCCCAGGCCCTCTGGGGGCTCCAGGCA 1500

1501 CAACGAAACCGCTTCTTCAGGACACCAAGATTCACTCCCTGGGAGCATGCCAA 1560

1561 GCTTCCGCGCAGAGCTGACGTGGAATGAGCGTCCGGACTGCCTTGGCTGCGCAG 1620

DB 1561 GCCTCTCGGCGACAGSAGCTGCACGTGGAAAGATGAACGCGTGGCGAGCTTGCCGTGCGAG 1820

1621 GAGGCCAAGGAGTTTCGCTCCTTCCGCGCGCGAGCAACGCTCTGAGTGAAGAAGATTCCCTGGC 1680

Db 1621 GAGCCAGGGGTTGGCTGTGTCTCCGGCCGCGAGACACCGTCTGGCTGAGGAGATCCTGGC 1688

1681 CAGAGTCTCGACATGGCGATAGTGTGACGCGTCAGCTGTACAGTCTTTCTTTA 1740

1741 TGTACGAGACCACTTCAAAAGACAGGCTTTTTCTACCGAAGATGTTTGAG 1800

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1741 TGTACGAGGACACAGTTTCAAAAAGACGGCTCTTTTCTACCGGAAAGGTGTGGAG 1800
QY 1801 CAAGTTGCAAGCATTTGGATCAGACAGCATTTGAAGAGGTGACGTGCGGAGCTGTTC 1860
Db 1801 CAAGTTGCAAGCATTTGGATCAGACAGCATTTGAAGAGGTGACGTGCGGAGCTGTTC 1860
QY 1861 GGAAGAGAGGTGACGAGCAGCATCGGGAGACCAAGGCGCGCTGCTGACGTCACGACTCCG 1920
Db 1861 GGAAGAGAGGTGACGAGCAGCATCGGGAGACCAAGGCGCGCTGCTGACGTCACGACTCCG 1920
QY 1921 CTTTATCCCCAAGCCTGACGGGCTGCGGCGATTTGAAACATGACCTACGTGTGGAGC 1980
Db 1921 CTTTATCCCCAAGCCTGACGGGCTGCGGCGATTTGAAACATGACCTACGTGTGGAGC 1980
QY 1981 CAGAACGTTTCCGAGAGAAAGAGGCGCGAGGCTCTACCTTGAGGGTGAAGCACTGTT 2040
Db 1981 CAGAACGTTTCCGAGAGAAAGAGGCGCGAGGCTCTACCTTGAGGGTGAAGCACTGTT 2040
QY 2041 CAGCGGTCTCACTACGAGCGGGCGGCGGCGCGCGCTCTGAGGGCGCTGTGTGGAG 2100
Db 2041 CAGCGGTCTCACTACGAGCGGGCGGCGGCGCGCGCTCTGAGGGCGCTGTGTGGAG 2100
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QY 2161 GCCGCTGAGCTGATCTTTGTCAAGGTGATGACGCGGCGGTACAGACCATCCCCA 2220
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QY 2221 GGAAGAGGCTCAGGAGGTGATGCGCAGCATCATCAACCCAGAAACAGGATCTGTGGG 2280
Db 2221 GGAAGAGGCTCAGGAGGTGATGCGCAGCATCATCAACCCAGAAACAGGATCTGTGGG 2280
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Db 2281 TCGGTATGCGGTGTGTCAGAAAGCCGCGCATGAGGCACTCCGCAAGGCTTCAAGAGCA 2340
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Db 2401 GACAGCGCGCTGAGGAGTCCGTGTGATCGAGCAGAGCTCTCTGTAAGAGGCGAG 2460
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QY 2581 CAGCGGTGCTACGAGGAGATGAGAAACAAGCTGTTTGGGGGATTCGCGGGAGCGGGCT 2640
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QY 2641 GCTCCTGCTTGGTGGATGATTTCTTGTGTGACACCTCACTCAACCCAGGAAAAC 2700
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QY 2701 CTTTCTCAGAGACCTGTGCTGAGGTGCTTCAAGTATGCTGTGCTGAGTGAATTTGCGGAA 2760
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QY 3841 AGGTGAGACCTTGAAGAGAGACCTTGAAGCTCTGAGGATTTGAGTGAACA 3901
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ORIGIN

QY	1	GGAGGCTGGTGGCTCTGCTGTGGAGACGTGGGAAGCCCTGGCCCCGGGCAACCCCGGAGTCC	60
Db	1	GCAGGCTGTGCTCTGTCTGGCACTTGGGAAGCCCTGGCCCCGGGCAACCCCGGAGTCC	60
QY	61	GGGCGCTCCCGCTGCTGGACCGCTGCGCTCCCTGTGTGGACCACTACCGGAGTGT	120
Db	61	GGGCGCTCCCGCTGCTGGACCGCTGCGCTCCCTGTGTGGACCACTACCGGAGTGT	120
QY	121	GGCGCTGGGACAGTTCGTGTGGGGGCGCTGGGGGCCCGAGGCGTGGGCGTGTGTGAGCGCGG	180
Db	121	GGCGCTGGGACAGTTCGTGTGGGGGCGCTGGGGGCCCGAGGCGTGGGCGTGTGTGAGCGCGG	180
QY	181	GGACCCGGGGCTTTCCGGCGCTGTGTGGCCAGTGCCTGTGTGTGCGTGTGCCTTGGACGC	240
Db	181	GGACCCGGGGCTTTCCGGCGCTGTGTGGCCAGTGCCTGTGTGTGCGTGTGCCTTGGACGC	240
QY	241	AGGGCGGGCCCCCGGGCGCCCCCTCCCTTCGCGAGGTGTCTGCTTGAAGAGCTGTGTGCG	300
Db	241	AGGGCGGGCCCCCGGGCGCCCCCTCCCTTCGCGAGGTGTCTGCTTGAAGAGCTGTGTGCG	300
QY	301	CCGAGTGTGACAGAGCTGTGTGGACCGGAGCGGACGAGAACGTGTGTGCTTCCGACTTGGC	360
Db	301	CCGAGTGTGACAGAGCTGTGTGGACCGGAGCGGACGAGAACGTGTGTGCTTCCGACTTGGC	360
QY	361	GGTGTGTGACGAGGGCGCGGGGGGGCCCCCGGAGGCCCTTACACCAACAGCGTGTGGACGCTA	420
Db	361	GGTGTGTGACGAGGGCGCGGGGGGGCCCCCGGAGGCCCTTACACCAACAGCGTGTGGACGCTA	420
QY	421	CTGTGCCCAACACGTTGACCGACGCACTTGGGGGGAGCGGAGCGTGTGGTGTGCG	480
Db	421	CTGTGCCCAACACGTTGACCGACGCACTTGGGGGGAGCGGAGCGTGTGGTGTGCG	480
QY	481	CCGCGTGGGCGACGACGTGTGCTGTTCACTGTGTGGACAAGCTGTGGCGCTTTTGTGTGGT	540
Db	481	CCGCGTGGGCGACGACGTGTGCTGTTCACTGTGTGGACAAGCTGTGGCGCTTTTGTGTGGT	540
QY	541	GGCTCTCCAGCTGTGCTTACAGAGTGTGTGGGCGCCCGCTGTACAGCTCGGCGCTGCAC	600
Db	541	GGCTCTCCAGCTGTGCTTACAGAGTGTGTGGGCGCCCGCTGTACAGCTCGGCGCTGCAC	600
QY	601	TGAGGCGGGCCCCCGGACACGCTAATGTGACCCCGAAGGCGTCTGGAGTGTCAAGGGC	660
Db	601	TGAGGCGGGCCCCCGGACACGCTAATGTGACCCCGAAGGCGTCTGGAGTGTCAAGGGC	660

[illegible]

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1801 CAAGTTGCAGAACATTTGGAATCAGACAGCATTTGAGAGAGTGTGACAGCTGTGCTG 1860
1861 GGAAGCAGAGGTGTGAGGAGCATGTGGAGACAGAGCCCGCTGTGAGTGTGAGTGTG 1920
1861 GGAAGCAGAGGTGTGAGGAGCATGTGGAGACAGAGCCCGCTGTGAGTGTGAGTGTG 1920
1921 CTTATCCCGCAAGCCGAGAGGCTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAG 1980
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Db	3901	CCCTGTACACAGGGGAGGACCCCTCACCTGGATGGGGGTCCCTGTGGSTCAAATTGGGGG	3960
QY	3961	GAGGTGCTGTGGAGTAATAATCATATATATGATTTTCAGTTTGAAAAAAA	4015
Db	3961	GAGGTGCTGTGGAGTAATAATCATATATATGATTTTCAGTTTGAAAAAAA	4015
RESULT 8			
LOCUS	AR243328	4015 bp	mRNA linear PAT 20-DEC-2002
DEFINITION	AR243328		
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VERSION	AR243328		
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 4015)		
TITLE	Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B., Harley,C.B. and Andrews,W.H. Human telomerase catalytic subunit: diagnostic and therapeutic methods		
JOURNAL	Patent: US 6475789-A 1 05-NOV-2002;		
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS  Morin,G.B. and Andrews,W.H.
TITLE     Promoter for telomerase reverse transcriptase
JOURNAL   Patent: US 6610839-A 1 26-AUG-2003;
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DB 2281 TCGGATGCGGATGCTGAGAGGCGGCGATGGGCGCTCCGCAAGGCTTCAAGAGCA 2340
QY 2341 CGTCTCTACCTTGAACAGACCTCCAGCGCTGATGACAGAGTTCGTGGCTCACTGAGGA 2400
DB 2341 CGTCTCTACCTTGAACAGACCTCCAGCGCTGATGACAGAGTTCGTGGCTCACTGAGGA 2400
QY 2401 GACCAAGCCGCTGAGAGGATGCGTGTGATGAGAGAGAGTCTCTCTTAAGAGAGCAG 2460
DB 2401 GACCAAGCCGCTGAGAGGATGCGTGTGATGAGAGAGAGTCTCTCTTAAGAGAGCAG 2460
QY 2461 CAGTGGCTCTTGAAGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATG 2520
DB 2461 CAGTGGCTCTTGAAGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATG 2520
QY 2521 CAAAGTCTTACGTCAGATGCAAGGAGATCCCGAGGCTCATCTTCCACGCTGTCTG 2580
DB 2521 CAAAGTCTTACGTCAGATGCAAGGAGATCCCGAGGCTCATCTTCCACGCTGTCTG 2580
QY 2581 CAGCCTGTGCTAGCGGAGCATGGAACAAAGCTGTTGCGGGGATTCGCGGGAGCGGCT 2640
DB 2581 CAGCCTGTGCTAGCGGAGCATGGAACAAAGCTGTTGCGGGGATTCGCGGGAGCGGCT 2640

QY 2641 GCTCTGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
DB 2641 GCTCTGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2700
QY 2701 CTTCTCAGAGACCTGCTGCTGAGTGTGCTGAGTATGCTGCTGCTGCTGCTGCTGCTG 2760
DB 2701 CTTCTCAGAGACCTGCTGCTGAGTGTGCTGAGTATGCTGCTGCTGCTGCTGCTGCTG 2760
QY 2761 GACAGGTGGAATCTTCCCTGATGAAAGAGAGGCTGGGTGGCAAGGCTTTTGTTCAGAT 2820
DB 2761 GACAGGTGGAATCTTCCCTGATGAAAGAGAGGCTGGGTGGCAAGGCTTTTGTTCAGAT 2820
QY 2821 GCCGGCCCAAGCTATTCCTGATGCGGCTGTGCTGATGATGATGATGATGATGATGATG 2880
DB 2821 GCCGGCCCAAGCTATTCCTGATGCGGCTGTGCTGATGATGATGATGATGATGATGATG 2880
QY 2881 GCAAGAGCTATCTCAGCTATGCTGAGCTTCATCAGAGCTCAGTCTTCACTTCAACCG 2940
DB 2881 GCAAGAGCTATCTCAGCTATGCTGAGCTTCATCAGAGCTCAGTCTTCACTTCAACCG 2940
QY 2941 CGGCTTCAAGGCTGGAGAGAAATGCTGCGAACTTTTGGGGCTTGGGCTGAGAGT 3000
DB 2941 CGGCTTCAAGGCTGGAGAGAAATGCTGCGAACTTTTGGGGCTTGGGCTGAGAGT 3000
QY 3001 TCACAGCTGTTTCTGATTTGAGTGAACAGCTCCAGAGGCTGAGAGTGAACATCTA 3060
DB 3001 TCACAGCTGTTTCTGATTTGAGTGAACAGCTCCAGAGGCTGAGAGTGAACATCTA 3060
QY 3061 CAAAGTCTCTGCTGACAGGCTGACAGGTTTCAAGCATGATGCTGACAGCTCCATTTCA 3120
DB 3061 CAAAGTCTCTGCTGACAGGCTGACAGGTTTCAAGCATGATGCTGACAGCTCCATTTCA 3120
QY 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGGGCGTCACTGCAAGCGGCTCCCT 3180
DB 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGGGCGTCACTGCAAGCGGCTCCCT 3180
QY 3181 CTGCTACTCATCTGAAAGCCAGAAACGACAGAGATGTCGTGAGGAGCCAGGCGCGC 3240
DB 3181 CTGCTACTCATCTGAAAGCCAGAAACGACAGAGATGTCGTGAGGAGCCAGGCGCGC 3240
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DB 3241 CGGCGCTGCTGCTGAGAGGCGGCTGAGTGTGTCACAGCATTTCTGCTCAAGCT 3300
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QY 3361 GCTGAGTGGAGAGCTCCGAGGAGCAGAGCTGAGCTGAGAGCGCAGCCAAACCGGC 3420
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QY 3601 CATGTCCGCTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660
DB 3601 CATGTCCGCTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660
QY 3661 GAGTGTCAAGCACAATGCGGCTTCACTTCCCAAGGCTGAGGCTGAGGCTTCAACCCA 3720
DB 3661 GAGTGTCAAGCACAATGCGGCTTCACTTCCCAAGGCTGAGGCTGAGGCTTCAACCCA 3720
QY 3721 GGGCAGCTTTTCTTACACAGAGCCCGCTTCACTCCCAATAGAAATAGTCCATCC 3780

Db	3721	GGGGCAGCTTTTCTCCACACGAGAACCGGGCTTCACCTCCCACTAGAGAAATGACCATCC	3780
QY	3781	CCAGATTGCGCATTTGTTCAACCCCTGGCGCTGCGCTCCCTTGGSCCTTCCACCCCAACATCC	3840
Db	3781	CCCAATTGCGCATTTGTTCAACCCCTGGCGCTGCGCTCCCTTGGSCCTTCCACCCCAACATCC	3840
QY	3841	AGGTGAGACCCCTGAGAGAGACCCCTGGAGCTCTGGGAAATTTGGAGTGAACCAAGGTGTG	3900
Db	3841	AGGTGAGACCCCTGAGAGAGACCCCTGGAGCTCTGGGAAATTTGGAGTGAACCAAGGTGTG	3900
QY	3901	CCCTGTACACAGCGAGAGACCCCTGACCTGGATGGGGGTCCCTGTGGTCAAAATTTGGGGG	3960
Db	3901	CCCTGTACACAGCGAGAGACCCCTGACCTGGATGGGGGTCCCTGTGGTCAAAATTTGGGGG	3960
QY	3961	GAGGTGCTGTGGGAGTAAATACTCAATATATGATTTTTCAGTTTGAATTTGAAAAAAA	4015
Db	3961	GAGGTGCTGTGGGAGTAAATACTCAATATATGATTTTTCAGTTTGAATTTGAAAAAAA	4015

RESULT	13
AR404030	
LOCUS	AR404030
DEFINITION	Sequence 1 from patent US 6627619.
ACCESSION	AR404030
VERSION	AR404030.1 GI:40152014
	4015 bp mRNA linear PAT 18-DEC-2003

ORGANISM	Unknown.	Unclassified.

REFERENCE	AUTHORS	TITLE	JOURNAL
1	(bases 1 to 4015) Cech, T. R., Lingner, J., Nakamura, T., Chapman, K. B., Morin, G. B., Harley, C. B. and Andrews, W. H.	Artisense compositions for detecting and inhibiting telomerase reverse transcriptase	US 6627619-A 1 30-SNP-2003;

FEATURES	Location/Qualifiers
source	1. .4015
	/ "United States" "Washington"

ORIGIN

Query Match	100.0%	Score	4015;	DB	6;	Length	4015;
Best Local Similarity	100.0%	Pred. No.	0;				
Matches 4015; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0

1 GCAGCGCTGCGTCTGCGCAGTGGGAAGCCCTGCCCCGGCCACCCCGCGATGCC 60

Db 1 GCAGGCTGCGTCTGTGCGCAGTGGGAAGCCCTGGCCCCCGCCACCCCCCGCAGTGC 60

Ov 61 GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 120

Db 61 GCGCGTCCCCGCTGCCGAGCGCTGCGCTCCTCCTGCTGCCGAGCCACTACCGCGAGTGT 120

121 GCCCGTGGCCACGTTTCGTGCGGCGCCCTGGGGGCCCCAGGCTGGCGGCTGGTCAGCGCCGG 180

DG 121 GCCCGTGGACAGATCCTGCCTCCGCCGTTCGTTTGCGTGGCA

OY 181 GGACC CGCGCGGCTTCCGCGCGGCTGATGGCCAGTAGCTGTGCGTGCCTGGAGCG 240

Db 181 GGACCGGGCGGCTTCCGCGCGGCTGCTGGCCAGTGCCTGATGTGCTGCCCTGGGAGC 240

DB

241 ACGGCGGGCCCCCGCCCTTTCGCACAGGTGTCTCCTGAAGAGACTGTGTGGC 300

301 CCGAGTCTGCACAGGCTGTGCCAGCCGCGCGCAAGACGTCGTGGCTTCGGCTTCGC 360

Db 301 CCGAGTCTGCAGAGCCTTGTCCAGCGCGGCGCAAGAACGTCGTGGCCTTCGGCTTCGC 360

361 GCTGCTGAGACGGGGCCCCGGGGGGCCCCCGAGGCTTACACCAAGCTGGCAGCTA 422
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421 CCTGCCCAACACGGTGAACCGACGACTGCGGGGGAAGCGGGCGTGGGGGCTGCTGCTCG 480

481 CCGCGGGGAGAGCACTGCTGGTTCACCTGCTGGACACGCTGCGCCTCTTTGTCCTGCT 540
421 CCTGCCACACCGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCGC 480

481 CCGCGTGGGCGACGCGTGTGTTCACTGCTGGCAGCTGCGCGCTTTTGTCTGGT 540

541 G G C T C C A G C T G G C C C T A C C A G G T G C G G G C C G C C G T G T A C C A G C T G G C G T G C C A C 600

D5
601 TCAGGCCCCGCCCCCGCCACAGCTTAGTGACC GCCGAAGGGGTCTGGATGC GAACGGGC

Db 601 TCAGGCCCGGGCCCCCGCCACGCTAGTGAGACCCCGAAGCGCTCGGATGCGAACGGGC 666

QY 661 CTGGAAACATAGCGCTCAGGGAGGCGGGGGTCCCCCTGGGCTGCACGCCCGGTCGAG 72
 Ph 661 CTGGAAACATAGCGCTCAGGGAGGCGGGGGTCCCCCTGGGCTGCACGCCCGGGTGCAG 72

721 GAGGCGCGGGGCAAGTCTGCCGTTGCCAAGAGGCCAGGCGTGCGC 78

Db 721 GAGCGCGGGGGCAGTGCACGCCGAACTCTGCCCTTGCACAAGAGGCCACAGCGCTGGCGC 78

781 TGCCTGAGCGGAGCGGACCGCTGGGCAAGGGTCTTGGCCCAACCGGGCAGGAC 84
 Db

[illegible]

D_b 841 GCGTGGACCAAGTGACCTGTTTCATGATGAGTATCACCCTCCACACCCGCCCGGC
QY 901 CACTCTTTGGAGGGTGGCTCTGTGGACGGCCACTCCACCCATTCCGTGGGCGCCA 96

Db 901 CACTCTTTGGAGGGTCCGCTCTGGCAGCGCCACTCCACCCATCCGTGGCCGCCA 96

961 GCACACACGCGGGCCCCCATCACATCGGGGCAACACGTCCTTGAGACACGGCCCTGTCC 10
961 GCACACGCGGGCCCCCATCCATCGGGCCACCAACGTCCTTGAGACACGGCCCTGTCC 10

1021 C C C G T G T A C G C C G A G A C C A A G C A C T T C C T A C T C C T C A G G C G A C A A G A G A C A C T G C G 10

Dbb
1021 CCGGCTGTACGCCGAGACCAGCACTTCTCTACTTCCTCAGGCAGACAAAGAGAGCAGCTGGC 10

1000 GCGGCGGCGTCCATCTCATCTCTCTGTGAGAGGCCACAGCTGACTGGAGCTCGAGGCTCTGTGA 11

05
 1081 GGCCTCTTCTACTACTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTCTGTGA 11

1141 GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCGCAGGTTGCCCGCCT 12

DB	1141	GACCATCTTTCGGGTTCCAGGCCCTCGATGACAGGACATCCCTCCAGAGTATGCCCCCCTC	1201
OV	1201	GCCCCAGCGTACTGCGCAATGCGGCCCTCTTTCTGAGCTGCTTGGGAACACGCGCA	1261

Db 1201 GCCCCAGCGCTACTGTGCATAATGCCGCCCTTTCTGAGCTGCTTGGGAAACCACGGGCA 1202

Oy 1261 GTGCCCTACGGGAGTGTCTCAAGACGACTGCCCGCTGCAGACTGGCGTACCCGAGC 13
 1261 GTGCCCTACGGGAGTGTCTCAAGACGACTGCCCGCTGCAGACTGGCGTACCCGAGC 13

DB 1261 GAGCCCTGTCGGCGGAGAAAGCCTCTGTGGCGGCCCGAGAGAGAGA 13

QY 1321 AGCCGGTGTCTGTGCCCCGGGAGAACCCCACAGGACTCTGTGGCGGCCCGAGAGAGAGA 13

Db 1321 AGCCGGTCTCTGCCCCGGAGAAAGCCCCAGAGGCTCTCTGCGGCCCCCGAGAGGAGGA 1322

OY	1381	CACAGATCCCGTCGCTGGTGAAGAGCCTCCGCAGACAGCAATCCCCTCCCTTTT
DB	1381	CACAGATCCCGTCGCTGGTGAAGAGCCTCCGCAGACAGCAATCCCCTCCCTTTT

1441 CGGCTTCGTGCGGCTGCTGCGCCGGCTGAGCCAGGCTCTGGGGCTCCAGCA 1
OY

Db 1441 CGGCTTCGTCCGGGCTGCTGCGCGCGGTGGTGGCCCCCAGGCTCTGTGGGCTCCAGCA 1

1501 CAACGACGCGCTTCTCTCAGAGACACAGAAAGTTTCATCTCTCGGGAGCATGCCAA 1560
1502 CACGAAACGCGCTTCTCTCAGAGACACAGAAAGTTTCATCTCTCGGGAGCATGCCAA 1560
1561 GCTTCGCTGACAGAGCTGACGTGAAAGATGAGCGGTGGGACTGCGCTTGGCTGCGAG 1620
1562 GCTTCGCTGACAGAGCTGACGTGAAAGATGAGCGGTGGGACTGCGCTTGGCTGCGAG 1620
1621 GAGCCGAGGGGTTGGCTGTTCCGCGCGCAGAGACCGTCTGCGGAGAGATCTGCGC 1680
1622 GAGCCGAGGGGTTGGCTGTTCCGCGCGCAGAGACCGTCTGCGGAGAGATCTGCGC 1680
1681 CAAGTTCCTGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
1682 CAAGTTCCTGACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
1741 TGTCAACGAGACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAGAGTGTCTGAG 1800
1801 CAAGTTCGAAACATTTGAAATGAAACAGACATTTGAAAGAGGTGACGCTGCGGAGCTG 1860
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1861 GGAAGCAGAGATCAGGACAGATCGGGAAGCAGGCGCGCTGCTGACGCTGCTGACGCTG 1920
1862 GGAAGCAGAGATCAGGACAGATCGGGAAGCAGGCGCGCTGCTGACGCTGCTGACGCTG 1920
1921 CTTGATCCCAAGCTTGAAGCTGAGCGGCTGCGGCTGATTTGAAACATGAGCTGATGAG 1980
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2042 CAGCGTGTCAACTGACGAGCGGAGCGGCGCGGCTGCTGAGGAGGAGGAGGAGGAGG 2100
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2461 GAGTGGCTCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520
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2941 CCGCTTCAAGGCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000
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3182 CTGCTACTCTCTGATTTGAGTGAAGAGATGATGATGATGATGATGATGATGATGATG 3240
3241 CCGGCTCTGAGGCTGAGGAGGCTGATGATGATGATGATGATGATGATGATGATGATG 3300
3242 CCGGCTCTGAGGCTGAGGAGGCTGATGATGATGATGATGATGATGATGATGATGATG 3300
3301 GACTGACACCGGTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
3302 GACTGACACCGGTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3360
3361 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
3362 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
3421 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480
3422 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3480
3481 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3540
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3601 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3660
3602 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3660
3661 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720

Db	3661	GAGTGTCCAGCAGACCTGCCTCTTCACTTCCCAAGGCTGGGGCTGGGCTCCACCCCA	3720
QY	3721	GGGCGAGCTTTTCTCTCACAGAGACCCGGCTTCCACTCCCAATAGCAATGCTCATCC	3780
Db	3721	GGGCGAGCTTTTCTCTCACAGAGACCCGGCTTCCACTCCCAATAGCAATGCTCATCC	3780
QY	3781	CCAGATTGCGCATTTGTTCAACCCCTGCGCCCTCCCTCTTTGCTCTTCACACCCCACTCC	3840
Db	3781	CCAGATTGCGCATTTGTTCAACCCCTGCGCCCTCCCTCTTTGCTCTTCACACCCCACTCC	3840
QY	3841	AGGTGGAGACCCCTGGAAGGACCCCTGGGAGCTCTGGAAATTTGGAGGACCAAGGCTG	3900
Db	3841	AGGTGGAGACCCCTGGAAGGACCCCTGGGAGCTCTGGAAATTTGGAGGACCAAGGCTG	3900
QY	3901	CCCTGTACACAGGCGAGACCCCTGCACTTGGATGGGGGTCCCTGTGGGTCAAAATTGGGG	3960
Db	3901	CCCTGTACACAGGCGAGACCCCTGCACTTGGATGGGGGTCCCTGTGGGTCAAAATTGGGG	3960
QY	3961	GAGGTGCTGTGGGAGTAAATATCTGAATATATGATTTTCAAGTTTGAATAAAAA	4015
Db	3961	GAGGTGCTGTGGGAGTAAATATCTGAATATATGATTTTCAAGTTTGAATAAAAA	4015

[illegible]

Db	361	GCTGCTGAGACGAGGAGCCCGGAGGAGCCCCCCCAAGGCTTACACACACAGCTGCGCAGGTA	420
Qy	421	CTGCCCCAACACGGTGAACCGACGCACTGCGAGGAGAGCGGAGCGTGAAGGCTGCTGCTCG	480
Db	421	CTGTCCCAACACGGTGAACCGACGCACTGCGAGGAGAGCGGAGCGTGAAGGCTGCTGCTCG	480
Qy	481	CCGCGTGAAGGAGAGAGTGTGGTTTAACTGCGTGAAGAGCTGCGGAGCTTTTGTCTGAT	540
Db	481	CCGCGTGAAGGAGAGAGTGTGGTTTAACTGCGTGAAGAGCTGCGGAGCTTTTGTCTGAT	540
Qy	541	GGCTCCGACGTGCGCTAACAGGATGTGCGGAGCCCGCTGTACCAAGCTGAGCGCTTGCAAC	600
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Qy	601	TCAGGCCCGGCCCCCGGCAACGCTGTGTGAACCCCGAAGCGCTGAGGATGGAACGGGCG	660
Db	601	TCAGGCCCGGCCCCCGGCAACGCTGTGTGAACCCCGAAGCGCTGAGGATGGAACGGGCG	660
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Qy	721	GAGGCGCGGAGGAGTGCACAGCCGAAGTCTGCGTTTGCCAGAAGGCCCAAGGCTGAGCGC	780
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Qy	781	TGCCCCGAGGCGGAGGAGAGCCCGGTGTGGAGAGGGTCTCTGAGGCACACCGGAGCAGGAC	840
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Qy	901	CACCTCTTTGAGAGGAGTGTGCTCTGTGGACAGCGCCACTTCCACCCCAATCCGTGAGCCGCA	960
Db	901	CACCTCTTTGAGAGGAGTGTGCTCTGTGGACAGCGCCACTTCCACCCCAATCCGTGAGCCGCA	960
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Qy	1021	CCCGGTATACGCCGAGACCAAGCACTTCTCTAATCCGAGGCGACAAAGAGAGAGCTGCG	1080
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Qy	1141	GACCATCTTTCTGAGGTTCAAGGCTCTGGAATCCCAAGGAGACTCCCGGAGAGTTGCGCGGCT	1200
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Db	1201	GCCCCAGCGCTACTGAGCAAAATGCGGCCCTGTATCTGTGAGCTCCCGGAGAGTTGCCCGCT	1260
Qy	1261	GTCGCTTACGAGGAGTCTCTAAGAGCGCATGCGCCGCTGGAAGCTGTGGAACACACGCGCA	1320
Db	1261	GTCGCTTACGAGGAGTCTCTAAGAGCGCATGCGCCGCTGGAAGCTGTGGAAGCTGTGGAAGC	1320
Qy	1321	AGCGGAGTGTGAGCGCGGAGAAACCCCAAGGCTCTGTGCGGAGCCCCGAGAGAGAGGA	1380
Db	1321	AGCGGAGTGTGAGCGCGGAGAAACCCCAAGGCTCTGTGCGGAGCCCCGAGAGAGAGGA	1380
Qy	1381	CACAGACCCCGGTGCGCTGTGAGCTGCTCCGCAAGCAACAGAGCCCTTGTGAGAGTGA	1440
Db	1381	CACAGACCCCGGTGCGCTGTGAGCTGCTCCGCAAGCAACAGAGCCCTTGTGAGAGTGA	1440
Qy	1441	CGGCTTCTGAGCGGAGCGTGCATGCGCGGCTGAGTGCAGGAGCTCTGAGGCTCCAGGCA	1500
Db	1441	CGGCTTCTGAGCGGAGCGTGCATGCGCGGCTGAGTGCAGGAGCTCTGAGGCTCCAGGCA	1500

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Qy	3721	GGGCGACGTTTTCCTCACAGGAGCCCGGCTTCCACTCCCAATAGTCATCC								
Db	3721	GGGCGACGTTTTCCTCACAGGAGCCCGGCTTCCACTCCCAATAGTCATCC								
Qy	3781	CCAGATTGCCATTGTTTCAACCCCTGCGCCCTGCTCTTTGCTTCCACCCCAATCC								
Db	3781	CCAAATTGCGCATTTGTTCAACCCCTGCGCCCTGCTCTTTGCTTCCACCCCAATCC								
Qy	3841	AGGTGAGAGCCCTGAGAGGACCTGTGGAGCTCTGGAAATTGGAGTGAACCAAGCTGTG								
Db	3841	AGGTGAGAGCCCTGAGAGGACCTGTGGAGCTCTGGAAATTGGAGTGAACCAAGCTGTG								
Qy	3901	CCCTGTACACAGCGGAGGACCTCTGACCTGTGATGGGGTCCCTGTGGTCAATTGGGGG								
Db	3901	CCCTGTACACAGCGGAGGACCTCTGACCTGTGATGGGGTCCCTGTGGTCAATTGGGGG								
Qy	3961	GAGGTGCTGTGGAGTAAATATCGAATATATGAGTTTTCAGTTTGAATGAAAAA								
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RESULT 15	AX019310	LOCUS	AX019310	4015 bp	DNA	1 linear	PAT 07-SEP-2000
DEFINITION	Sequence 10 from Patent W09940221.	AX019310					
ACCESSION	AX019310.1	GI:10043297					
VERSION							

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiod; Homnidae; Homo.
AUTHORS	1 Dahn,M.W., Phelps,R.C. and Brockmeyer,C.
TITLE	Method for quantitatively analyzing tumor cells in a body fluid and test kits suited therefor
JOURNAL	Patent: WO 9940221-A 10 12-AUG-1999;
FEATURES	DAHM MICHAEL W (DE); PHELPS ROBERT C (DE); BROCKMEYER CARSTEN (DE)
	Location/Qualifiers

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ORIGIN

Query Match	100.0%;	Score 4015;	DB 6;	Length 4015;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4015; Conservative	0;	Mismatches	0;	Gaps 0;

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Db	1	GCAAGGCTGCTGCTCTGCTGCTGACACTGGAAAGCCCTGGCCCCGAGCCACCCCGCATATCC	60	
QY		61	GCGGCTCCCGCTCCGATCCGAGCCCTGCGCTCCCTGCTGCGACCACTACCGAGAGTCT	120
Db		61	GCGGCTCCCGCTCCGATCCGAGCCCTGCGCTCCCTGCTGCGACCACTACCGAGAGTCT	120
QY		121	GCGCGTGGGCAAGTTCGTGTCGGCGGCTGGAGAGCCCGAGGAGTGGCGAGTGTGACAGCGG	180
Db		121	GCGCGTGGGCAAGTTCGTGTCGGCGGCTGGAGAGCCCGAGGAGTGGCGAGTGTGACAGCGG	180
QY		181	GGACCCGCGGCGCTTTCCGCGCGCTGTGTGACCAAGTGTGCTGTGTGCGTGTCCCTTGGAGCC	240
Db		181	GGACCCGCGGCGCTTTCCGCGCGCTGTGTGACCAAGTGTGCTGTGTGCGTGTCCCTTGGAGCC	240
QY		241	ACGGCGGCGCCCGCGCGCGCCCTCTCTTCGCGCAGGATGTCTCTCGAAGAGACTGTGTGAC	300
Db		241	ACGGCGGCGCCCGCGCGCGCCCTCTCTTCGCGCAGGATGTCTCTCGAAGAGACTGTGTGAC	300
QY		301	CCGAGTGTGACAGAGACTGTGTGCGAGCGCGCGCGAAGAACTGTGTGCGCTTGGCTTGCC	360

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QY	361	GCTGCTGAGACGGGAGCCCGCGGGAGCCCCCGGAGGCTTTCACACCAAGCGTGTGGCAGCTA	420
Db	361	GCTGCTGAGACGGGAGCCCGCGGGAGCCCCCGGAGGCTTTCACACCAAGCGTGTGGCAGCTA	420
QY	421	CTGGCCCCAACGSGTGAACGACGCACTGTGGGGGAGAGGGGAGCGTGTGGGAGCTGTCTGTCTGC	480
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Db	901	CACCTCTTTTGGAGGAGTGTGCGCTCTGTGGCAGCGCACCTCCACCCATTCGTGTGGCGGCA	960
QY	961	GCACCAAGCGGGGCCCCCATTCACATGTGCGGCGCACAGTCCCTGTGGGACAGAGCCTTGTGCC	1020
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QY	1081	GCCCTCTCTTCTACTCAGCTCTGTGAGGCGCCAGCTGAATGGCGCTGTGGAGGCTGTGTGGA	1140
Db	1081	GCCCTCTCTTCTACTCAGCTCTGTGAGGCGCCAGCTGAATGGCGCTGTGGAGGCTGTGTGGA	1140
QY	1141	GACCATCTTTCTGGGTTCCAGGCGCTGTGATGCCAGAGGATCTCCCGGAGGTTTGCCTCCGCT	1200
Db	1141	GACCATCTTTCTGGGTTCCAGGCGCTGTGATGCCAGAGGATCTCCCGGAGGTTTGCCTCCGCT	1200
QY	1201	GCCCCAGGCGCTACTGGCAAAATGCGGCGCCCTGTCTTTCTGTGAGCTGTCTTGGAAACAGCGCGCA	1260
Db	1201	GCCCCAGGCGCTACTGGCAAAATGCGGCGCCCTGTCTTTCTGTGAGCTGTCTTGGAAACAGCGCGCA	1260
QY	1261	GTGCCCCCTTACGGGAGTGTCTCTCAGAGCGCATCTGCCCGCTGTGGAAGCTGTGTGATCCCAAGC	1320
Db	1261	GTGCCCCCTTACGGGAGTGTCTCTCAGAGCGCATCTGCCCGCTGTGGAAGCTGTGTGATCCCAAGC	1320
QY	1321	AGCGGATGTCTGTGCGCGGAGAAAGCCCAAGGCTCTGTGGCGGCGCCCGAGAGAGAGGA	1380
Db	1321	AGCGGATGTCTGTGCGCGGAGAAAGCCCAAGGCTCTGTGGCGGCGCCCGAGAGAGAGGA	1380
QY	1381	CACAGACCCCGTGTGCTGTGTGACCTGTCCGACAGCAGACGCCCTGTGGCAGGTGTA	1440

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Db 3481 GAGCAGACCAAGAGCCCTGTCAAGCGCGGCTTCAAGTCCAGGAGAGGAGGAGGCGGCG 3540
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Search completed: October 29, 2004, 20:54:42
 Job time : 16400 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 09:37:01 : Search time 7840 Seconds
(without alignments)
5261.451 Million cell updates/sec

Title: US-10-044-692-2

Perfect score: 5961
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Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO_epool/US10044692/runat_28102004_103655_1370/app_query.fasta_1.1287
-DB=EST -QFMT=fastap -SUFFIX=rbt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_esc2: *
3: gb_hic: *
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5: gb_esc4: *
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7: gb_esc6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2168	36.4	1584	9	AY407350
3	1805	30.3	1835	9	AY407351
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5	1028	17.2	851	5	BU702370
6	875	14.7	851	4	BG917907
7	776	13.0	492	4	BM824748
8	771.5	12.9	664	5	BQ258274
9	682	11.4	1424	3	CR688161

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14	567	9.5	409	7	CN274427	CN274427	170005313
15	566	9.5	866	2	BB651920	BB651920	BB651920
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22	457	7.7	724	5	BX889962	BX889962	BX889962
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27	425	7.1	409	1	AA311750	AA311750	EST182469
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ALIGNMENTS

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DEFINITION	Homo sapiens TERT gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY407349				
VERSION	AY407349.1	GI:39763320			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
	1 (bases 1 to 1826)				
	Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarawal, A.,				
	Todd, M.A., Tanendau, D.M., Civeallo, D.R., Lu, F., Murphy, B.,				
	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,				
	Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous				
	gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1826)				
AUTHORS	Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarawal, A.,				
	Todd, M.A., Tanendau, D.M., Civeallo, D.R., Lu, F., Murphy, B.,				
	Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,				
	Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,				
	Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering				
	them based on alignment.				
FEATURES	Location/Qualifiers				
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ORIGIN

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Percent Similarity:	86.66%	Conservative:	0
Best Local Similarity:	86.66%	Mismatches:	81
Query Match:	44.37%	Indels:	0
DB:	9	Gaps:	0

US-10-044-692-2 (1-1132) x AY407349 (1-1826)

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QY      546 HisTriLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyrValThrGlu 565
DB      63 CACTGGCTGATGAGTGTGTACGTCTGACGCTCTCAAGTCTTTTATATGCAAGGAG 122
QY      566 ThrThrPheGlnIlyAsnArgLeuPhePheTyrArgIysSerValTTPSerIlyLeuGln 585
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QY      586 SerIleGlyIleArgGlnHisIleuIysArgValGluLeuArgGluLeuSerGluAlaGlu 605
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QY      606 ValArgGlnHisArgGluAlaArgProAlaIleuLeuThrSerArgLeuArgPheIlePro 625
DB      243 CTCAGGACAGATTCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCGCTTCATCCCC 302
QY      626 LysProAspGlyLeuArgProIleValAsnMetAspTyrValValGlyAlaArgThrPhe 645
DB      303 AAGCTGACGGGCGCGCCGATGTGAACATGACATCACTCGGGAGCCAGAACCTTC 362
QY      646 ArgArgGlnIlyAsnArgGluArgLeuThrSerArgValIlyAlaLeuPheSerValIleu 665
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QY      786 LeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSerSerGlyLeu 805
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DB      903 GTCCAGATGCCAGGGAGATCCGACAGGCTCCATCTCTCCACGCTGCTCGAGCCTGTGC 962
QY      846 TyrGlyAspMetGluAsnIlyLeuPheAlaGlyIleArgArgAspGlyLeuLeuLeuArg 865
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DEFINITION Pan troglodytes TERT gene, VIRUAL, TRANSCRIPT, partial sequence,
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ACCESSION genomic survey sequence.
AY407350
VERSION AY407350.1 GI:39763321
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
AUTHORS 1 (bases 1 to 1584)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J., Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1584)
AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
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Query Match: 36.37% Indels: 0
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DB 1203 GGCCTATTCCTCGTGGTGGCTGCTGCTGAGCACCCGGAACCTTGGAGTGCAGAGCAG 1262
QY 946 TyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgLysPheLys 965
DB 1263 TACTCAGCTATGCCCGGACCTCCATCNNNNCAGCTCACCTTCAACCGCGGCTTCAAG 1322
QY 966 AlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysSerLeu 985
DB 1323 GCTGGAGAGAAATGCTGTCGAAACCTTTGGGGCTTGGCGCTGAAGTGCACAGCCTG 1382
QY 986 PheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyrLysIleLeu 1005
DB 1383 TTTCGTGATTTGCAAGTGAACAGCTTCCAGAGCGTGTGACCAACATCTCAANNCTCTC 1442
QY 1006 LeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHisGlnGlnVal 1025
DB 1443 CTGTGTCAGCGTACAGGTTTACCGCATGTGTGTCAGACTCCCATTTTCATCAGCAAGTT 1502

QY 1026 TPLYSASPProThrPhePheLeuArgValIleSerAspThrAlaSerLeuCysTyrSer 1045
DB 1503 TGGAGAACCCACCATTTTCTCGGCATCATCTTGACACGCGCTCCCTGCTACTCTC 1562
QY 1046 TLeuLeuAlaLeuAsnAla 1052
DB 1563 ATCCTGAAAGCCAGAACGCA 1583

RESULT 3
AY407351 1835 bp DNA linear GSS 15-DEC-2003
LOCUS Mus musculus TERT gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY407351
VERSION AY407351.1 GI:39763322
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 1835)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
AUTHORS 2 (bases 1 to 1835)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..1835
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/gene="TERT"
/locus_tag="HCM2861"

Alignment Scores:
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Score: 1805.00 Matches: 373
Percent Similarity: 69.56% Conservative: 52
Best Local Similarity: 61.05% Mismatches: 176
Query Match: 30.28% Indels: 11
DB: 9 Gaps: 3

US-10-044-692-2 (1-1132) x AY407351 (1-1835)

QY 529 ValProAlaAlaGluHisArgLeuArgGluIleLeuAlaLysPheLeuHisTrpLeu 548
DB 12 GTCGCCGCGAGAGACCGCTCTGAGGAGAGATCTGGCTACGTTCTCGTTCTGGCG 71
QY 549 MetSerValTyrValValGluLeuLeuAspSerPhePheTyrValThrGluThrThrPhe 568
DB 72 ATGACACATACCTGCTACAGCTGCTTAGGTCATCTTTACATCACAGAGACACATTTC 131
QY 569 GlnTyrAsnArgLeuPhePheTyrArgLysSerValTrpSerLysLeuGlnSerIleGly 588
DB 132 CAGAAACACAGGCTCTTCTTCTACCGTTACAGTGTGTGAGCAAGCTGCGACGACATTGGA 191
QY 589 IleArgGlnHisLeuLysArgValGlnLeuArgLysLeuSerGluAlaGluValArgGln 608

DB 192 GTCAGGCAACACCTTGAGAGAGTGGCTACCGAGAGCTGTCAAGAGAGAGTCCAGCAT 251
QY 609 HisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArgPheIleProLysProAsp 628
DB 252 CACCGAGACACTGGCTAGCCATGCCATCTGCACATCGCGTTTCATCCCAAGCCCAAC 311
QY 629 GlyLeuArgProIleValAsnMetAspTyrValValGlyAlaArgThrPheArgArgGlu 648
DB 312 GGCCTGGCGGCCCATTTGTGAACATGATTATGACATGGTACAGACGACTTGGGCAAGAG 371
QY 649 Lys-ArgAlaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeuAsnTyrGln 668
DB 372 AAGCAGGGCCGACGATTCACCGACCGAGTCTCAAGCTCTTCAGAGATCTCAACATATA 431
QY 668 uArgAlaArgArgProGlyLeuLeuGlyAlaSerValIleuGlyLeuAspAspIleHisArg 688
DB 432 GCGAGACAAACATCTCACCCTTATGGGGCTTCTGACTGGGTATGAATGACATCTACAG 491
QY 688 gAlaTrpArgThrPheValIleuArgValArgAlaGlnAspProProGluLeuTyrPhe 708
DB 492 GACCTGGCGGCGCTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
QY 708 eValLysValAspValThrGlyAlaTyrAspThrIleProGlnAspArgLeuThrGluVal 728
DB 552 TGTAAAGNN 611
QY 728 ILeAlaSerIleIleLysProGlnAsnThrTyrCysValArgArgTyrAlaValAlaGln 748
DB 612 NNN 671
QY 748 nLysAlaAlaHisGlyHisValArgLysAlaPheLysSerHisValSerThrLeuThrAs 768
DB 672 NNN 731
QY 768 pLeuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGluThr-----SerProLe 786
DB 732 CCTCCAGCATACATGAGGCGAGCTCTTAAAGATCTGCGAGATTGACATGCCAGTGCACCT 791
QY 786 uArgAspAlaValIleGluGlnSerSerSerLeuAsnGluAlaSerSerGlyLeuPhe 806
DB 792 GAGGAATCTCGTTGTCATGAGCAGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 851
QY 806 eAspValPheLeuArgPheMetCysHisHisAlaValArgIleArgGlyLysSerTyrVa 826
DB 852 NNN 911
QY 826 lGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCysSerLeuCysTyr 846
DB 912 GCAGTGCCAGGCGCATCCCGCAGGCGCTCCAGCCTATCCACCTGCTGCGAGCTGTGTT 971
QY 846 rGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeuLeuLeuArgLe 866
DB 972 CGAGACATGAGAAACACAGCTGTTGCTGAGGAGTGGAGATGGGTGCTTTTACGTTT 1031
QY 866 uValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThrPheLeuArgTh 886
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QY 886 rLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLysThrValAlaAs 906
DB 1092 CCTGCTTCATGCGCTCTCGATATGAGTATGAGTAACTTGACAGAAACAGTGTGTGA 1151
QY 906 nPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAlaHisGln 926
DB 1152 CTTCCCTGTGAGCGCTGTACCTGGGTGTGACAGTCCATACAGCTGCTCAGCTG 1211
QY 926 yLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGlnValGlnSerAspTyr 946
DB 1212 CCGTTTCCCTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1271
QY 946 rSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPheLysAl 966

Db	1272	CTCAGGTTATCCAGACCTCAATTAAAGCAGCGCTCACCTTCCAGAGTGTCTTCAAGC	1331
Qy	966	AGLYArgAsnMetArgArgVLeuPheGlyValLeuArgLeuLysCySHISerLeuPh	986
Db	1332	TGGGAAGCCATGGGGAAACAAGCTTCGTCCGCTCTGGGTTGAAGTGCACGGTCTATT	1391
Qy	986	ELeuAspLeuGlnValAsnSerLeuGlnThrValCySHraSniLeuTyrLysIleLeuLe	1006
Db	1392	TCTGACTTCGAGGTGAACAGCTTCCAGACAGTCTGCATCAATATATACAGATCTTCTT	1451
Qy	1006	uLeuGlnAlaTyrArgPheHISaLcySVaIleuGlnLeuProPheHISglnGlnValTr	1026
Db	1452	GCTTCAGCGCTCAAGGTTCCATGATGATGTGATTTCAGCTTCCTTTGACAGCGGTGAG	1511
Qy	1026	PLyAsnProThrPhePheLeuArgValIISerAspThrAlaSerLeuCySTyrSerI	1046
Db	1512	GAAGAACCTCCATCTTTCTGGGGCATCATCTCCAGCCMACCATCTCGCTCTATGCTAT	1571
Qy	1046	eLeuLysAlaLysAsnAla-----GlyMetSerLeuGlyAlaLysGlyAlaAl	1062
Db	1572	CTGGAAGGTCAAGATTC-AGTGAATCCCCAGAGATGACACTTAAGGCTCTGGGCTCC-	1628
Qy	1062	AGLYProLeuProSerGlnAlaValGlnTrpLeuCySHISglnAlaPheLeuLeuLysLe	1082
Db	1629	-----TTTCTCTCTGGAAGCGGACATTTGGCTCTGCATCACAGGCTTCCGTCTCAACT	1681
Qy	1082	uThrArgHISArgValIlnTyrValProLeuLeuGlySerLeuArgThrAlaGlnThrGl	1102
Db	1682	GGCTGCTCATCTGTGCATCTCAATATGTCCTCTGGGACCTCTGAGGACAGCGCCAAAAC	1741
Qy	1102	nLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsnProAl	1122
Db	1742	GCTGTCGCGGAGCTCCGAGGCGCACATGACATCTCTTAAAGCTGACGTGACCCAGC	1801
Qy	1122	aleuProSerAspPheLysThrIleLeuAsp	1132
Db	1802	CTTAAGCACAGACTTTCAGACCATTTTGGAC	1852
RESULT 4			
LOCUS	BM453198	925 bp	mRNA linear EST 05-FEB-2002
DEFINITION	AGENCOURT 6387556 NIH_MGC_71	Homo sapiens	CDNA clone IMAGE:5529840
ACCESSION	BM453198		
VERSION	BM453198.1	GI:18502238	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 925)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.lnl.gov		
	Plate: L14M12208 row: p column: 01		
	High quality sequence stop: 646.		
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Source			
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	/db_xref="taxon:9606"		
	/clone="IMAGE:5529840"		
	/tissue_type="telomysarcoma"		
	/lab_host="DH10B (phage-resistant)"		

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/clonase IIb="N1H_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt
Average insert size 2.1 kb. "

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Alignment Scores:			
Pred. No.:	2..2e-87	Length:	925
Score:	1406.00	Matches:	274
Percent Similarity:	98.92%	Conservative:	0
Best Local Similarity:	98.92%	Mismatches:	1
Query Match:	23.59%	Indels:	2
DB:	4	Gaps:	0
US-10-044-692-2 (1-1132) x BM453198 (1-925)			
OY	699	AlAGlaSPPrpPrpProgluLeuLyrPheValysValaSPValThrglValaTyrAsp	71E
Db	3	GCCACGAGACCCGCGCTGAGCTGTACTTGTCAAGGTGAGATGACCGGCGGTACGAC	62
OY	719	ThrIleProgluInaSPArgLeuThrgluValIleIleAserIleIleLysProgluInaSPThr	73E
Db	63	ACCATTCGCCAGAGACAGGCTCACGAGGTGCATCGGCACACATCATTAACCCACAGAACG	122
OY	739	TyrCysValaArgArgTyrAlaValaValGlnLysValaIleAsiGlyHisValaArgLysAla	75E
Db	123	TACTGCGTGTGGGTATCGCTGGTCCGAAAGCGCCGCTCATGGGCAAGTCCGACAGGCC	182
OY	759	PheLysSerHisIalSerThrlleuThraSPleuGlnInProTyrTmeArgGlnPheValaIa	77E
Db	183	TTCAAGGACCACTCTTCACTTGACAGACCTTCACGCGTACATGCGACAGTGTGGCT	242
OY	779	HisLeuGlnGlnIuThrSerProleuLyrASpAlaValaIleGluGlnSerSerLeu	79E
Db	243	CACCTGACGAGACACAGCCCGCTGAGGATGCCGCTGCATCATGACAGACAGCTCTCCG	302
OY	799	AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisIleAlaVal	81E
Db	303	AATGAGGCGCAGTGGCTCTTCCGACGCTTCTCATACCTTCATGTGCCACACGCGCTG	362
OY	819	ArgIleArgGlySerSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSer	83E
Db	363	CGATTCAGGGGCAAGTCTTACGTCACAGTCCAGGAGATCCGACAGGGCTCCATCTCTCC	422
OY	839	ThrlleuLysSerLeuLysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArg	85E
Db	423	ACCGTGTCTGCAGCGCTGTGTCTACGCGGACACAGAGAACAAAGCTGTTGGCGGGATTCG	482
OY	859	ArgAspGlyLeuLeuLeuLyrLeuValaAspAspPheLeuLeuValThProHisLeuThr	87E
Db	483	CGGACGCGGCTGCTCTCGCTGGTGGGTGATGATTCCTGTTGGTGACACCTCACCTCAC	542
OY	879	HisAlaLysThrPheLeuArgThrlleuValaArgGlyValaProGluTyrGlyCysValaVal	89E
Db	543	CACGCGAAACCTTCTCTCAGAACCTCGGTCCAGAGTGTCCGTGATATAGGCTGGGTGG	602
OY	899	AsnLeuArgIysThrValaValaSPNepProValGluAspGluAlaLeuGlyIleThrAla	91E
Db	603	AACCTTGGGAAAGCACTGATGAACCTTCCTGTAGAAAGACAGGCGCTGGGTGGACCGCT	662
OY	919	PheValGlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArg	93E
Db	663	TTTGTTCAGATGCCGCGCCACCGGCTCATATTCCTCTGTGTGGGCTGTCTGTGAATACCGG	722
OY	939	ThrlleuGlnValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeu	95E
Db	723	ACCGTGAAGGTGACAGACCACTACCTCACTATGCCCGGACCTCATATAGAGCCAGTCTC	782
OY	959	ThrPheAsnArgGlyPheLysAla--GlyArgAspMetArgArgLys	973
Db	783	ACCTTCAACCGCGGCTTCAAAAGGCTGGGAAGAAACATCGTCTGCAAA	829

DB: 4 Gaps: 0

US-10-044-692-2 (1-1132) x BM824748 (1-492)

QY 905 ValAsnProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAla 924
 Db 1 GTGAACCTTCCTGTGAGAGACAGAGCCCTGGGTGGACAGCTTTGTTGTCAGATGGCGGC 60

QY 925 HisGlyLeuPheProThrProCysGlyLeuLeuLeuAspThrArgThrLeuGluValGlnSer 944
 Db 61 CACGGCTATTCCTCGTGGAGCGGCTGCTGCTGATACCCGAGCCTGGAGGTGCAGAGC 120

QY 945 AspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPhe 964
 Db 121 GACTACTCCAGCATGATCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCGCGCTTC 180

QY 965 LysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCysHisSer 984
 Db 181 AAGGCTGGGAGAAACGCTGCAAACTCTTGGGGCTCTTGGCGCTGAAGTGTCAAGC 240

QY 985 LeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyrLysIle 1004
 Db 241 CTGTTTGTGATTTGACGTGAGGAGCAGCTCCAGCGGTGTGCACCAATCTACAGATC 300

QY 1005 LeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHisGln 1024
 Db 301 CTCTGCTGACGAGGCTACAGGTTTCAAGCATGTGTGTGAGCTCCCATTTCAACAGCA 360

QY 1025 ValThrLysAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeuCysTyr 1044
 Db 361 GTTGTGAAGAACCCCACTTTTCTGCGGTATCTCTGACAGCGGCTCCCTGCTAC 420

QY 1045 SerIleLeuLysAlaLysAsnAla 1052
 Db 421 TCCATCTCGAAGCCCAAGACGA 444

RESULT 8 BQ258274 664 bp mRNA linear EST 06-MAY-2002
 LOCUS BQ258274 NISC kp11904.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone
 DEFINITION IMAGE:5409222, mRNA sequence.
 BQ258274
 ACCESSION BQ258274.1 GI:20459030
 VERSION BQ258274.1 GI:20459030
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 664)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 CDNA Library Preparation: J. Baker (Stanford University)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC)
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 info@image.lnl.gov
 MGI:1845958
 Place: LHAM12043 row: N column: 7
 Seq primer: Sp6 primer.
 Location/Qualifiers
 1. 664
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 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
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 /clone_lib="Baker mouse embryo e7.5"
 /note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA
 made by oligo-dt priming. Directionally cloned into
 SalI/NotI sites using the following 5' adaptor:
 5'-TCACCCACGCGCCG-3'. Size-selected for average insert
 size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
 University)."

ORIGIN

Alignment Scores:
 Prid. No.: 1,659-43 Length: 664
 Score: 771.50 Matches: 153
 Percent Similarity: 72.03% Conservative: 17
 Best Local Similarity: 64.83% Mismatches: 45
 Query Match: 12.94% Indels: 21
 DB: 5 Gaps: 2

US-10-044-692-2 (1-1132) x BQ258274 (1-664)

QY 352 ProSerLeuThrGlyAlaArgArgLeuValGluThrIlePheLeuGlySerArgProTyr 371
 Db 10 CCTAATGACTGGAGGCGCAGAGACCTGTGAGATCATCTTTCTGGGCTCAAGGCTTAG 69

QY 372 MetProGlyThrProArgArgLeuProArgLeuProGlnAlaGlyTyrTyrGlnMetArgPro 391
 Db 70 ACATCAGACCACTGTCAGAGACACACCGTCTATCGGCTGATCTGCGAGATGCGGCC 129

QY 392 LeuPheLeuGluLeuLeuGlyAsnHisAlaGlnCysProTyrGlyValLeuLeuLysThr 411
 Db 130 GTTGTCAACAGCTGCTGTGTAACCAAGAGTGCACATATGTCAACACTCTCAGGTCA 189

QY 412 HisCysProLeuArgAlaAla-----ValThrProAlaAlaGlyValCysAlaArg 428
 Db 190 CATTGCAAGTTTCCAGACGAAACCAACAGGTGACAGATGCTTG----- 234

QY 429 GlnUysProGlnGlySerValAlaAlaProGluGluGluAspThrAspProArgArgLeu 448
 Db 235 -----AACCCAGCCCAACCGCACCTC 255

QY 449 ValGlnLeuLeuArgGlnHisSerSerProTyrGlnValTyrGlyPheValArgAlaCys 468
 Db 256 ATGAGATTGCTCGGCTGCACAGAGTCCCTGCGAGATATGTTTCTTCGGGCTGT 315

QY 469 LeuArgArgLeuValProProGlyLeuTyrGlySerArgHisAsnGluArgArgPheLeu 488
 Db 316 CTCTGCAAGTGTGTCTGCTAGTCTTGGGGGTACAGGCAACAAAGAGCGCGCTTCTT 375

QY 489 ArgAsnThrLysLysPheIleSerLeuGlyLysHisAlaLysLeuSerLeuGlnGluLeu 508
 Db 376 AAGAACCTTAAGAGATTCATCTGTGGGAAATACGGCAGACTTCACTGAGGAACTG 435

QY 509 ThrTyrLeuMetSerValArgAspCysAlaTyrPheArgArgSerProGlyValGlyCys 528
 Db 436 ATGTGAAAGATGAATAATAGAGATTGCGACTGCGCAGAGCCACAGGAAAGACCT 495

QY 529 ValProAlaAlaGluHisArgLeuArgGluGluIleLeuAlaLysPheLeuHisTyrPheLeu 548
 Db 496 GTCCCGCTGCAGAGACCGTCTGAGGAGAGAGATCTGCTACAGTCTCTGTTGCGCTG 555

QY 549 MetSerValTyrValAlaGluLeuLeuArgSerPhePheTyrValThrGluThrThrPhe 568
 Db 556 ATGACACATACGTGTACAGCTGCTTAGGTCAATCTTTTACATCAGAGACACATTC 615

QY 569 GlnLysAsnArgLeuPhePheTyrArgLysSerValTyrSerLysLeu 584
 Db 616 CAGAGAAAGAGGCTCTTCTTCAACGTAAGATGTGAGCAAGCTG 663

RESULT 9 CR688161 1424 bp mRNA linear HTC 12-AUG-2004
 LOCUS CR688161
 DEFINITION Tetraodon nigroviridis full-length cDNA.

ACCESSION CR688161
 VERSION CR688161.1 GI:5118608
 KEYWORDS HTG, cDNA; full-length; Tetraodon nigroviridis.
 SOURCE Tetraodon
 ORGANISM Tetraodon
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae.
 1 (bases 1 to 1424)
 REFERENCE
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -
 : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 The sequences are based on single pass reads.
 More information available at
 http://www.genoscope.cns.fr/tetraodon.
 FEATURES
 source 1..1424
 /organism="Tetraodon"
 /mol_type="mRNA"
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 Best Local Similarity: 43.91% Mismatches: 140
 Query Match: 11.44% Indels: 8
 Gaps: 3
 DB: 3
 US-10-044-692-2 (1-1132) x CR688161 (1-1424)

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 QY ArgLeuLeuCySerLeuPheLeuSerLeuGlnValAlaSerLeuGlnThrValCys 998
 DB 617 AGACGAAAGTGCAGAGCTTGTCTTATCTTAAAGACCACTCTCTTGAAGCCATCTAT 676
 QY ThrAenIeTyLysIleLeuLeuGlnAlaTyAArgPheHlaCyValLeuGln 1018
 DB 677 AAGATATCTACAAATTAATCTGCTTACAGCAGCTCAGATTCATGTGTCTCAGGT 736
 QY 1019 LeuProPheHlaGlnIleValTyrLysAenProThrPheLeuArgValIleSerAsp 1038
 DB 737 CTGCGCTTGTGTCAGACTGTGCTTAAGAACCCAGATCTTCTGCTATATATGAGCT 796
 QY 1039 ThrAlaSerLeuCyTySerIleLeuValAlaValAenAlaGlyMetSerLeuValAla 1058
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 QY 1059 LysGlyAlaAlaGlyProLeuProSerGlnAlaValAlaGlnTyrLeu-CysHlaGlnAlaPhe 1078
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 QY 1078 eLeuLeuLysLeuThrArgHlaArgValThrTyValProLeuLeuGlySerLeuArgTh 1098
 DB 905 CTGCTGAGTGTGCTCAAAACATGACGCTCTATTAAGATGCTGCTCCACACTGCAAAA 964
 QY 1098 rAlaGlnThrGlnLeuSerArgValGlyLeuProGlyThrThrLeuThrAlaLeuGlnAla 1118
 DB 965 ACGAAGCGCAGTGTTAAGACAGCGCTGAGAGACTGAGTGGCCAGAGTCCGACAGGC 1024
 QY 1118 aAlaAenProAlaLeuProSerAspPheLeuThrIle 1130
 DB 1025 TGCTCAGCCAGAGAGCCAGTGAATCTTCTGCAATT 1061
 RESULT 10
 CFS31069 649 bp mRNA linear EST 12-SEP-2003
 LOCUS UI-M-FY0-GSP-C-19-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 DEFINITION IMAGE:30355746 5', mRNA sequence.
 CFS31069
 ACCESSION CFS31069.1 GI:34583033
 VERSION CFS31069.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/
 1 (bases 1 to 649)
 REFERENCE
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgs@bbs-riemail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mouse1.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: PYX-5.
 FEATURES
 source 1..649
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30355746"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	2,696-36	Length:	649
Score:	667.50	Matches:	153
Percent Similarity:	46.32%	Conservative:	17
Best Local Similarity:	41.69%	Mismatches:	32
Query Match:	11.20%	Indels:	165
		Gaps:	3

US-10-044-692-2 (1-1132) x CF531069 (1-649)

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QY 1 MetProAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
Db 42 ATGACCGCGCTCTGCTGCGCGCGCTCTCTGCTGCGCGCGCGCGCGCGCGGAG 101
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
Db 102 GTGTGGCGCGCTGGAGACCTTGTGCGCGCTGGCGCGCGCGCGCGCGCGCGCTTGGCA 161
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 162 CCGCGGGAGCGGAGATCTACCGCATTTGGTGTCCCAATGGCTCAGTGTGCAGCTGG 221
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnAlaSerCysLeuValGlnLeu 80
Db 222 GGCTCAGACCTCCACCTCGCGACCTTCTTCCACAGGGGTGTATCCCTGAAAGACTG 281
QY 81 ValAlaArgValLeuGlnArgLeuCysGlyValArgValAlaValAsnValLeuAlaPheGly 100
Db 282 GTGGCCAGGTTGTGACAGACTCTGCGAGGCGAAGAGAAACGTGGCTTTGGC 341
QY 101 PheAlaLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrSerValArg 120
Db 342 TTGTAGCTGTTAAACGAGCGCAGAGCGGCGCTCCCATGGCTTCACTAGTAGCGTGGT 401
QY 121 SerTyrLeuProAlaThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
Db 402 AGCTACTGTCACACACTGTTATTTGAGACCTGTGCTGTCACTGTGTGATGATGACTCTG 461
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 462 TTGAGCCAGTGGGAGAGACCTGTGTCTTACCGTGTGCGACACTGTGCTTATCTT 521
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db 522 CTGGTGGCCCCCAGCTGTGCTTAC----- 545
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db 545 ----- 545
QY 201 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 545 ----- 545
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLeuArgProArgArg 240

```

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Db 545 ----- 545
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
Db 546 ----- 557
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaProAlaGlu 280
Db 557 ----- 557
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 557 ----- 557
QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
Db 558 ----- 569
QY 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
Db 569 ----- 569
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 570 ---AAACCTCATTTCTACTCAGCANCTCCAGCTTAACCTTACTGCGGCGCAGAGACTG 626
QY 361 ValGluThrIlePheLeuGly 367
Db 627 GTGAGATCATCTTCTTCTGGC 647

```

RESULT 11

CF531121 688 bp mRNA linear EST 12-SEP-2003
 UI-M-FY0-CSP-m-21-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 IMAGE:30355988 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Seq primer: pYX-5.

Location/Qualifiers

1..688

/organism="Mus musculus"

/mol type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30355988"

/tissue type="whole brain"

/dev stage="embryo 13.5,14.5,16.5,17.5,18.5"

/lab host="DH10B (T1 phage resistant)"

/clone lib="NIH BMAP FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	3,456-36	Length:	688
Score:	666.50	Matches:	154
Percent Similarity:	46.34%	Conservative:	17
Best Local Similarity:	41.73%	Mismatches:	32
Query Match:	11.18%	Indels:	166
	7	Gaps:	2

US-10-044-692-2 (1-1132) x CF531121 (1-688)

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Oy 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
Db ATGACCCGCGCTCTCTGTTGCCCGCGGTGCGCTCTCTGCGCAGCCGATACCGGAG 138
Oy 21 ValLeuProLeuAlaThrPheValArgArgGluGlyProGlnGlyTyrPheGluValGln 40
Db GTGTGGCCGCTGGCAACCTTTGTGGCGCGCTGGGGCCCGAGGCGGCGGCTGTGCA 198
Oy 41 ArgGlyAerProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db CCGCGGAGACCCCAAGATCTACCGCACTTGTGGTCCCATGCTACTGATGCACTGG 258
Oy 139 GGTGAGCCGCTGGCAACCTTTGTGGCGCGCTGGGGCCCGAGGCGGCGGCTGTGCA 198
Oy 41 ArgGlyAerProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db CCGCGGAGACCCCAAGATCTACCGCACTTGTGGTCCCATGCTACTGATGCACTGG 258
Oy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuGlyGluLeu 80
Db GGGTCAAGCCCTCCACCTGCTTCTCCACAGAGTGTCACTCCCTGAAGAGCTG 318
Oy 259 GGGTCAAGCCCTCCACCTGCTTCTCCACAGAGTGTCACTCCCTGAAGAGCTG 318
Oy 81 ValAlaArgValLeuGlnArgGluCysGluArgGlyAlaLeuAsnValLeuAlaPheGly 100
Db GTGGCCAGGCTGTGGAGAGCTGTGGCGGCAACGAGAGAAACCTGTGCTTTGGC 378
Oy 319 GTGGCCAGGCTGTGGAGAGCTGTGGCGGCAACGAGAGAAACCTGTGCTTTGGC 378
Oy 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
Db TTTGAGCTGCTTACAGAGCCAGAGGCGGCTCCCATGCTTCACTACTGACGCTGCT 438
Oy 379 TTTGAGCTGCTTACAGAGCCAGAGGCGGCTCCCATGCTTCACTACTGACGCTGCT 438
Oy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATrpglyLeuLeu 140
Db AGCTACTGCTCCCAACACTGTATTGAGACCTGCGGTGTCAGTGTGCATGATGCTACTG 498
Oy 439 AGCTACTGCTCCCAACACTGTATTGAGACCTGCGGTGTCAGTGTGCATGATGCTACTG 498
Oy 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db TTGAGCCGAGTGGGCGAGCAGCTGTGCTTACCTGCTGCGACACAGTCTTTATCTT 558
Oy 499 TTGAGCCGAGTGGGCGAGCAGCTGTGCTTACCTGCTGCGACACAGTCTTTATCTT 558
Oy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db CTGGTGCCCCCAACGCTGTGCTTAC----- 582
Oy 559 CTGGTGCCCCCAACGCTGTGCTTAC----- 582
Oy 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db 582 ----- 582
Oy 201 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 582 ----- 582
Oy 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
Db 582 ----- 582
Oy 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyrAlaHisProGln 260
Db 583 ----- 598

```

```

Oy 260 YArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGln 280
Db 598 ----- 598
Oy 280 uGlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGln 300
Db 598 ----- 598
Oy 300 YArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPr 320
Db 598 ----- 598
Oy 320 oCysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLeuGlnGln 340
Db 599 ----- 603
Oy 340 nLeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLe 360
Db 604 TCTAAACCCCTCATCTCTACTCAGCANCCTCAGCCTTAAGTGAAGGCGGCGAGAGACT 663
Oy 360 uValGlnThrThrIlePheLeuGlySer 368
Db 664 GGTGGAGATCATCTTCTGGGCTCA 688

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RESULT 12

AA281296 389 bp mRNA linear EST 14-AUG-1997

z108g02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5', mRNA sequence.

AA281296 1 GI:1924194

AA281296.1 GI:1924194

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo.

1 (bases 1 to 389)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 2187 Std Error: 0.00

Seq primer: -28mb3 rev2 ET from Amersham

High quality sequence stop: 385.

Location/Qualifiers

1..389

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:712562"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_GCB1"

/note="vector: pT73D-Pac (pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI). Dr. David Allman (NCI) and Dr. Gerald Mari (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer

15'-GTTACCATCTGAAGTGGAGCGCGCCCTCATTTTCTTTTCTT-3'

] Double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:	3,83e-35	Length:	389
Score:	646.00	Matches:	127
Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	98.45%	Mismatches:	0
Query Match:	10.84%	Indels:	0
DB:	1	Gaps:	0

US-10-044-692-2 (1-1132) x AA281296 (1-389)

QY 542 AAlayPheleuHistrleuMetSerValTYValValGluLeuLeuArgSerPhePhe 561
 DB 1 GCCAACTTCTGACGCTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTGTGAGTGTG 60
 QY 562 TYValTYHThrThrThrPheGlnLYSAARGLeuPhePheTYArgLYSerValTTP 581
 DB 61 TATGTACGAGACGACGCTTTCAAAAGAACAGGCTTTTTCACCGAAGAGTGTCTG 120
 QY 582 SerLYLeuGlnSerLYLeuArgGlnHistrleuArgValGlnLeuArgGlnLeu 601
 DB 121 AGCAAGTGTCAAGACATGGATCAAGACACTTAAGAGGAGTGTGAGTGTGAGTGTG 180
 QY 602 SerGluAGluValArgGlnHistrleuArgGlnValArgProAlaLeuLeuThrSerArgLeu 621
 DB 181 TCGAAGACGAGGTCAGGACGATCGGAAAGCCAGCCGCTGTGAGTGTGAGTGTG 240
 QY 622 ArgPheLeuProLYSProArgGlyLeuArgProLYSValLeuMetAspTYValValGly 641
 DB 241 CGCTTACCTCCCAAGCCTGACGCGCTGCGCCATGTGTAACTGACATCACTGCTG 300
 QY 642 AAlayThrPheArgArgGluLYSArgAlaGluArgLeuThrSerArgValLYSAlaLeu 661
 DB 301 GCCAAGACGCTTCCGACAGAAAGAGGCGGACGCTGTCTACCTCGAGGAGTGTGAGTGTG 360
 QY 662 PheSerValLeuArgTYArgGlnValGlnValGlnValGlnValGlnValGlnVal 670
 DB 361 TTCAGCGCTGTCAACTACGAGCGGCG 387

RESULT 13
 BB618671
 LOCUS
 DEFINITION
 BB618671 RIKEN full-length enriched, 8 days embryo Mus musculus
 cDNA clone 5730412M20 5', mRNA sequence.
 BB618671
 ACCESSION
 BB618671.1 GI:16458173
 VERSION
 BB618671.1
 KEYWORDS
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 599)

REFERENCE
 AUTHORS
 Arakawa,T., Carrinci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
 Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
 Kono,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
 Ono,H., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
 Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Saitama-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
 Carrinci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)

FEATURES
 source
 location/Qualifiers
 1..599
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="5730412M20"
 /sex="mixed"
 /dev_stage="8 days embryo"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 8 days embryo"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCTCGAAGCTCTTTTCTTTTCTTTT 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rct = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGATCTCGAAGCTCTTTTCTTTTCTTTT 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda phage I. Cloning sites, 5' end: SalI, 3' end: BamHI."

ORIGIN
 Alignment Scores:

Pred. No.:	2.35e-32	Length:	599
Score:	610.00 <td>Matches:</td> <td>121 </td>	Matches:	121
Percent Similarity:	83.85% <td>Conservative:</td> <td>14 </td>	Conservative:	14
Best Local Similarity:	75.16% <td>Mismatches:</td> <td>26 </td>	Mismatches:	26
Query Match:	10.23% <td>Indels:</td> <td>0 </td>	Indels:	0
DB:	2 <td>Gaps:</td> <td>0 </td>	Gaps:	0

US-10-044-692-2 (1-1132) x BB618671 (1-599)

QY 1 MetProAlaArgAlaProArgCysArgAlaValArgSerLeuArgSerHistrArgGlu 20
 DB 115 ATGACCCGGGCTCTCTGTTGCCCCGGGGGCGCTCTCTGCGACGCGATACGGAGG 174
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
 DB 175 GTGTGCGCGTGGCACTTTGTGCGGCGCTGTGCGGCGCGAGGACAGGCGCTGTGCA 234
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValArgGlnCysLeuValCysValProTTP 60
 DB 235 CCGGGGAGCCCGAAGATCAACGCACTTTGTTGCCCAATGCTAGTGTGATGCACTGG 294
 QY 61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80

Db		295	GGCTCACAGCTCCACCTGCGCAGACTTTCCTTCCACCAAGGTATCCCTTAAGAAGCTG	354
Qy		81	VAlAaaRgVAlLeuGlARgLeuCysGIuaRglYAlaLyAsenValleuAlaphneCIy	100
Db		355	GTCGCCAGGGGTGTGCAGAGACTCTGCAGCGCAAAGAAACGTGTGGCTTTGGC	414
Qy		101	PheAlaleuLeuApBgLYAlARgLIgLYProBoGuAlaPheThrThSeraValArg	120
Db		415	TTTAGAGCTGCTTAACGAGGCGCAGAGGCGGGCTCCCATGCGCTTCACTAGTAGGGTGCT	474
Qy		121	SerTYLeuProAntHrValThAspAlaleuARgISerGIYAlATPrGIYleuDen	140
Db		475	AGCTAACCTTGCCCAACACTGTATTATGAGACCCTGCTGTCAATGTGTGATGATCTACTG	534
Qy		141	LeuARgARgAlGLIYAspAspValleuValHisleuLeuAlaArGYsaIAleuPheVal	160
Db		535	TTGAGCGGAGTGGGGGAGACGACTGTGTACTACGCTGAGCACACTGTGCTTTATCTT	594
Qy		161	Leu	161
Db		595	CTG	597
RESULT 14				
LOCUS	CN274427	409 bp	mRNA	linear EST 16-MAY-2004
DEFINITION	17000531326763 GRN_ES Homo sapiens CDNA 5', mRNA sequence.			
ACCESSION	CN274427			
VERSION	CN274427.1 GI:47290841			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 409) Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lekowski, J. and Stanton, L.M. Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R Regenerative Medicine Genon Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel.: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@genon.com Insert Length: 409 Std Error: 0.00.			
JOURNAL COMMENT	Location/Qualifiers			
FEATURES	source	1..409	/organism="Homo sapiens"	
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			/db_xref="taxon:9606"	
			/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"	
			/clone_lib="GRN ES"	
			/note="Oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p13), H7 (p25), and H9 (p26) maintained in feeder-free conditions"	
ORIGIN				
Alignment Scores:				
Pred. No.:	1,286-29	Length:	409	
Score:	567.00	Matches:	108	
Percent Similarity:	99.08%	Conservative:	0	
Best Local Similarity:	99.08%	Mismatches:	1	
Query Match:	9.51%	Indels:	0	
DB:	7	Gaps:	0	
US-10-044-692-2 (1-1132) x CN274427 (1-409)				
Qy	1 MecProAtgAlaProArgCyaaRgAlaValArgSerLeuLeuArgSerHisTyARgGlu	20		

Dn		82	ATGCGGGCCCTCCCGCTCCAGCCGTGCCTTGTGCGCAGCACTACCGGAG	141
Qy		21	VallueProLeuAalathrPheValArgArgLeuglyPProGlnIyTPdArgLeuValGln	40
Dn		142	GTCGTGCCGTGCACAGTTGTCGCGCGCCTTGAGGCCCAAGGAGCTGCGCTGTGCAG	201
Qy		41	ArgGLyAspProbaAlaApheargAlaleuValAlAGInCyseuValCysevalProTrp	60
Dn		202	CGCGGGACC CGG GGG GTT TCC GCG CCG CTG TGCC AGT GC CCAG TGC GTG TC GCG CCG	261
Qy		61	AspAlaArgProPProfoAlaAlaProSerPheArgSlnValSerCyseuLySGluLeu	80
Dn		262	GAGCGACGCGCCCCCGCCGCCCTCTTCCGCCAGGTGTCTGCTGAAGGACTG	321
Qy		81	ValAlaArgValleuglnArgLeuCyseGluArgLyAlaLysanValleuAaphely	100
Dn		322	GTCGCGCAGTGTCTGACAGAGCTGTGTGGAGCGCGCGAGAAGACGTGTGCTTGACG	381
Qy		101	PheAlaLeuLeuAspGlyAlaArgLy	109
Dn		382	TTCGCGCTGTGACGCGGCGCGCGG	408

RESULT 15

BE371943

LOCUS BE371943

DEFINITION 601217728F1 NCI CGAP Lu29 Mus musculus cDNA clone IMAGE:3586614 5', mRNA sequence.

ACCESSION BE371943

VERSION BE371943.1 GI:9317215

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 866)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
Plate: LHM6748 row: h column: 07
High quality sequence stop: 639.
Location/Qualifiers

FEATURES

Source

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Alignment Scores:

Pred. No.: 4,72e-29

Score: 566.00

Percent Similarity: 82.31%

Best Local Similarity: 73.47%

Query Match: 9.50%

Length: 866

Matches: 108

Conservative: 13

Mismatches: 26

Indels: 0

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QY      825 TyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCysSerLeu 844
      64 TATACCGACAGTCCAGGGGCAATCCCCCAAGGCTCCAGCTTATCCACCTGCTGTGCAAGTCTG 123
QY      845 CysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAspGlyLeuLeuLeu 864
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QY      865 ArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThrPheLeu 884
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QY      885 ArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgLysThrVal 904
      244 AGCACCTGGTCCATGGCGCTTCTGAGTATGATGATGATATAAATTGCAGAGACAGTGT 303
QY      905 ValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAla 924
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QY      925 HisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluValGlnSer 944
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Search completed: October 28, 2004, 15:17:31
 Job time : 7866 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2004, 10:30:52 ; Search time 7841 Seconds

(without alignments)
5260.780 Million cell updates/sec

Title: US-10-044-692-2

Perfect score: 5961

Sequence: 1 MPRAPRCRAVSLRSHYRE.....TALEMANPALPDPFKITLD 1132

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 segs, 1821965908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=EST -QFMT=fastp -SUFFIX=1st -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human0.cdi -LIST=45
-DOCALL=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=txt -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MAP -LARGEBUFFER -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :

EST:*
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2: gb_est2:*
3: gb_hic:*
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8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2168	36.4	1584	9	AY407350
3	1805	30.3	1835	9	AY407351
4	1406	23.6	925	4	BM453198
5	1028	17.2	851	5	BU702370
6	875	14.7	851	4	BC917907
7	776	13.0	492	4	BM624748
8	771.5	12.9	664	5	BO258274
9	682	11.4	1424	3	CR688161

10	667.5	11.2	649	7	CF531069	CF531069	UI-M-FY0-
11	666.5	11.2	688	7	CF531121	CF531121	UI-M-FY0-
12	646	10.8	389	1	AA281296	AA281296	UI-M-FY0-
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23	449.5	7.5	632	6	CA353864	CA353864	625469 NC
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25	437	7.3	703	5	BE531258	BE531258	BE531258
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ALIGNMENTS

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DEFINITION
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ACCESSION
AY407349.1 GI:39763320
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 1826)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
AUTHORS
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity:	86.66%	Mismatches:	81
Query Match:	44.37%	Indels:	0
DB:	9	Gaps:	0

US-10-044-692-2 (1-1132) x AY407349 (1-1826)

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QY      586 SerIlyGlyIleArgGlnHISleuIysArgValGlnLeuArgGlnLeuSerGlnAlaGlu 605
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QY      866 LeuValAspAspPheLeuLeuValThrProHISLeuThrHISAlaIlySerPheLeuArg 885
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QY      926 GlyLeuPheProTyrCyGlyLeuLeuLeuAspThrArgThrLeuGlnValGlnSerAsp 945
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genomic survey sequence.
AY407350 GI:39763321
GSS.
Pan troglodytes (chimpanzee)
SOURCE
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
1 (bases 1 to 1584)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1584)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment
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QY 966 AlaGlyArgAsnMetArgArgLysLeuPheGlyValIleuArgLeuLysGlyHisSerLeu 985
DB 1323 GCTGGAGAGAAATGCGTGCAGAACTTTTGGAGTCTTGGCTGAAGTCAAGCTCG 1382
QY 986 PheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyrLysIleLeu 1005
DB 1383 TTTCGTGATTTCAAGTGAACAGCTTCAGAGAGGTGTGACCAACATCAANNATTCCTC 1442
QY 1006 LeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHisGlnGlnVal 1025
DB 1443 CTGCTGACAGGCTACAGGTTTACCGATGTGTGCTGACAGCTCCCATTTATCAGCAAGTT 1502

QY 1026 TrpLysAspProThrPhePheLeuArgValIleSerAspThrAlaSerLeuCysTyrSer 1045
DB 1503 TGGAAAGACCCCACTTTTCCGCGCATCATCTGACACGGCCCTCCCTCTACTCC 1562
QY 1046 IleLeuLysAlaLysAla 1052
DB 1563 ATCTGAAAGCCAAAGACCA 1583
RESULT 3
AY407351
LOCUS AY407351 1835 bp DNA linear GSS 15-DEC-2003
DEFINITION Mus musculus TERT gene, VIRTUAL TRANSCRIPT, partial sequence,
AY407351
ACCESSION AY407351
VERSION AY407351.1 GI:39763322
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1835)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniatsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1835)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sniatsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
1..1835
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1835
/gene="TERT"
/locus_tag="HCM2861"
ORIGIN
Alignment Scores:
Pred. No.: 1.17e-114 Length: 1835
Score: 1805.00 Matches: 373
Percent Similarity: 69.56% Conservative: 52
Best Local Similarity: 61.05% Mismatches: 176
Query Match: 30.28% Indels: 11
DB: 9 Gaps: 3
US-10-044-692-2 (1-1132) x AY407351 (1-1835)
QY 529 ValProAlaAlaGluHisArgLeuArgGluGluIleLeuAlaLysPheLeuHisTrpLeu 548
DB 12 GTCCCGCGTCAGAGACCGCTCTGAGGAGAGAGATCTGGCTACGTTCTCTGGCTGG 71
QY 549 MetSerValTyrValValGluLeuLeuArgSerPhePheTyrValThrGluThrThrPhe 568
DB 72 ATGGACATACCTGCTTACAGCTCTTACGTCATTTTACATCAACAGAGCACCATTTC 131
QY 569 GlnTyrAsnArgLeuPhePheTyrArgLysSerValTrpSerLysLeuGlnSerIleGly 588
DB 122 CAGAGAAACAGGCTCTTCTTACCGTAAAGAGTGGTGAGCAGAGTGCAGAGCATTGGA 191
QY 589 IleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGluAlaGluValArgGln 608

DB 192 GTACAGCAACACCTTGAGAGAGTGGCGCTACAGGAGCTGTACAGAGAGAGTCCAGCAT 251
QY 609 HisArgGluAlaArgProAlaLeuLeuThrSerArgLeuArgPheIleProLysProLys 628
DB 252 CACACAGAACCTGGCTAGCGCCATCTGCACATCGCGCTTATCCCAAGCCCAAC 311
QY 629 GlyLeuArgProIleValAsnMetAspTyrValValGlyAlaArgThrPheArgGlu 648
DB 312 GGCCTGGCGCCATTGTGATGATGAGTTTATGACATGGTATCCAGAGCTTTGGCCAGAG 371
QY 649 Lys-ArgAlaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeuAsnTyrG 668
DB 372 AAGCAGGGCCGACATTCACCCAGCGTCTCAAGACTCTCTTACAGATGCTCAACTATGA 431
QY 668 ValArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGlyLeuAspAspIleHisAr 688
DB 432 GCGACAAACATCTTCACCTTATGGGCTTCTGTACTGGGTATGATGACATCTTACG 491
QY 688 GAlATrPArGThrPheValIleuArgValArgAlaGlnAspProProGluLeuTyrPh 708
DB 492 GACCTGGCGGCTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
QY 708 eValLysValaLysValThrGlyAlaTyrAspThrIleProGlnAspArgLeuThrGluVa 728
DB 552 TGTAAAGNN 611
QY 728 IleAlaSerIleIleLysProGlnAsnThrTyrCysValaArgArgTyrAlaValaGl 748
DB 612 NNN 671
QY 748 nLysAlaAlaHisGlyHisValaArgLysAlaPheLysSerHisValSerThrLeuThrAs 768
DB 672 NNN 731
QY 768 PleuGlnProTyrMetArgGlnPheValAlaHisLeuGlnGluThr-----SerProLe 786
DB 732 CCTCAGACATACATGAGGAGCGATTCCTTAAGATCTGACAGATTCAGATGACAGTGCAC 791
QY 786 ValArgAspAlaValValIleGluGlnSerSerSerLeuAsnGluAlaSerSerGlyLeuPh 806
DB 792 GAGGAATCTCGTTGTATCATGACAGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 851
QY 806 eAspValPheLeuArgPheMetCysHisHisAlaValaArgLysSerTyrVa 826
DB 852 NNN 911
QY 826 LglnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeuLeuCysSerLeuCysTyr 846
DB 912 GCAGTGCAGAGGATCCCCCAGGCGCTCCAGCTTACCACTGCTCAGCTGTGTGTTT 971
QY 846 rGlyAspMetGluAsnLysLysPheAlaGlyIleArgArgAspGlyLeuLeuArgLe 866
DB 972 CAGAGACATGGAGAACAGAGCTGTGTGCTGAGAGGAGGAGGTGGCTTTTACGTTT 1031
QY 866 uValaAspAspPheLeuLeuValThrProHisLeuThrHisAlaLysThrPheLeuArgTh 886
DB 1032 TGTGATGACTTCTGTGTGTGAGCGCTCAGTTGACCAAGCAAAACCTTCTCAGAC 1091
QY 886 rLeuValaArgGlyValaProGluTyrGlyCysValaValaLeuArgLysThrValaLys 906
DB 1092 CCTGTGTACATGCGCTTCTGTGATGAGGTGATGATGAACCTTGCAAGAGACAGTGTGAA 1151
QY 906 nPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAlaHisG 926
DB 1152 CTTCCTGTGAGCTGTGTACCTGGGTGGTGGACCTCAATACAGAGCTGCTCAGCT 1211
QY 926 yLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluValaGlnSerAspTyr 946
DB 1212 CCGTTTCCCTGGGTGTGGCTTGTGCTGCTGACACCTCAAGCTTTGGAGGTGTTCTGACTA 1271
QY 946 rSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPheLysAl 966

BU702370 851 bp mRNA linear EST 15-JUL-2003
 LOCUS UI-M-FIO-byx-f-12-0-UI-r1 NIH BMAP_F10 Mus musculus cDNA clone
 DEFINITION IMAGE:6400523 5', mRNA sequence.
 ACCESSION BU702370
 VERSION BU702370.1 GI:23627105
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 851)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seg primer: pyx-5.
 Location/Qualifiers
 1. 851
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6400523"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5dpc"
 /lab_host="D10B (T1 phage resistant)"
 /clone_lib="NIH BMAP F10"
 /note="Organ: Brain; Vector: pyx-Asc; Site 1: Ecor I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with NotI and then cloned
 directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CAGCCACGAC. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemm Chiu, Ph.D.,
 program coordinator."

ORIGIN

Alignment Scores:
 Pred. No.: 3,6e-61 Length: 851
 Score: 1028.00 Matches: 197
 Percent Similarity: 80.85% Conservative: 31
 Best Local Similarity: 69.86% Mismatches: 52
 Query Match: 17.25% Indels: 2
 DB: 5 Gaps: 1

US-10-044-692-2 (1-1132) x BU702370 (1-851)

QY 738 ThrTTCyGValAArgTyrAlaValAlaGlnlyAlaAlaHisGlyHisValArglys 757
 Db 6 ACGTACTGATGATCCGAGTGAAGTGGCCGAGAGATGACCAAGGCCAAATGCCAAG 65
 QY 758 AlaPheLysSerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheVal 777
 Db 66 TCCTTTAGAGACAGGTCAACCCCTCTGTGACCTCCAGCCATACATGGCCAGTTCTT 125

QY 778 AlaHisLeuGlnGluThr-----SerProLeuArgAspAlaValAlaIleGlnGlnSer 795
 Db 126 AAGCATCTGCAGAGATTTCAGATCCAGTGCAGAGAACTCCGTTGTATTCAGACAGAGC 185
 QY 796 SerSerLeuArgGlnAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHis 815
 Db 186 ATCTCTATGAATGAGAGACAGCAGCCGTTGTGACTTCTCCTCAGACTTCTGCGCTCAC 245
 QY 816 HisAlaValArgIleArgGlyIleSerSerTyrValGlnCysGlnGlyIleProGlnIleSer 835
 Db 246 AGTGTGCTGAAGATTTGTCAGACAGTGTATACCGCAGTGCAGAGGATCCCGAGGCTCC 305
 QY 836 IleLeuSerThrLeuLeuLeuCysSerLeuCysTyrGlyAspMetGluAlaHisLeuPheAla 855
 Db 306 ACCCTATCCACCCTGCTGCTGAGTGTGTGTTTCGAGACATGAGAACAGCTGTTGCT 365
 QY 856 GlyIleAlaArgArgAspGlyLeuLeuLeuArgLeuValAspAspPheLeuValThrPro 875
 Db 366 GAGGTGCAGCCGGGAAATGGTGTCTTTACGTTTGTGTGATGACTTCTGTGTGACGCT 425
 QY 876 HisLeuThrHisAlaIleThrPheLeuArgThrLeuValArgGlyValProGlnIleArg 895
 Db 426 CACTTGACCAACGAAACAAACCTTCTCAGACACCTGTCATGCGCTTCTGAGATGAG 485
 QY 896 CysValAlaAsnLeuArgLysThrValAlaAsnProValGluAspGluAlaLeuGly 915
 Db 486 TGCATGATAAACTTCGACAGACAGTGGTGAACCTCCGTGGACCTGGTACCTGGGT 545
 QY 916 GlyThrAlaPheValAlaGlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeu 935
 Db 546 GGTGACGCTCCATACACAGTGCCTGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTG 605
 QY 936 AspThrArgThrLeuGluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArg 955
 Db 606 GACATCTCAGACTTTCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665
 QY 956 AlaSerLeuThrPheAsnArgLysGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPhe 975
 Db 666 ACGACCTTCACCTTCACAGATGTCCTTCANAGCTGGAGACCATCGGAACANCGCTCTG 725
 QY 976 GlyValIleuArgLeuLysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGln 995
 Db 726 TCGGTCTTGGCGGTGAAGTGCACGCTATTTCTTACGCTTGCAGAGTAAACAGCTCCAG 785
 QY 996 ThrValCysThrAsnIleTyrIleLeuLeuLeuGlnAlaTyrArgPheHisIleCys 1015
 Db 786 ACGTCTGCATCAATATATACAGATCTTCTGCTTCANCGCTACAGGTTCCATCATGT 845
 QY 1016 ValIleu 1017
 Db 846 GTGATT 851

RESULT 6

BG917907 851 bp mRNA linear EST 05-JUN-2001
 LOCUS 602820830F1 NCI CGAP Mam6 Mus musculus cDNA clone IMAGE:494987 5',
 DEFINITION mRNA sequence.
 ACCESSION BG917907
 VERSION BG917907.1 GI:14298383
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 851)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DB: 4 Gaps: 0

US-10-044-692-2 (1-1132) x BQ258274 (1-492)

QY 905 ValAsnProValGluAspGluAlaLeuGlyThrAlaPheValGlnMetProAla 924
 Db 1 GTGAACCTCTCTGTAAAGACAGAGCCCTGGGGGACGGCTTTGTTTCAGATGCCGCC 60
 QY 925 HisGlyLeuPheProTyrCysGlyLeuLeuAspThrArgThrLeuGluValGlnSer 944
 Db 61 CACGGCTATTCCTCCGTGGGGCTGCTGCTGATACCCGAGCCCTGGAGGTGCAGAGC 120
 QY 945 AspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPheAsnArgGlyPhe 964
 Db 121 GACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCACTTCAACCGCGCTTC 180
 QY 965 LysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeuLysCysHisSer 984
 Db 181 AAGGCTGGAGGAGACATGCTCCGAACTCTTGGGGCTCTGGGCTGAAGTGCACAGC 240
 QY 985 LeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsnIleTyrLysIle 1004
 Db 241 CTGTTCTGATTTGGAGGTGAACAGCTCCAGAGCTGTGCACCAACTTCAAGATC 300
 QY 1005 LeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuProPheHisGln 1024
 Db 301 CTCCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGTGCTGAGCTCCCATTTTATCAGCA 360
 QY 1025 ValTyrPheAsnProThrPhePheLeuArgValIleSerAspThrAlaSerLeuCysTyr 1044
 Db 361 GTTTGGAAGAACCCCAATTTTCTGCGGTATCTGTGACAGCGGCTCCCTGCTAC 420
 QY 1045 SerIleLeuLysAlaLysAsnAla 1052
 Db 421 TCCATCCTGAAGCCAGAAAGCA 444

RESULT 8

BQ258274 664 bp mRNA linear EST 06-MAY-2002

LOCUS NISC_Kp11g04.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone

DEFINITION IMAGE:5409222, mRNA sequence.

ACCESSION BQ258274

VERSION BQ258274.1 GI:20459030

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 664) NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

TITLE Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: csgbbs-remail.nih.gov

cDNA Library Preparation: J. Baker (Stanford University)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CCAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

info@image.lnl.gov

MGI:1845958

Plate: LLM12043 row: N column: 7

Seq primer: SP6 primer:

Location/Qualifiers

1..664

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CD-1"

/db_xref="taxon:10090"

/clone="IMAGE:5409222"

/tissue_type="embryo, late gastrula"

ORIGIN

Alignment Scores:
 Pred. No.: 1.65e-43 Length: 664
 Score: 771.50 Matches: 153
 Percent Similarity: 72.03% Conservative: 17
 Best Local Similarity: 64.83% Mismatches: 45
 Query Match: 12.94% Indels: 21
 DB: 5 Gaps: 2

US-10-044-692-2 (1-1132) x BQ258274 (1-664)

QY 352 ProSerLeuThrGlyValArgArgLeuValGluThrIlePheLeuGlySerArgProTyr 371

Db 10 CCTAATGACTGGGCGCAGAGACTGGTGAATCACTTTCTGGGCTCAAGGCTTAG 69

QY 372 MetProGlyThrProArgArgLeuProArgLeuProGlnArgTyrTyrGlnMetArgPro 391

Db 70 ACATGAGACCACTCTGACAGACACACGCTTACGCTGATCTGAGTACGAGATGCGGCC 129

QY 392 LeuPheLeuGluLeuLeuGlyValAsnHisAlaGlnCysProTyrGlyValLeuLeuLysThr 411

Db 130 CTGTTCCAAAGCTGCTGTGTGAACCATGACAGAGGCAATATGTCAAGACTCTCAGGTCA 189

QY 412 HisCysProLeuArgAlaAla-----ValThrProAlaAlaGlyValCysAlaArg 428

Db 190 CATTGACAGTTTCGACAGCAACCAACAGGTGACAGTGCCTTG----- 234

QY 428 GlnLysProGlnGlySerValAlaAlaProGluGluGluAspThrAspProArgArgLeu 448

Db 235 -----AACACCAGCCACCGCACTC 255

QY 448 ValGlnLeuLeuArgGlnHisSerSerProTyrGlnValTyrGlyPheValArgAlaCys 468

Db 256 ATGGAATTTGCTCGCTGCTGACAGCATGCTCCCTGAGGATATGTTTCTTCGGGCGCTGT 315

QY 468 LeuArgArgLeuValProProGlyLeuTyrGlySerArgHisAsnGluArgArgPheLeu 488

Db 316 CTCTGCAAGGTGTGTGCTAGTCTCTGGGGTACCAAGCAACATGACGCGCTTCTTT 375

QY 488 ArgAsnThrLysLeuPheIleSerLeuGlyLysHisAlaLysLeuSerLeuGlnGluLeu 508

Db 376 AAGAACTTAAAGATTCATCTGTTGGGAAATACGGCAAGCTATCTCGAGAACTG 435

QY 509 ThrTyrLeuMetSerValArgAspCysAlaTyrLeuArgArgSerProGlyValGlyCys 528

Db 436 ATGTGGAAGATGAAGATAGAGATTCACCTGCTCCGAGAGCCAGGAGAGACCGT 495

QY 529 ValProAlaAlaGluHisArgLeuArgGluGluIleLeuAlaLysPheLeuHisTyrLeu 548

Db 496 GTCCCGCTGACAGACCGCTGAGGAGAGAGATCTGCTACGTTCTGTGTGGCTG 555

QY 549 MetSerValTyrValValGluLeuLeuArgSerPhePheTyrValThrGluThrPhe 568

Db 556 ATGACACATACGTGTACAGCTGCTTACGTCATTTTATCATCATCAGAGACATTC 615

QY 569 GlnLysAsnArgLeuPhePheTyrArgLysSerValTyrSerLysLeu 584

Db 616 CAGAGAACAGGCTCTTCTTACCGTTAAGAGTGTGAGCAAGCTG 663

RESULT 9

CR688161

LOCUS

DEFINITION

Tetradon nigroviridis full-length cDNA.

1424 bp

mRNA

linear

HTC 12-AUG-2004

ACCESSION CR688161
 VERSION CR688161.1
 KEYWORDS GI:51186068
 SOURCE HTC: CDNA; full-length; Tetraodon nigroviridis.
 ORGANISM Tetraodon
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae.
 1 (bases 1 to 1424)
 REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -
 JOURNAL (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT The sequences are based on single pass reads.
 More information available at
 http://www.genoscope.cns.fr/tetraodon.
 FEATURES
 source
 1..1424
 /organism="Tetraodon"
 /mol_type="mRNA"
 /db_xref="taxon:47144"
 /tissue_type="Eyes"
 ORIGIN
 Alignment Scores:
 Pred. No.: 8,77e-37 Length: 1424
 Score: 682.00 Matches: 155
 Percent Similarity: 58.36% Conservative: 51
 Best Local Similarity: 43.91% Mismatches: 140
 Query Match: 11.44% Indels: 8
 DB: 3 Gaps: 3
 US-10-044-692-2 (1-1132) x CR688161 (1-1424)

Db 561 ACTTTAGCCCCCTGCTGCTGACAGCAAAATGAGAGAACTAT-GGC---TTC 616
 Qy ArgLeuysCyShiSerLeuPheLeuaspLeuValaLanSerLeuThirValCys 998
 Db 617 AGACTGAAGTGCATGCTTTGTTGATCTTAAGACCACTCTTGGAACTCTAT 676
 Qy 999 ThrAniLeTyrIleLeuLeuLeuValaTyrArgPheHisaCysValLeuGln 1018
 Db 677 AAGATATCTCAAAATTAATCTGCTTCAAGCATGAGTTCCATGTGTGCTCAGGT 736
 Qy 1019 LeuProPheHisaGlnValTTrpLysAnProThrPhePheLeuArgValIleSerasp 1038
 Db 737 CTGCCCCCTTGGTCAGACTGTTGCTTAAGAACCCAGCATCTTCTGATATAGGAT 796
 Qy 1039 ThrAlaSerLeuCyTyrSerIleLeuLysAlaLysAnAlaGlyMetSerLeuGlyAla 1058
 Db 797 ATGGCTGAGTACCAATCATCTGCTCAGGCTCAGCAACAT-----GGCACT 844
 Qy 1059 LysGlyAlaAlaGlyProLeuProSerGlnAlaValaGlnTrpLeu-CysHisaGlnAlaP 1078
 Db 845 AAAGCTCAGACTGCTGCTGTGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
 Qy 1078 eleuLeuLysLeuThrArgHisaGlnValTTrpValProLeuLeuGlySerLeuArgTh 1098
 Db 905 CTTCCTGCTGCTGTCCAAACATCGACGTCTATTAAGATGCTGCCACACTGCMAA 964
 Qy 1098 rAlaGlnThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuAla 1118
 Db 965 ACGGAGGCGCAGTTTAAAGCAGGCGCTGAGAGACTGAGGTTGGCCAGAGTCCAGAGC 1024
 Qy 1118 aAlaAnProAlaLeuProSerAspPheLysThrIle 1130
 Db 1025 TGCTCAGCCAGAGAGCCAGTGCATTTTGGCAATT 1061
 RESULT 10
 CFS31069 649 bp mRNA linear EST 12-SEP-2003
 LOCUS UI-M-FY0-GSP-C-19-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 DEFINITION IMAGE:30355746 5', mRNA sequence.
 ACCESSION CFS31069
 VERSION CFS31069.1 GI:34583033
 KEYWORDS
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 649)
 REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mouse1.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.
 FEATURES
 source
 1..649
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30355746"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: Bcor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Bcor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	2,69e-36	Length:	649
Score:	667.50	Matches:	153
Percent Similarity:	46.32%	Conservative:	17
Best Local Similarity:	41.69%	Mismatches:	32
Query Match:	11.20%	Indels:	165
DB:	7	Gaps:	3

US-10-044-692-2 (1-1132) x CF531069 (1-649)

```

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgIu 20
DB 42 ATGACCCGGGCTCTGTTGCCCCGGGGGCGCTCTCTGCGACGAGTACCAGGAG 101
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
DB 102 GGTGGCGCGCTGGCAACCTTTGGCGCGCGCTGGCGCGCGAGGAGGAGGGGCTGTGGCA 161
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 162 CCGGGGACCCAGAGATCAACCGCACTTGTGCGCAATGCTACTGTGCACTGCACTGG 221
QY 61 AspAlaArgProProAlaAlaPheArgPheArgGlnValSerCysAspLeuArgIu 80
DB 222 GGCTCAGACCTCCACCTCCGACCTTCTTCCACCAAGTGTCTCCTGAAAGACTG 281
QY 81 ValAlaArgValLeuGlnArgLeuGlyCysGlnArgGlyValAlaLysValLeuAlaPheGly 100
DB 282 GTGGCCAGGTTGTGTGAGAGACTCTGCGAGCGCAAGAGAAACGTGCTGGCTTTGGC 341
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrHisSerValArg 120
DB 342 TTGAGCTCTTAACGAGCCAGAGCGGGGCGCTCCCATGCGCTTCACTGTGCGCGT 401
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTyrGlyLeuLeu 140
DB 402 AGCTACTTCCCAACACTGTATTGAGACCTGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 461
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 462 TTGAGCGGAGTGGGCGAGCACTGTGTGTCTACTGCTGTGCACTGTCTCTTATCTT 521
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 522 CTGGTGGCCCCCAGCGTGTGCTTAC----- 545
QY 181 AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
DB 545 ----- 545
QY 201 ArgAlaTyrPAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 545 ----- 545
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240

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DB 545 ----- 545
QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
DB 546 ----- 557
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGln 280
DB 557 ----- 557
QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 557 ----- 557
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
DB 558 ----- 569
QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
DB 569 ----- 569
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 570 ----- 626
QY 361 ValGlnThrHisPheLeuGly 367
DB 627 GTGGAGATCATCTTTGTGGGC 647

```

RESULT 11

CF531121 688 bp mRNA linear EST 12-SEP-2003
 UI-M-FY0-GSP-M-21-0-UI-rl NIH_BMAP_FY0 Mus musculus cDNA clone
 IMAGE:3035598 5', mRNA sequence.

DEFINITION

LOCUS

CF531121

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgi.mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1998)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousef1.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seg primer: pYX-5.
 Location/Qualifiers
 1. 688
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:3035598"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (TI phage resistant)"
 /clone_lib="NIH BMAP FY0"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: Bcor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pX-vec vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGCAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	3,456-36	Length:	688
Score:	666.50	Matches:	154
Percent Similarity:	46.34%	Conservative:	17
Best Local Similarity:	41.73%	Mismatches:	32
Query Match:	11.18%	Indels:	166
	7	Gaps:	2

US-10-044-692-2 (1-1132) x CF531121 (1-688)

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OY 1 MetProArgAlaProArgCysAlaValArgSerLeuArgSerHisTyraArgGlu 20
DB ATGACCCGGGCTCTGTTGCCCGGGTGGCGCTCTGCTGCGCAGCCGATACCGGGAG 138

OY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPheLeuValGln 40
DB GTGTGGCGCGTGGCAACCTTTGTGGCGCGCTGGGGCCGAGGGCAGGGCGCTTGGCAA 198

OY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB CCGGGGAGCCCAAGATCTACCGCACTTTGTTGCCCATGCTTACTGATGCACTGG 258

OY 61 AspaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
DB GGGCTACAGCTCCACCTGCTGCTTCTTCCACAGATGTCTCATCTCGAAGAGCTG 318

OY 81 ValAlaArgValLeuGlnArgLeuGlyGlyValAlaValAsnValLeuAlaPheGly 100
DB GTGGCGAGGGTGTGGAGACTGTGGCGGCAAGAGAAACCTGTGCTTTTGGC 378

OY 101 PheAlaLeuAspGlyValArgGlyProProGlnAlaPheThrThrSerValArg 120
DB TTTGAGCTGCTTACAGAGCCAGAGCGGCGCTCCCATGSCCTTCACTGATGCGTGC 438

OY 121 SerTyrLeuProAsnThrValThrAspaLeuArgGlySerGlyAlaTyrPheLeuLeu 140
DB AGCTACTTGGCCCAACCTGTATTGTAGACCTGCGGTGTCAGTGGTGCATGCTACTG 498

OY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB TTGAGACCGAGTGGGCGACACCTGCTGCTACTGCTGCGACACTGTCTTATATCT 558

OY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB CTGGTGGCCCGCCACGCTGCTCTAC----- 582

OY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
DB 582 ----- 582

OY 201 ArgAlaTyrPheAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 582 ----- 582

OY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 582 ----- 582

OY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyr-AlaHisProGln 260
DB 583 ----- 598
CAGGGGAGATGGCCAN-----

```

```

OY 260 YArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGln 280
DB 598 ----- 598

OY 280 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGln 300
DB 598 ----- 598

OY 300 YArgGlnHisAlaGlyProProSerThrSerArgProProAlaProTyrPheThrPr 320
DB 598 ----- 598

OY 320 OCysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLeuGlnGln 340
DB 599 ----- 603.
GAGCG

OY 340 nLeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLe 360
DB 604 TCTAAACCCCTCATCTCTACTCAGCANCCTCAGCCTTACTGACTGGGCGCAGAGACT 663

OY 360 nValGlnThrIlePheLeuGlySer 368
DB 664 GTGGAGATCATCTTTCTGGGCTCA 688

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RESULT 12

AA281296 389 bp mRNA linear EST 14-AUG-1997
 z108902.r1 NCI_GCAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5',
 mRNA sequence.

AA281296.1 GI:1924194
 EST.

VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 389)
 NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL
 COMMENT
 Email: cgaps-remail.nih.gov

This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 2187 Std Error: 0.00

Seq primer: -28m13 rev2 ET from Amersham
 High quality sequence stop: 385.
 Location/Qualifiers

FEATURES

source

1.389
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:712562"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /clone_lib="NCI_GCAP_GCB1"
 /note="Vector: pT73D-Pac (pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI). Dr. David Altman
 (NCI) and Dr. Gerald Matli (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 15'-TGTACCAATCTGAAGTGGAGCGCGCGCTCATTTTCTTTTCTT-3'
 1. Double-stranded cDNA was ligated to Eco RI adaptors
 (pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Db 295 GGCCTCAGACCTCCACCTGCGACCTTTCCTTCACACAGGTGTCACTCCCTGAAGAGCTG 354
.....
Qy 81 ValAlaArgValLeuGlnArgLeuGlyGlyValAlaValAsnValLeuAlaHeGly 100
.....
Db 355 GTGGCCAGGGTGTGTGACAGACTGTGCGAGCGCAACGAGAAACGTGTGCTTTTGGC 414
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Qy 101 PheAlaLeuLeuAspGlyValaArgGlyGlyProGluAlaPheThrThrSerValArg 120
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Db 415 TTTGAGCTGCTTAACGAGCGCCAGAGCGGCGCTCCCATGCGCTTCACTAGTACGCTGCT 474
.....
Qy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeu 140
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Db 475 AGCTACTTGCACACACTGTATTGAGACCTGCGGTGTCAGTGTGATGATGCTACTG 534
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Qy 141 LeuAlaArgValGlyAlaAspValLeuValHisLeuLeuAlaArgGlyAlaLeuPheVal 160
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Db 535 TTGACCCAGATGGGGGAGCACTGCTGTCTACTGCTGGCACACTGTCTTATCTT 594
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Qy 161 Leu 161
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Db 595 CTG 597
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RESULT 14
CN274427 409 bp mRNA linear EST 16-MAY-2004
LOCUS 17000531326763 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN274427.1 GI:47290841
VERSION CN274427.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 409)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 409 Std Error: 0.00.
Location/Qualifiers
FEATURES
source 1..409
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_lib="GRN_ES"
/note="Oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

Db 82 ATGCCGCGCGCTCCCGCTGCGAGCCCTGCGCTCCCTGCGCGAGCAGCTACCGCGAG 141
.....
Qy 21 ValLeuProLeuAlaThrPheValaArgArgLeuGlyProGlnGlyTrrArgLeuValGln 40
.....
Db 142 GTGGCTCCGCTGGCCACCTTGTGTGGGGCTGGGGGCCCAAGGGGTGGCGGCTGGGACG 201
.....
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValaGlnCysLeuValCysValProTrp 60
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Db 202 CCGGGGACCCGGCGGCTTTCCGCGCGCTGTGGCCAGTGCCTGTGTGGCTGCGCTG 261
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Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGlyLeu 80
.....
Db 262 GACGACAGCGCGCGCGCGCGCGCGCGCTTCCTCCGCGAGGTCTCTGCTGAAGAGCTG 321
.....
Qy 81 ValAlaArgValLeuGlnArgLeuGlyGlyValAlaValAsnValLeuAlaHeGly 100
.....
Db 322 GTGGCCAGATGTCTGCAAGGCTGTGCGAGCGCGCGGGAAGAGTCTGCTTCAAGC 381
.....
Qy 101 PheAlaLeuLeuAspGlyValaArgGly 109
.....
Db 382 TTGCGCTGTGAGCGGGCGCGCGG 408
.....
RESULT 15
BE371943 866 bp mRNA linear EST 21-JUL-2000
LOCUS 601217728P1_NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586614 5',
DERIVATION mRNA sequence.
ACCESSION BE371943
VERSION BE371943.1 GI:9317215
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 866)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
UNPUBLISHED (1999)
COMMENT Contract: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LILAM8748 row: h column: 07
High quality sequence stop: 639.
Location/Qualifiers
FEATURES
source 1..866
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="3586614"
/tissue_type="spontaneous tumor, metastatic to mammary.
stem cell origin."
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Alignment Scores:
Pred. No.: 1 286-29 Length: 409
Score: 567.00 Matches: 108
Percent Similarity: 99.08% Conservative: 0
Best Local Similarity: 99.08% Mismatches: 1
Query Match: 9.51% Indels: 0
Gaps: 0
US-10-044-692-2 (1-1132) x CN274427 (1-409)

ORIGIN
Alignment Scores:
Pred. No.: 4 726-29 Length: 866
Score: 566.00 Matches: 108
Percent Similarity: 82.31% Conservative: 13
Best Local Similarity: 73.47% Mismatches: 26
Query Match: 9.50% Indels: 0

Qy 1 MetProArgAlaProArgCysArgAlaValaArgSerLeuArgSerHisTyrArgIlu 20


```

VERSION      BT452535.1  GI:25941846
KEYWORDS     EST.
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE    1 (bases 1 to 753)
              Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
              Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.U.
              A Comprehensive Collection of Chicken cDNAs
              Curr. Biol. 12 (22), 1965-1969 (2002)
AUTHORS      12445392
              22335534
              12445392
TITLE        Contact: Simon Hubbard
              Department of Biomolecular Sciences
              University of Manchester Institute of Science and Technology
              (UMIST)
JOURNAL      PO Box 88, Manchester, M60 10D, UK
MEDLINE      Tel: 01612008930
              Fax: 01612360409
PUBMED       Email: Simon.Hubbard@umist.ac.uk.

FEATURES
    source
        1..753
            location/Qualifiers
            ..
            /organism="Gallus gallus"
            /mol_type="mRNA"
            /strain="Layer"
            /db_xref="taxon:9031"
            /clone="CHEST696F7"
            /sex="Female"
            /dev_stage="adult"
            /lab_host="DH10B"
            /clone_idb="CSEQRBN14"
            /note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
            EcorI; Site_2: NotI; This normalized library was
            constructed from 1 million independent clones. cDNA
            synthesis was initiated using an oligo(dT) primer, using
            methylated C in the first strand synthesis reaction.
            Following this first strand reaction, double-stranded cDNA
            was bluntend, ligated to NotI adapters, digested with
            EcorI, size-selected, and cloned into the NotI and EcorI
            compatible sites of a custom modified MCS of the
            pBluescript (KS+) vector. The library was normalized in 2
            rounds using conditions adapted from Soares et al., PNAS
            (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
            (1996): 791, except that a significantly longer
            reannealing hybridization was used."

ORIGIN
Alignment Scores:
Pred. No.:      1,34e-25      length:      753
Score:          515.00      Matches:      100
Percent Similarity: 74.55%      Conservative: 23
Best Local Similarity: 60.61%      Mismatches:  42
Query Match:    8.64%      Indels:      0
DB:              Gaps:      0

US-10-044-692-2 (1-1132) x BU452535 (1-753)
Qy      968  ArgAsnMetAArgIyIsleuphegiValleuAglueLyCySHISerleupheleu 987
          :::::::::::
Db      5  AAAAACAATGAATGCAAAATGACTGACGCTCCAAACTGAATGCCATCTTACTCTT 64
          :::::::::::
Qy      988  AspleugInValasnsSerleuGlnThrValCySThrAsnIleTyTlyIsIleuenuleu 1007
          :::::::::::
Db      65  GACTTAAAGATCAACAGCCTTCAGACAGTTCCTTAATTAACATCTACCAAGATATTTTACTT 124
          :::::::::::
Qy      1008  GAlAlATyArGrpPheHisAlaCySValleuGlnleuProPheHisGlnGlnValATrpIys 1027
          :::::::::::
Db      125  CAGGCTTACGGTTCATGCGCTGTGTCTTCAGCTTCATTCACACAGAAAGTTAGAAAT 184
          :::::::::::
Qy      1028  AsnProThrPhePheleuA-gValIIIsersAspThrAlaSerleuCySfIyIserIleu 104
          :::::::::::

```

Db	185	AATCTGATTTCCTTCTTAAGATCATCTCTGTACTACCTGTTCACTGCTATTATTCCTG	244
Oy	1048	LYSALAALYSASPAALAGIYwEtsErleuglYalalyglYlaIAAIGlyProleuProser	1067
Db	245	AAAGCTAAAATAATCCAGAGATTTCCTTAGTGACCAAGAATGATCTGGATGTCCTCCTTTT	304
Oy	1068	GUAlaIVaIGltThPLeuCysHtISGlInAlPhEleuLeuYlsLeuthArXhIsArgVal	1087
Db	305	GAGGCACGAAGATGGCTGTGCTACCATCGCTTCATTCGTCAAACTGTCCAACACAAAGTT	364
Oy	1088	ThTYrVaIpLeouLeuGISerLeuArghTrAlaGINrhInLeuSerArgLySeu	1107
Db	365	ATTACCAAATGCTTACTTAAGCCCCCTTAAAGTCTATAAGATGCATCTGTTGGGAAGATC	424
Oy	1108	ProGLYThrThrLeuthrAlaLeuGIuaIAaIIaIAaSProAlaLeuProSerAspPhe	1127
Db	425	CCAAGGATATCTATGAGACTGCTGAAGACGGTGAAGCAACAATCCGCTTTGTCAAAATTC	484
Oy	1128	LyeThrIleLeuASP	1132
Db	485	AAAACTATACTGCAC	499
RESULT 19	CNS05902	846 bp	mRNA linear EST 28-APR-2004
LOCUS	AGNCOCURF_22432746 NIH_ZGC_7	Danio rerio cDNA clone IMAGE:7267941	
DEFINITION	5', mRNA sequence.		
ACCESSION	CNS05902		
VERSION	CNS05902.1	GI:46818526	
KEYWORDS	EST.		
SOURCE	Danio rerio (zebrafish)		
ORGANISM	Danio rerio		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Actinopterygii; Neopterygii; Teleostei; Ostariophysi;		
TITLE	Cypriniformes; Cyprinidae; Danio.		
JOURNAL	1 (bases 1 to 846)		
COMMENT	NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 RmlDA07 Bethesda, MD 20892 Email: dsgrahbs@remail.nih.gov Tissue Procurement: Len Zon, Harvard Tissue Library Preparation: Open Biosystems cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LRAM15246 row: h column: 19 High quality sequence start: 21 High quality sequence stop: 756. Location/Qualifiers 1. 846 /organism="Danio rerio" /mol_type="mRNA" /db_xref="taxon:7955" /clone="IMAGE:7267941" /tissue_type="whole body" /lab_host="DH10B" /clone_idb="NIH_ZGC_7" /note=vector: pEXpress1; Site_1: NotI; Site_2: EcoRV; Bulk tissue was collected from a whole adult individual from the Tübingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pEXpress-1. Library was size-selected for >1 kb fragments and normalized. A non-normalized version of this library is also available (NIH_ZGC_10). Library was constructed by Open Biosystems (Huntsville, AL)"		

Db 234 GAATTAGAGAGGTTTTCATGCGAGAGTTATGCTTCTTATCATCAAG 293
 Qy 957 rleutrhPheAsnArgGlyPheValArgValAsnMetArgValLeuPheGlyVal 977
 Db 294 TCTTTCTTCATTCAGTAGAATAGCTGGGAAACATGTAATGCAATTCATCGAGCT 353
 Qy 977 lLeuArgLeuValSerHisSerLeuPheLeuValAsnSerLeuGlnThrVal 997
 Db 354 CCGCAACAGTAATGATGATCTTCTTCTGACTTAAGATCAACAGCTTCACAGAGT 413
 Qy 997 lCysThrAsnIleTyrIleValLeuLeuGlnAlaTyrArgPheHisAlaCysValIle 1017
 Db 414 TCTAATTAACATCTCAAGATATTTTACTTCAGGCTTACAGGTTTCATGCTGCTTCT 473
 Qy 1017 uGlnLeuProPheHisGlnGlnValTyrPheAsnProThrPhePheLeuArgValIle 1037
 Db 474 TCGCTTCCTTCATTCACCGAAGATGAGATATCTGATTTCTTCTTCAAGATCATCTC 533
 Qy 1037 rAspThrAlaSerLeuValSerTyrSerIleLeuValAlaValAsnAlaGlyMetSerLeuGln 1057
 Db 534 TGATACGCTTCATGCTGCTATTTTATCTGAAAGCTTAATAATCCAGAGGTTCTTAGG 593
 Qy 1057 ValAlaValGlyAlaAlaGlyProLeuProSerGlnAlaValGlnTyrLeuValSerGlnAla 1077
 Db 594 TAGCAAAAGATGATCTGGCAT-GTTCCTTGGAGCGACGAGATGCTGTGCTACCATGC 652
 Qy 1077 aPheLeuLeuValSerLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArg 1097
 Db 653 CTTGATTTGTAACATGTCACCAACCAAAAGTTATTAACAATGCTTACTTAAGCCCTTA 712
 Qy 1097 gThrAlaGlnThrGlnLeuSerArgValSerProGlyThrThrLeuThrAlaLeuGlnAla 1117
 Db 713 AAGCTATAGATGATCTGTGGGAAAGATCCAGGAGATCTTAATGGAACCTGTGAAGA 772
 Qy 1117 aAlaAlaAsnProAlaLeuProSerAspPheVal 1128
 Db 773 CGGAGCCGAACCATCGCTTGTCCAGAAATTCAAA 806

RESULT 21 CA380121 668 bp mRNA linear EST 06-NOV-2002
 LOCUS CA380121 659344 NCCGWA 1RT Oncorhynchus mykiss cDNA clone 1RT49P11_B_H06 5',
 DEFINITION mRNA sequence.
 ACCESSION CA380121.1 GI:24701509
 VERSION CA380121.1 GI:24701509
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 668)
 Rexroad, C.B. 3rd, Lee, Y., Keele, J.W., Karanicheva, S., Brown, G.,
 Koop, B., Gahr, S.A., Palti, Y., and Quackenbush, J.
 Sequence analysis of a rainbow trout cDNA library and creation of a
 gene index
 JOURNAL Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
 COMMENT Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@nccgwa.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified by
 cross_match v0.990329.
 Seq primer: AGCGATTAACAATTTCACACAGA.
 Location/Qualifiers
 1. 668
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="1RT49P11_B_H06"

/tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="NCCGWA 1RT"
 /note="Vector: pCMV SPOR6; Site 1: NotI; Site 2: SalI;
 library made from pooled tissue from brain, gill, liver,
 spleen, muscle, and kidney."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.57e-22 Length: 668
 Score: 463.00 Matches: 102
 Percent Similarity: 58.19% Conservative: 33
 Best Local Similarity: 43.97% Mismatches: 85
 Query Match: 7.77% Indels: 12
 Gaps: 4
 Db: 6

US-10-044-692-2 (1-1132) x CA380121 (1-668)

Qy 451 LeuLeuArgGlnHisSerSerProTyrGlnValTyrGlyPheValArgAlaCysLeuArg 470
 Db 7 CTCCTGCCCGACGACAGTGCACCTCACGGGTGATCTTGTGTCAAGAGTCCCTCAAC 66
 Qy 471 ArgLeuValProProGlyLeuTyrGlySerArgHisAsnGlnArgArgPheLeuAsn 490
 Db 67 GCGGTGTCCTCCCGAGGTTCTGGGGTCCGACCATACGATTCAAATTCCTGTCGCA 126
 Qy 491 ThrLysLysPheIleSerLeuGlyLysHisAlaLysLeuSerLeuGlnGlnLeuThrTrp 510
 Db 127 CTCAGGAACCTTCCTGTCATGGGACATTTGAGAGATGATCATGCTGCTGAGATGTGG 186
 Qy 511 LysMetSerValArgAspCysAlaTyrLeuArgArgSerProGlyValGlyCysValPro 530
 Db 187 AAGATGAAGGTGAATGACTGTGATTTGGCTGAAGATCGCAAG--ACGGGCGCTGCCG 243
 Qy 531 AlaAlaGlnHisArgLeuArgGlnGlnIleLeuAlaLysPheLeuHisTrpLeuMetSer 550
 Db 244 CCCAGTGAAGCTGTCGTATTCGACGCGGCTGTAGGCCAGCTCCGTGGCTGCTGGAT 303
 Qy 551 ValTyrValAlaGlnLeuLeuArgSerPhePheTyrValThrGlnThrPheGlnLys 570
 Db 304 GGCTATGCTGATGGCTGTGAGCTATGTTCTACGTCACAGAGAGATGGACAGAG 363
 Qy 571 AsnArgLeuPhePheTyrArgLysSerValTrpSerLysLeuGlnSerIleGlyIleArg 590
 Db 364 AACGACCTGGCTTCTACAGATACAGATCTGGGCCAAGCTGCAGAGCTGGCTTCACT 423
 Qy 591 GlnHisLeuLysArgValGlnLeuArgGlnLeuSerGlnAlaGlnValArgGlnHisArg 610
 Db 424 GGTCACTCTCTAAGAGTCAAGATGTCAGAGTTGACCTGCGCCAGGTG-----ACG 474
 Qy 611 GluAlaArgProAlaLeuLeuThrSerArgLeuArgPheIleProLysProAspGlyLeu 630
 Db 475 TCGCTCCCGCAACCACTGTCCCTCCGCTCCGCTCCCTTATCCCAAGACCGAAGGATG 534
 Qy 631 ArgProIleValAsnMetAspTyrValValGlyAlaArgThrPheArgArgGlnLysArg 650
 Db 535 AGACCATACACAG-----GTCAAGGGGCT-----GACCCCAA 570
 Qy 651 AlaGlnArgLeuThrSerArgValLysAlaLeuPheSerValLeuAsnTyrGlnArgAla 670
 Db 571 ACAAGGTGTTCCAGACCCGTGGAAGAGCGTTAGATGCTAGTGTCTGTGTACGG 630
 Qy 671 ArgArgProGlyLeuLeuGlyLysSerValLeuGly 682
 Db 631 TCCTTCCTCTCTCTGCTGAGCTCTACAGTGTGGGG 666

RESULT 22 EX889962 724 bp mRNA linear EST 27-JUL-2004
 LOCUS EX889962 tcdk Oncorhynchus mykiss cDNA clone tcdk0041c.i.20 5prim,
 DEFINITION mRNA sequence.
 ACCESSION EX889962
 VERSION EX889962.2 GI:43411444

KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 724)
AUTHORS Govoroun,M., Guiguen,Y. and Le Gac,F.
TITLE Construction and primary characterization of normalized cDNA
libraries in rainbow trout, *Oncorhynchus mykiss*
JOURNAL Unpublished (2003)
COMMENT On Dec 18, 2003 this sequence version replaced gi:40140362.
Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenassupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0041 row: i column: 20
Seq primer: M13R.
Location/Qualifiers
1..724
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="cdk041c.1.20"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="cdk"
/note="Vector: pT7TD-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution : AGENAE Ressource centre. Francois PLOMI,
Francis Pluimel@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Alignment Scores:
Pred. No.: 1.35e-21 Length: 724
Score: 457.00 Matches: 106
Percent Similarity: 58.47% Conservative: 39
Best Local Similarity: 42.74% Mismatches: 89
Query Match: 7.67% Indels: 15
DB: Gaps: 5
US-10-044-692-2 (1-1132) x BX889962 (1-724)

OY 486 ArgPheLeuAArgAsnThrLysLysPheLeuGlyLysHisAlaLysLeuSerLeu 505
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 2 AAATTCCTGTCGCGACGAGCACTTCCTGTCATGCGCAAGTTGACGAGATGTCATTG 61
OY 506 GlnGluLeuThrTrpLysMetSerValaLysArgProGly 525
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 62 GCTGAGCTGATGTGAAGATGAAGTGAATGACTGATGCTGAAGTCAAGCAAG-- 118
OY 526 ValGlyCysValProAlaAlaGlnHisArgLeuArgGluGlnIleLeuAlaLysPheLeu 545
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 119 ACAGCCCGCTGCGCCCGCAGTGAAGCTGTGATTCGAGCCGGGTGTAGCCAGCTCCG 178
OY 546 HisTrpLeuMetSerValTrpValGluLeuLysSerPhePheTrpValThrGlu 565
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 179 GCTTGCTGCTGATGAGTGTGCTGAGGCTGCTGAGAGCTATGTTCTACCTCACAGAG 238
OY 566 ThrTrpPheGlnLysAsnArgLeuPheTrpArgLysSerValTrpSerLysLeuGln 585
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 239 AGCAGGAGACAGAAAGACACCTGCGCTTCTACAGTACCAAGCTGCGCCAAAGCTGCGAG 298
OY 586 SerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGlnAlaGln 605

Db 299 GAGCTGCTTTCAGTGTCTACCTCTCTAAAGCTCAGAGTGCAGAGTGCACCTGCGCCAG 358
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
OY 606 ValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeuAsnPheLeuPro 625
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 359 GGG-----ACGTGCTCCGCCCAAAACACACTGCTCCCTCGGCTCGCTTCATATCCC 409
OY 626 LysProAspGlyLeuArgProIleValAsnMetAspTrpValValaGlyAlaArgThrPhe 645
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 410 AAGACCGAAGGATAGACCATTCACAGG-----GTCATAGGGGGCT----- 451
OY 646 ArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeuPheSerValLeu 665
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 452 -----GACGCCAAACAAGGTTGTTCCAGACCCGCTGGAAGAGAGCTGTATGATGTGCTA 505
OY 666 AsnTrpGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeuGlyLeuAspArg 685
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 506 GGTGTCTGTGAACGGTCTCTCTCTCTCTGAGCTGTACAGTGTGGGGGTGAACCGAC 565
OY 686 IleHisArgAlaTrpArgThrPheValLeuArgValaGlnAlaAspProProProGlu 705
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 566 ATCCACAGAGTCTCTCTTC-----ATCACCCCTGCTCAGAAAGACAAACACACAGCGG 619
OY 706 LeuTrpPheValLysValaAspValThrGlyAlaTrpThrIleProGlnAspArgLeu 725
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 620 CTCTACTTGTTCAGAGTGAATGATGATGAGTGGGCTGTAGACAGTCAACCCAC-ACTCAGCTC 678
OY 726 ThrGluValIleAlaSerIleIle 733
|||||:::|||||:::|||||:::|||||
Db 679 TTGAGAGTGAATGTCACAGTCTCTG 702

RESULT 23
CA353864
LOCUS
DEFINITION 632 bp mRNA linear EST 05-NOV-2002
625469 NCCCMW 1RT Oncorhynchus mykiss cDNA clone 1RT74012_C_H06 5',
mRNA sequence.
ACCESSION CA353864
VERSION CA353864.1 GI:24599035
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 632)
AUTHORS Rexroad,C.B. 3rd, Lee,Y., Keele,J.W., Karaycheva,S., Brown,G.,
Koop,B., Gahr,S.A., Palti,Y. and Quackenbush,J.
TITLE Sequence analysis of a rainbow trout cDNA library and creation of a
gene index
JOURNAL Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
COMMENT Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: cirexroad@ncccmw.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim.alc option. Vector identified by
cross match v0.990329.
Seq primer: AGCGATGATCAATTTCACACAGCA.
FEATURES
source
1..632
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="1RT74012_C_H06"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="NCCCMW 1RT"
/note="Vector: pCMV SPOR6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

ORIGIN

Alignment Scores:

Pred. No.: 3,64e-21 Length: 632
 Score: 449.50 Matches: 102
 Percent Similarity: 55.978 Conservative: 34
 Best Local Similarity: 41.988 Mismatches: 68
 Query Match: 7.54% Indels: 40
 Gaps: 2

US-10-044-692-2 (1-1132) x CA353864 (1-632)

QY 773 MetArgGlnPheValAlaHisLeuGlnGluThrSerProLeuArgAspAlaValIle 792
 Db 17 ATGAAAGGCTTGTAGTGTGCGCAAGAGAGGCGAAAGTTCACATCTCCATCTGGG 76
 QY 793 GlnGlnSerSerSerLeuGlnAlaSerSerglyLeuPheAspValPheLeuArgPhe 812
 Db 77 GAGCAGCATTTCTCCACAGATATTCAATGGCAAGACGTCTGGAGGCTTGACCCAGATG 136
 QY 813 MetCysHisHisAlaValAlaArgIleArgGlyLysSerTyrValGlnCysGlnGlyIlePro 832
 Db 137 CTCTCTAGCTGAGTTCAGCTTGGGAAAGAAATCGTCCGTACAGGAGGTACGGGATTCCT 196
 QY 833 GlnGlnSerIleLeuSerThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 852
 Db 197 CAGGGGTCGCGGAGTGTCTGCTGGCTGCTCTGTTACGGGCAATGAGAACCTT 256
 QY 853 LeuPheAlaGlyIle--ArgArgAspGlyLeuLeuLeuArgLeuValAlaAspPheLeu 871
 Db 257 CTGTTTCTTAACGTCAGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 316
 QY 872 LeuValThrProHisLeuThrHisAlaLysThrPheLeuArgThrLeuValAlaArgGlyVal 891
 Db 317 CTCTACCTCTGACCTGAGCAGGACAGACAGACCTTCTTCAAGACCTGATGGGCGGAGTA 376
 QY 892 ProGlnTyrGlyCysValAlaAsnLeuArgGlyThrValAlaAsnPheProValGluAsp 911
 Db 377 CCACGGTACGGGTGTGTGAGAACCCCAAGAAAGGTGCTGTAACTTCCCTTT-GAC--- 432
 QY 912 GluAlaLeuGlyGlyThrAlaPheValGlnMetProAlaHisGlyLeuPheProTyrCys 931
 Db 432 ----- 432
 QY 932 GlyLeuLeuLeuAspThrArgThrLeuGluValGlnSerAspTyrSerSerTyrAlaArg 951
 Db 433 -----TACGCTGGC 441
 QY 952 ThrSerIleArgAlaSerLeuThrPheAsnArgGlyPheIysAlaGlyAlaAsnMetArg 971
 Db 442 CTATCCCTGCGGCTACAGCTGAGCTGCTCCCTCCACTGCGGGGCGCAACAAACGAG 501
 QY 972 ArgGlyLeuPheGlyValLeuArgLeuLysCysHisSerLeuPheLeuAspLeuGlnVal 991
 Db 502 AGGAAGCTCATGCTCATCTTGAATTCAGAGGACAGCCCTCTTCTTCTGAGACTCAGAAC 561
 QY 992 AsnSerLeuGlnThrValCysThrAsnIleTyrIysIleLeuLeuLeuGlnAlaTyrArg 1011
 Db 562 AACTCCCTGAGAGGCTGTATAGCAACGTCACAGTATAGTGTGCTGACGCGTTCAGG 621
 QY 1012 PheHisAla 1014
 Db 622 TTCATGCTCC 630

RESULT 24
 BE396925 715 bp mRNA linear EST 21-JUL-2000
 LOCUS 601290610F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621050 5',
 DEFINITION mRNA sequence.

ACCESSION BE396925
 VERSION BE396925.1 GI:9342230
 KEYWORDS EST, human
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc
 DNA Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM294 row: C column: 03
 High quality sequence stop: 634.

FEATURES

source
 1..715
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3621050"
 /issue_type="Burkitt Lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_8"
 /note="Organ: lymph; vector: pOT87; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 location/qualifiers

ORIGIN

Alignment Scores:
 Pred. No.: 1.15e-20 Length: 715
 Score: 443.50 Matches: 98
 Percent Similarity: 90.09% Conservative: 2
 Best Local Similarity: 88.29% Mismatches: 6
 Query Match: 7.44% Indels: 5
 Gaps: 1

US-10-044-692-2 (1-1132) x BR396925 (1-715)

QY 525 GlyValGlyCysValProAlaAlaGluHisArgLeuArgGlnIleLeuAlaLysPhe 544
 Db 373 GGGGTGGCTGTGTTCCGCGCCGACAGACACCTCTGCTGAGAGATCTGGCCAAATTC 432
 QY 545 LeuHisThrPheMetSerValTyrValValGluLeuLeuArgSerPhePhe-TyrValIth 564
 Db 433 CTGCACTGGCTGATGAGTGTGATGCTGTCGAGCTGCTCAGGTCTTTTATATGTCAC 492
 QY 564 rgIuThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTTPSerIyle 584
 Db 493 GGAACACAGTTTCAAAAGAACAGAGGCTTTTTCACCGGAAGAGTCTGAGCAAGTT 552
 QY 584 uGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlnLeu-SerGlnuA 604
 Db 553 GCAAGCATTGGATGACAGACGACTTGAAAGGGTGCAGCTGCGGAGACTGTGGAAG 612
 QY 604 lagluValArgGlnHisArg--GluAlaArgProAlaLeuLeuThrSerArgLeuArgPh 623
 Db 613 CAGAGGTCAAGGAGCATCGGGAACCAAGCCCTGCTGATGACGTCCAC---TCCGT 669
 QY 623 eileProLysProAspGlyLeuArg 631
 Db 670 TCATCCCAAGCTGAAGGGGCTGGCG 694

RESULT 25
 EX886589 703 bp mRNA linear EST 27-JUL-2004
 LOCUS EX886589
 DEFINITION EX886589 tcdk Oncorhynchus mykiss cDNA clone tcdk0036c.p.02 5prim,

ACCESSION	BX86589	mRNA sequence.
VERSION	BX86589.2	GI:42819050
KEYWORDS	EST.	
SOURCE	Oncorhynchus mykiss (rainbow trout)	
ORGANISM	Oncorhynchus mykiss	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE	Actinopterygii; Neopterygii; Teleostei; Euteleostei;	
REFERENCE	proactanctoperygii; Salmoniformes; Salmonidae; Oncorhynchus.	
JOURNAL	1 (bases 1 to 703)	
COMMENT	Govoroun,M., Guiguen,Y. and Le Gac,F. Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss unpublished (2003) On Dec 18, 2003 this sequence version replaced gi.40135983. Contact: Guiguen Y INRA - SCRIBE Campus de beaulieu, RENNES cedex, 35042, France Tel : 02.23.48.50.09 Fax: 02.23.48.50.20 Email: Yann.Guiguen@beaulieu.rennes.inra.fr Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence. Plate: 0036 row: p column: 2 Seq primer: M13R. Location/Qualifiers 1..703 /organism="Oncorhynchus mykiss" /mol_type="mRNA" /db_xref="taxon:8022" /clone="tcdk0036c.p.02" /tissue_type="multi-tissues" /dev_stage="from embryos to adults" /lab_host="DH10B" /clone_id="tcdbk" /note="Vector: pRTTID-pac; AGENAE Rainbow trout multi-tissues - normalized + 2 subtractions; Clone distribution : AGENAE Ressource centre, Francois PUMI, Francois.Pumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREGE), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"	
FEATURES		
source		
Alignment Scores:		
Pred. NO.:	3.17e-20	Length: 703
Score:	437.00	Matches: 95
Percent Similarity:	64.2%	Conservative: 31
Best Local Similarity:	48.4%	Mismatch: 70
Query Match:	7.3%	Indels: 1
DB:	5	Gaps: 0
US-10-044-692-2 (1-1132) x BX86589 (1-703)		
QY	935 leuapthrraragthrleugluvalglnserrapyrserstyryalaargthrsertle	954
Dd	1 CTGAATACACACACCCTGAGCGTTCA-CACAATPACGCACGTACGGCTGACTTCCTG	59
QY	955 ArgAlaSerLeuThrPhaAsnArgGlyPheUylsalagiAygAsnMetArgArgUyleu	974
Dd	60 CGCTACACCCCTGACCCCTGAGCTCCGCCCATCGCGGGGAGCAAATMAAGGAAAGCTC	119
QY	975 PheGlyValLeuArgUylLeuUysCyHisSerLeuPheLeuAAPleUGlnValAsnSerleu	994
Dd	120 ATGTCATCCTTAAGTATTCAAGTGCCACGCCCTCTTCCTGAACTCAAAACCACTCCCTG	179
QY	995 GlnThrValCyUthAsnIleTyrlsyleuleuleuGlnAlaTyArgPheHisaIa	1014
Dd	180 GAGCGTGTCTATTACGAACGTCTATAAGTTAGTGTGCGAAGGCGTTCAGGTTCCATCC	239
QY	1015 CysValLeuGlnLeuProPheHisGlnGlnValTrpylvaenProThrPhePheLeuArg	1034

Db	Accession	Source	Organism	Reference Authors Title Journal Comment	
Db	240	TGTCACAGAGTTTGCCGTTTGGTGCACAAAGATGGCCGAAACCACTGCTACTTCTCAAT	299		
Db	1035	Val11eSeraphinAl1aserLeuCYtySer11eLeuysAl1alyAsnAl1glyMet	1054		
Db	300	CTGATTCGGAGCTTGGCGAGTACCAACCAACCATTAATCACTTCCGACCAAGATG	359		
Db	1055	SerLeuG1yAl1alySG1yAl1aAG1yProLeuProSerG1uAl1aVal1G1nTripleCYs	1074		
Db	360	TCTTTAGGCTGTAGAGCTTTTAACAGTACGCTTCAATATAGAGAGTAAAGATATATAC	419		
Db	1075	HisG1nAl1aPheLeuLeuLysLeuThrArgHisArgValThrTyValProLeuLeuG1y	1094		
Db	420	TGTCGGCTTCTCCGTGTGTTCTGTCCGTCATGCCCCCTCTACTCACTCTCTGCT	479		
Db	1095	SerLeuArgThrAl1aG1nThrG1nLeuSerArg1yLeuProG1yThrThrLeuThrAla	1114		
Db	480	CCGCTACGACACCGTAAAGAGACCTGAGGGGAGGCGGTTTGAGATTGACCCGA	539		
Db	1115	LeuG1uAl1aAl1aAsnProAl1aLeuProSerAspPheLysThrIle	1130		
Db	540	ATCAGACAGGCTGCCACACCCAAATGCTGAGACTTCAAGGCCATC	587		
RESULT 26					
LOCUS	CF531258	344 bp	mRNA	linear	EST 12-SEP-2003
DEFINITION	UT-M-PYO-cgp-h-01-0-UT.r1 NIH_BMAP_FY0		Mus musculus	CDNA clone	
ACCESSION	CF531258				
VERSION	CF531258.1	GI:34583222			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 344)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cga@rs-1@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mouse1.html This clone was contributed by the Brain Molecular Anatomy Project (BMAP)				
FEATURES	Seq primer: PYX-5.				
SOURCE	Location/Qualifiers				
	1..344				
	/organism="Mus musculus"				
	/mol_type="mRNA"				
	/db_xref="taxon:10090"				
	/strain="C57BL/6"				
	/cd_xref="taxon:30355848"				
	/clone="IMAGE:30355848"				
	/tissue_type="whole brain"				
	/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"				
	/lab_host="DH10B (T1 phage resistant)"				
	/clone_lib="NIH_BMAP_FY0"				
	/note="Organ: Brain; Vector: PYX-Asc; Site: 1; Ecor I; Site: 2; Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National				

ORIGIN Institute of Mental Health (NIMH), Hemlin Chirn, Ph.D.,
program coordinator."

Alignment Scores:

Pred. No.: 1,25e-20 Length: 344
Score: 436.00 Matches: 85
Percent Similarity: 79.82% Conserved: 6
Best Local Similarity: 74.56% Mismatches: 23
Query Match: 7.31% Indels: 0
DB: 7 Gaps: 0

US-10-044-692-2 (1-1132) x CF531258 (1-344)

QY 904 ValValAspPheProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetPro 923
DB 1 GTGGTGAACCTTCCTCCGTGAGCCTGTGTACCTGGGGTGGAGCTCCATACAGAGCTGCT 60
QY 924 AlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluValGln 943
DB 61 GCTCACTGCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 944 SerAspTyrSerSerTyrAlaArgThrSerLeuArgAlaSerLeuThrPheAsnArgGly 963
DB 121 TGTGACTACTCAGGTTATGCGCCAGACCTCAATTAAAGACGACCTCACTTCCAGAGTGTTC 180
QY 964 PheValAlaGlyArgAsnMetArgArgGlyLeuPheGlyValLeuArgLeuLysCysHis 983
DB 181 TTCAAGAGCTGGAGAACCATGCGGAACAAGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 984 SerLeuPheLeuAspLeuGluValAsnSerLeuGlnThrValCysThrAsnLeuTyrLys 1003
DB 241 GGTCTATTCTTACACTTGCAGGTGAACAGCTCCAGACGCTGCATCANTATATACAG 300
QY 1004 IleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeu 1017
DB 301 ATCTTCCTGCTCAGGCTTACAGGCTTCCATGATGATGATG 342

RESULT 27 409 bp mRNA linear EST 19-APR-1997
AA311750
LOCUS EST182469 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA
DEFINITION
ACCESSION AA311750
VERSION AA311750.1 GI:1964077
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 409)

REFERENCE
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fullmer, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinsock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, M.-C.,
Clayton, R.A., Cline, T.R., Colton, M.D., Earle-Hughes, J., Fink, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glock, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palacios, R.F., McDonald, L.A., Nguyen, D.T., Pelligino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.D., Sauder, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Peng, D.-F., Ferris, A.A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, U., Xu, C., Yu, G.L., Ruben, S.M.,
Drillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
JOURNAL MEDLINE PUBMED
96026280 756098

COMMENT

Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@igf.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers

FEATURES

source 1..409
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):158964"
/db_xref="taxon:9606"
/cell_type="T-lymphocyte"
/clone_id="Jurkat T-cells VI"
/note="Vector: pBluescript SK-, Site_1: EcoRI, Site_2:
XhoI"

ORIGIN

Alignment Scores:
Pred. No.: 9.44e-20 Length: 409
Score: 425.00 Matches: 80
Percent Similarity: 97.56% Conserved: 2
Best Local Similarity: 97.56% Mismatches: 2
Query Match: 7.13% Indels: 0
DB: 1 Gaps: 0

US-10-044-692-2 (1-1132) x AA311750 (1-409)

QY 866 LeuValAspAspPheLeuLeuValThrProHisLeuThrHisAlaLeuThrPheLeuArg 885
DB 3 TTGGGGATGATTTCTTGTGTGACACTCACCACCGAAGAAACCTTCTCAGG 62
QY 886 ThrLeuValArgGlyValProGluTyrGlyCysValAlaAsnLeuArgLysThrValVal 905
DB 63 ACCCTGTCGAGGAGTCCCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 122
QY 906 AsnProValGluAspGluAlaLeuGlyGlyThrAlaPheValGlnMetProAlaHis 925
DB 123 AACTTCCCTGTAAGAGACGAGCCTGGGTGGACAGGCTTTTNTTCAATGCCGCCAC 182
QY 926 GlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeuGluValGlnSerAsp 945
DB 183 GCGNATTTCCCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 242
QY 946 TyrSer 947
DB 243 TACTCC 248

RESULT 28 679 bp mRNA linear EST 21-JUL-2000
BE396606
LOCUS BE396606
DEFINITION 601289077F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619674 5',
MRNA sequence.
ACCESSION BE396606
VERSION BE396606.1 GI:9341882
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 679)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at: image.lnl.gov
Plate: L10M290 row: 1 column: 19
High quality sequence start: 2
High quality sequence stop: 656.
Location/Qualifiers

FEATURES

source

1..679
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3619674"
/issue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH MGC 8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:

Pred. No.: 2,05e-19 Length: 679
Score: 425.00 Matches: 89
Percent Similarity: 96.74% Conservative: 0
Best Local Similarity: 96.74% Mismatches: 1
Query Match: 7.13% Indels: 2
DB: Gaps: 0

US-10-044-692-2 (1-1132) x BE396606 (1-679)

OY 525 GtYValGtYCyValAProAla-AlaGluHisArgLeuArgGluGluLeuAlaLeuAlaLeu 544
Db 372 GGGGTTGGCTGTCTCCGGCTCGACAGACACGCTGCTGCTGAGAGATCTGGCCAAATT 431
OY 544 eleuHisTrp-LeuWetSerValTyrValValGluLeuLeuArgSerPhePheTyrValT 564
Db 432 CCTGCACTGTCTGATGATGTGTGCTGCTGACGCTGCTGCTTTTATGTCA 491
OY 564 hrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTTPSerVal 584
Db 492 CGGAACCAAGCTTCAAAAGAACAGAGCTCTTTTTCACCGAAGAGTGTCTGAGCAAGT 551
OY 584 euGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGluA 604
Db 552 TCCAAAGCATTCGATTCACACAGCACTTCAAGAGGTCGACGTCGCGAGCTGTCTCGAAG 611
OY 604 laGluValArgGlnHisArgGluAlaArgPro 614
Db 612 CAGAGCTGACGACGATCGGAAGCCAGGCCG 643

RESULT 29
LOCUS BU111946 835 bp mRNA linear EST 25-NOV-2002
DEFINITION 603127172P1 CSECHL13 Gallus gallus cDNA clone ChEST98p18 5', mRNA
sequence.
ACCESSION BU111946
VERSION BU111946.1 GI:25315846
KEYWORDS EST
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 835)
Boardman,P.E., Sanz-Baquero,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs

REFERENCE
AUTHORS
TITLE

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335334
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

1..835
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, HiseX"
/db_xref="taxon:9031"
/clone="ChEST98p18"
/dev_stage="22"
/lab_host="DH10B"
/clone_lib="CSECHL13"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
ligate in double stranded adaptor containing BspI and
BamHI sites [5'ggcgcgtgcgagcccgatccgcaaaaaag]
[5'aattcttttcgatccgcggcgccagc]"

ORIGIN

Alignment Scores:

Pred. No.: 3.3e-19 Length: 835
Score: 424.00 Matches: 107
Percent Similarity: 50.90% Conservative: 34
Best Local Similarity: 38.63% Mismatches: 74
Query Match: 7.11% Indels: 63
DB: Gaps: 2

US-10-044-692-2 (1-1132) x BU111946 (1-835)

OY 592 HisLeuLysArgValGlnLeuArgGluLeuSerGluAlaGluValArgGlnHisArgGlu 611
Db 184 CATTTTGCCTAAGTACATCTACGCTCTTCTTTCAGAGACATGCACTGATCCCTCA 243
OY 612 AlaArgProAlaLeuLeuThrSerArgLeuArgPheIleProLysProAspLysLeuArg 631
Db 244 AAAAGTATTTTCCATATTCATCAAGGCTCCGCTTCATTCCTAAATGAATGATTATACA 303
OY 632 ProIleValaMetCaspTyrValValGlyAla-ArgThrPheArgGluLysArgAl 651
Db 304 CCCGTAGTAAGACTAAGCCGTGTGTTGAAGAGCAGAACTCAGCAGAGAACAGACAGA 363
OY 651 agLuarGluThrSerArgValLysAlaLeuPheSerValLeuAsnTyrGluArgAlaArg 671
Db 364 AAGG-----
OY 671 gArgProGlyLeuLeuGlyAlaSerValLeuGlyLeuAspAspIleHisArgAlaTrpArg 691
Db 367 -----
OY 691 gThrPheValLeuArgValArgAlaGlnAspProProProGluLeuTyrPheValLysVal 711
Db 368 -----
OY 711 AspValThrGlyAlaTyrAspThrIleProGlnAspArgLeuThrGluValIleAlaSer 731
Db 373 TGATGTATCCAGAGCTTTGATACCATTCCTACAAAGAACTTGTGAGAGTATATTCACA 432
OY 731 rIleIleLysPro-----GlnAsnThrTyrCySValArgArgTyrAlaValAlaGlnLys 749
Db -----

Db 433 GGTCTGAAACCTGAGACCAACTGCTAATGAAATGAGTGTATGCAATGATATATAT 492
 QY 749 salalahlslgylhlsvalargyalaphelysserhlsvalserthrleuthrasple 769
 Db 493 TACCCCACTGAAAAAGCAGAACTCTATAGAGACATGTTTCTACTTCGAGATTT 552
 QY 769 uclnprotyrmetarglnphevalalahlslenglnlurthrserproleuargaspal 789
 Db 553 TATTCAGACATGAGACAGTTTGTGTCCAGCTTCAGAGCCATTCATTAGAAATGC 612
 QY 789 aalvalallieglnlinserserserleuansnglnlasergerglyleupheaspvalph 809
 Db 613 AATAGATGTGACACATGCTTACTTATATGGAACATTCACCTCTTACTTCTTCT 672
 QY 809 eleuargpmetcyshlsishlsalavalargylleargyllyssetryvalglncysgl 829
 Db 673 TCTTCAATGTTATCATATATACATCTCTGAGATTTGGCACAGTACTATATACAGTCTC 732
 QY 829 nglylleptroglnglyserlleuserthrleuleucysserleucyetyrglyasphe 849
 Db 733 TGGAAATCCACAGAGGCTCCATTTGTC--AACTTACTTTCAGCTTATGCTACGAGACAT 790
 QY 849 tgluan-lysleu-phealaglylleargargaspglyleuleu 863
 Db 791 GGAAACCAATTAATCTCTGTGGATCCAGAGATGGAGTCTA 835

RESULT 30 649 bp mRNA linear EST 07-AUG-2000
 BE514070
 LOCUS 601316575F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634962 5',
 DEFINITION mRNA sequence.
 ACCESSION BE514070
 VERSION BE514070.1 GI:9721282
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 649)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LLCM330 row: f column: 19
 High quality sequence stop: 628.

FEATURES

source

1. .649

Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3634962"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_8"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN

Alignment Scores:
 .Pred. No.: 3.09e-19 Length: 649

Score: 422.00 Matches: 87
 Percent Similarity: 95.74% Conservative: 3
 Best Local Similarity: 92.55% Mismatches: 2
 Query Match: 7.08% Indels: 2
 DB: 2 Gaps: 0

US-10-044-692-2 (1-1132) x BE514070 (1-649)

QY 525 GLYVALGLCYVSLPPOALAAAGLHLSARGLEUARGGLUGLULEALALYSPPH 544
 Db 368 GGGGTGGCTGTGTCCGCGCAGACACCGCTTGGCTAGAGATCTCGCCAACTTC 427
 QY 545 Leu-HisTrpleuMetserValTyValValGluLeuLeuArgSerPhePheTyVal1th 564
 Db 428 CTGCACTGGCTATGATGTGTACGTCTGCACTCTCAGGCTCTTCTTTATGTCTAC 487
 QY 564 tgluThrThrPheGlnLysAsnArgLeu-PhePheTyArgLysSerValTrpSerLysL 584
 Db 488 GGAGACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAGAGATGTCTGGAGCAAGT 547
 QY 584 euGlnSerTlleGlyTlleArgGlnHisLeuLysArgValGlnLeuArgGlnLeuSerGln 604
 Db 548 TCGAAGGATTGGAATCAGACACACTTGAAGAGGCTCAGCTCGGAGACTGTGGAAG 607
 QY 604 laglvalarglnhlsarglnlalaargproalaleu 616
 Db 608 CAGAGTCAAGCAGCATCGGAGAGAGCCCGCTGATG 645

RESULT 31 610 bp mRNA linear EST 07-AUG-2000
 BE514188
 LOCUS 601316376F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634987 5',
 DEFINITION mRNA sequence.
 ACCESSION BE514188
 VERSION BE514188.1 GI:9721400
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 610)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: LLCM330 row: g column: 20
 High quality sequence stop: 610.

FEATURES

source

1. .610

Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3634987"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_8"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN

Alignment Scores:

Pred. No.: 1.63e-18 Length: 610
 Score: 411.00 Matches: 80
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.89% Indels: 0
 DB: 2 Gaps: 0

US-10-044-692-2 (1-1132) x BBS14188 (1-610)

QY 525 GYVAlGlyCyValProAlaAlaGluHisArgLeuArgGluGluIleuAlaLysPhe 544
 Db 369 GGGGTGGCTGTGTCCGGCCGACAGCACCGCTGCGGAGAGATCCTGGCCAAAGTTC 428
 QY 545 LeuHISTPLeuMetSerValTyrValValGluLeuLeuArgSerPhePheTyrAlaThr 564
 Db 429 CTGCACTGGCTGATAGTGTACGTCGAGCTGCTCAGGCTCTTTTATATGTCACG 488
 QY 565 GlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTyrPserLysLeu 584
 Db 489 GAGACACAGCTTTCAAAGACAGCGCTTTTCTACCGAGAGAGTCTCGAGCAAGTTG 548
 QY 585 GlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeuSerGluAla 604
 Db 549 CAAAGCATTTGAAATGACAGACACTTGAAGAGGTGACGCTCGGAGAGCTGTGCGAAGCA 608

RESULT 32

BUI39751

LOCUS BUI39751 696 bp mRNA linear EST 25-NOV-2002
 DEFINITION 60134527F1 CSEQCHL24 Gallus gallus CDNA clone CHEST116f8 5', mRNA sequence.

ACCESSION BUI39751

VERSION BUI39751.1 GI:25354188
 KEYWORDS EST

SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 696)

REFERENCE

AUTHORS

Boadman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

JOURNAL

MEDLINE

PUBMED

Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)

PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. 696

FEATURES

source

/organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hixex"
 /db_xref="taxon:9031"
 /clone="CHEST116f8"
 /dev_stage="16 day embryo"
 /lab_host="DH10B"
 /clone_1fb="CSEQCHL24"
 /note="Organ: brain; Vector: pBluescript II KS(+); Site 1:
 EORI; Site 2: NotI; Modification of pBluescript II KS(+)
 [Stratagene] vector to accommodate cDNA produced with the
 T-strimmed protocol (Construction of uni-directionally
 cloned cDNA libraries from messenger RNA for improved 3'
 end DNA sequencing by Glenn Fu, et al. U.S. Patent #
 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
 ligate in double stranded adaptor containing BsgI and
 BamHI sites [5'gcccgcgtgcagcccgatccgcaaaaaag]

ORIGIN

[5'aattcttttttcggatccggggctgcagc]"

Alignment Scores:
 Pred. No.: 2.39e-17 Length: 696
 Score: 395.50 Matches: 85
 Percent Similarity: 64.74% Conservative: 27
 Best Local Similarity: 49.13% Mismatches: 58
 Query Match: 6.63% Indels: 3
 DB: 5 Gaps: 2

US-10-044-692-2 (1-1132) x BUI39751 (1-696)

QY 9 AlaValArgSerLeuLeuArgSerHisTyrArgGluValLeuProLeuAlaThrPheVal 28
 Db 72 GCGGTCTCGGCGCGCTCGGGGCTGCTACGCCAGGCGCAGCCCTCGAGCCCTTCGTC 131
 QY 29 ArgArgLeu-----GlyProGlnGlyTyrArgLeuValGlnArgGlyAspProAla--- 45
 Db 132 CGGCGCTGACAGAGAGGTGGACCGGAGAGTTCGAGTCTCGAGCGACGACCGCTCAG 191
 QY 46 AlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyrAspAlaArgProPro 65
 Db 192 TGGTACCGGACCTTGTGTGCGAGTGTGTGCTGCTCCCGCGTGTCTGCGGCATC 251
 QY 66 ProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeuValAlaArgValLeu 85
 Db 252 CCGCGCCCATCTGCTTCCAGCAGATATTCAGTACAGAGAGTATCATCAAGATCTT 311
 QY 86 GlnArgLeuGlyGluArgGlyAlaLysAsnValLeuAlaPheGlyPheAlaLeuLeuAsp 105
 Db 312 CAGAGCTGTGTGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 371
 QY 106 GlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArgSerTyrLeuProAsn 125
 Db 372 GAGAACAGTGTCACTTCAGACTTTCGATCTTGTGTATATACGATATCTGTCAT 431
 QY 126 ThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeuLeuArgValGly 145
 Db 432 ACTGTACAGAAACCATTCGCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
 QY 146 AspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSer 165
 Db 492 GACGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
 QY 166 CysAlaTyrGlnValCysGlyProProLeuTyrGlnLeu 178
 Db 552 AACTGTACAGCTGCTGCGGCAACCAATTATGAACCTT 590

RESULT 33

LOCUS

BY783093 343 bp mRNA linear EST 23-MAR-2004

DEFINITION BY783093 RIKEN full-length enriched, 17.5 days embryo whole body

ACCESSION

BY783093

VERSION BY783093.1 GI:39709732
 KEYWORDS EST

SOURCE

ORGANISM

AUTHORS

Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 343)
 Carinaci, P., Waki, K., Shiraki, T., Kono, H., Shibata, K., Itoh, M.,
 Aizawa, K., Aikawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S.,
 Sugahara, Y., Saito, R., Otsu, N., Fukuda, S., Sato, K., Watanabe, A.,
 Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A.,
 Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Baisel, K.,
 Pavani, W., Aidinis, V., Nakagawa, A., Heid, W.A., Iwata, H., Kono, T.,
 Nakachi, H., Lyons, P., Wells, C., Hume, D.A., Fagiolini, M.,
 Hensch, T.K., Brinkmeier, M., Camper, S., Hirota, K., Mombaerts, P.,
 Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.
 Targeting a complex transcriptome: the construction of the mouse
 full-length cDNA encyclopedia

JOURNAL
MEDLINE
PUBMED
COMMENT

Genome Res. 13 (6B), 1273-1289 (2003)

22703353
12819125

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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.jp/>) for
further details.

FEATURES
Location/Qualifiers

1..343
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L930172A03"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_idb="RIKEN full-length enriched, 17.5 days embryo
whole body"

ORIGIN

Alignment Scores:

Pred. No.: 3,16e-17 Length: 343
Score: 387.00 Matches: 77
Percent Similarity: 86.00% Conservative: 9
Best Local Similarity: 77.00% Mismatches: 14
Query Match: 6.49% Indels: 0
DB: 6 Gaps: 0

US-10-044-692-2 (1-1132) x BY783093 (1-343)

QY 70 SerPheArGInValSerCyLeuLygIuLeuValAlaArgValLeuGlnArgLeuGys 89
Db 11 TCCTTCCACAGGTGTCTATCCCTGAAAGAGCTGTGGCGAGGTTGGACAGACTCTGC 70
QY 90 GluArgGlyAlaValAsnValLeuAlaPheGlyPheAlaLeuAspGlyAlaArgGly 109
Db 71 GAGCGCAACGAGAAAGCTGTGCTTTGGCTTTGAGCTTTACGAGGCCAGAGGC 130
QY 110 GIVProPGIuAlaPheThrThrsSerValArgSerTyLeuProAsnThrValThrAsp 129
Db 131 GGGCTCCACAGGCTTCACTAGTACGCTGCGTACCTTGGCCCAACACTGTTATGAG 190
QY 130 AlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArgValGlyAspAspValLeu 149
Db 191 ACCCTGGCGTGTGAGTGTGATGATGCTACTGTTGACCCGAGTGGGAGACCTGCTG 250
QY 150 ValHisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAlaTyGln 169
Db 251 GTCTACCTGTGGACACACTGTGCTCTTATCTTGTGTGCCCCCAGCTGTGCTACAG 310

RESULT 34

LOCUS BY784804 338 bp mRNA linear EST 23-MAR-2004

DEFINITION BY784804 RIKEN full-length enriched, 17.5 days embryo whole body

ACCESSION BY784804 GI:39711443

VERSION BY784804.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 338)
Garnini, P., Waki, K., Shiraki, T., Komno, H., Shibata, K., Itoh, M.,
Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S.,
Suzahara, Y., Saito, R., Oeato, N., Fukuda, S., Sato, K., Matsubara, A.,
Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A.,
Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustinich, S., Beisei, K.,
Pavan, W., Aidi, V., Nakagawa, A., Held, W. A., Iwata, H., Kono, T.,
Nakanishi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M.,
Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P.,
Muramatsu, M., Okazaki, Y., Kawai, J.,
Targeting a complex transposon: the construction of the mouse
full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.jp/>) for
further details.

FEATURES
Location/Qualifiers

1..338
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L930188J05"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_idb="RIKEN full-length enriched, 17.5 days embryo
whole body"

ORIGIN

Alignment Scores:

Pred. No.: 4,99e-17 Length: 338
Score: 384.00 Matches: 76
Percent Similarity: 86.00% Conservative: 10
Best Local Similarity: 76.00% Mismatches: 14
Query Match: 6.44% Indels: 0
DB: 6 Gaps: 0

US-10-044-692-2 (1-1132) x BY784804 (1-338)

QY 70 SerPheArGInValSerCyLeuLygIuLeuValAlaArgValLeuGlnArgLeuGys 89
Db 11 TCCTTCCACAGGTGTCTATCCCTGAAAGAGCTGTGGCGAGGTTGTGACAGACTCTGC 70
QY 90 GluArgGlyAlaValAsnValLeuAlaPheGlyPheAlaLeuAspGlyAlaArgGly 109
Db 71 GAGCGCAACGAGAAAGCTGTGCTTTGGCTTTGAGCTTTACGAGGCCAGAGGC 130
QY 110 GIVProPGIuAlaPheThrThrsSerValArgSerTyLeuProAsnThrValThrAsp 129
Db 131 GGGCTCCACAGGCTTCACTAGTACGCTGCGTACCTTGGCCCAACACTGTTATGAG 190
QY 130 AlaLeuArgGlySerGlyAlaTrpGlyLeuLeuLeuArgValGlyAspAspValLeu 149
Db 191 ACCCTGGCGTGTGAGTGTGATGATGCTACTGTTGACCCGAGTGGGAGACCTGCTG 250
QY 150 ValHisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAlaTyGln 169
Db 251 GTCTACCTGTGGACACACTGTGCTCTTATCTTGTGTGCCCCCAGCTGTGCTACAG 310

RESULT 35
 BY775178 mRNA linear EST 23-MAR-2004
 LOCUS BY775178
 DEFINITION Mus musculus full-length enriched, 17.5 days embryo whole body
 M385178.1 GI:39701816
 VERSION BY775178.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 336)
 Alarwa, K., Arakawa, T., Ishii, Y., Saeki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Otsu, N., Fukuda, S., Sato, K., Watanabe, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustinich, S., Beisel, K., Pavan, W., Aldini, V., Nakagawa, A., Heid, W. A., Iwata, H., Kono, T., Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Henrich, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, U. and Hayashiraki, Y.
 Targeting a complex transcritpome: the construction of the mouse full-length cDNA encyclopedia
 Genome Res. 13 (6B), 1273-1289 (2003)
 22703353
 12819125
 COMMENT Contact: Yoshinide Hayashiraki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site (http://genome.gsc.riken.jp/) for further details.
 FEATURES
 source Location/Qualifiers
 1..336
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6J"
 /db_xref="taxon:10090"
 /clone="U930091N09"
 /tissue_type="whole body"
 /dev_stage="17.5 days embryo"
 /clone_lib="RIKEN full-length enriched, 17.5 days embryo whole body"
 ORIGIN
 Alignment Scores:
 Pred. No.: 9 386-17 Length: 336
 Score: 380.00 Matches: 77
 Percent Similarity: 85.00% Conservative: 8
 Best Local Similarity: 77.00% Mismatches: 15
 Query Match: 6 37% Indels: 0
 DB: 6 Gaps: 0
 US-10-044-692-2 (1-1132) x BY775178 (1-336)
 QY 70 SerpheaTgTnValSerCysLeuYsgLueValAlaArgValLeuGlnArgLeuCyS 89
 DB 11 TCCTTCACACGAGTGTGATCCCTGAAGAGGCTGTGGCCAGGCTTGACAGAGCTG 70
 QY 90 GUAAGGGLAAlaValLeuAlaPheGlyPheAlaLeuLeuAspGlyAlaArgGly 109
 DB 71 GAGCGCAACGAGAAACGTGCTTTGGCTTTGAGCTGCTTAACGAGCGCAGAGCG 130

QY 110 G1PProGluAlaPheThrThrsValArgSerTyrLeuProAsnThrValThrAsp 129
 DB 131 GGGCTCCACGAGCTTACTACTAGCTGAGTACTGCTGAGTCCACACCTGTTATGAG 190
 QY 130 AlaLeuArgGlySerGlyAlaTfPGLyLeuLeuAlaGValGlyAspAspValLeu 149
 DB 191 ACCCTGCGTGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 250
 QY 150 ValHisLeuLeuAlaArgCysAlaLeuPheValLeuValAlaProSerCysAlaTfGln 169
 DB 251 GCTACCTGCTGGACACTGCTGCTTATCTTCTGAGTCCGCCCGAGTGTGCTTACG 310
 RESULT 36
 AW244516/c
 LOCUS AW244516/c
 DEFINITION 347 bp mRNA linear EST 25-JAN-2002
 BR. ENDO6809 Bain Rancourt retinoic acid induced ES cell neural differentiation subtration library Mus musculus cDNA clone 06809 similar to gp[AF073311][AF073311 Mus musculus telomerase catalytic subunit mRNA, complete cds, mRNA sequence.
 AW244516
 AW244516.1 GI:8051265
 EST.
 VERSION AW244516.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 347)
 Bain, G., Mansergh, F. C., Wide, M. A., Hane, J. E., Ito, G. A., Rancourt, S. L., Ray, W. J., Yoshimura, Y., Tsunaki, T., Gottlieb, D. I., and Rancourt, D. E.
 ES cell neural differentiation reveals a substantial number of novel ESTs
 Funct. Integr. Genomics 1 (2), 127-139 (2000)
 21652683
 11793228
 COMMENT Contact: Rancourt DE
 Department of Biochemistry and Molecular Biology
 University of Calgary
 3330 Hospital Drive N.W., Calgary, Alberta, T2N 4N1, Canada
 Tel: 403 220 2888
 Fax: 403 283 8727
 Email: rancourt@calgary.ca; URL: http://www.acs.ucalgary.ca/
 rancourt
 DNA sequencing by: University Core DNA Services, University of Calgary. Submitted sequence has been trimmed at both ends to remove the adaptor oligos containing the EcoRI sites, i.e. GAATTCGACCTA (beginning) and TAGTCGATTC (end) removed. Therefore, reported insert length is longer than actual EST sequence length.
 Insert length: 359 Std Error: 10.00
 Seq primer: T3 Or T7.
 FEATURES
 source Location/Qualifiers
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 /mol_type="mRNA"
 /strain="129"
 /db_xref="taxon:10090"
 /clone="06809"
 /cell_type="embryonic stem (ES) cell"
 /cell_line="D3"
 /lab_host="DMS alpha"
 /clone_lib="Bain Rancourt retinoic acid induced ES cell neural differentiation subtration library"
 /note="vector: pBluescript II SK+ (Stratagene), Site_1: EcoRI, Site_2: EcoRI; Library constructed by Dr. Gerard Bain (present address: Hoechst-ARIAD Genomic Center, ARIAD Pharmaceuticals Inc., 26 Landsdowne Street, Cambridge, Massachusetts, 02139-4234, U.S.A.). To isolate cDNAs corresponding to mRNAs which are upregulated during the neural differentiation of ES cells in vitro, the subtractive hybridization technique of Wang and Brown (1) was employed. Poly(A)+ RNA was prepared from both undifferentiated ES cells and from embryoid bodies which had been cultured for 4 days in the absence of RA followed


```

Db      272 CTCAGGCCA---TTATTGAGACCAAGCATTTCTTACTCCAGGGAGATGCGCAAG 328
Qy      340 GlnLeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArg 359
      329 CGCTTAACCCCTCATCTTCTACTACTGACCAACCTTCAGACCTTAATTGACTGGGGCCAGGAGA 388
Qy      360 LeuValGluThrL11PheLeuGlySerArgProTpmPmeProGlyThProArgArgLeu 379
      389 CTGGTGAGATCATCATCTTCTGGCTTCAGGCTTACGACATCATGACCACTCTGCAAGACA 448
Qy      380 ProArgLeuProGluArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsn 399
      449 CACCGCTTATCGCGTGTGATCTGCGAGATGCGGCCCTCTTCCACAGCTGCTGGAGAC 508
Qy      400 HisAlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAla--- 418
      509 CAGCAGAGTGCACCAATATGTCAGACTCTCAGGTCAATTCAGATTCGAAACACCAAC 568
Qy      419 -----ValThrProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAla 436
      569 CAACAGGTGACAGATCCCTTG----- 589
Qy      437 AlaProGlnGluGluSerThrAspProArgArgLeuValGlnLeuLeuArgLysSer 456
      590 -----AAACACGACCCACGCGACCTCATGATTGCTCCGCTGCACAGC 634
Qy      457 SerPro 458
      635 AGTCCC 640
Db
RESULT 39
CK392784      619 bp      mRNA      linear      EST 29-DEC-2003
LOCUS      K0850A03-5 NIA Mouse 8.5-dpc Whole Embryo cDNA Library (Long) Mus
DEFINITION      musculus cDNA clone NIA:K0850A03 IMAGE:30083138 5', mRNA sequence.
ACCESSION      CK392784
VERSION      CK392784.1 GI:40383303
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 619)
Pao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)
JOURNAL
MEDLINE      21429098
PUBMED      11544199
COMMENT      Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun-grc.nia.nih.gov
Plate: K0850 row: A column: 03
Seq primer: M13 Reverse
High quality sequence stop: 619
POLYA=No.
FEATURES
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1..619
location/Qualifiers
/mol_type="mRNA"
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taabst:K0850A03-5"
/db_xref="taxon:10090"
/clone="NIA:K0850A03 IMAGE:30083138"
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tissues at 8.5-days postcoitum"
/dev_stage="8.5-days postcoitum"
/lab_host="DH10B"
/clone_11b="NIA Mouse 8.5-dpc Whole Embryo cDNA Library
(Long)"

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/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI. Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://igsun-grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 13 embryos at 8.5-days postcoitum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTTACTTCTAGTCCGAGCGGCCCTTTTCTTTT-3'] from 9.1 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker Lr-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Pao (NIA)."

ORIGIN

Alignment Scores:

Pred. No.:	2,24e-15	Length:	619
Score:	366.00	Matches:	97
Percent Similarity:	55.61%	Conservative:	22
Best Local Similarity:	45.33%	Mismatches:	79
Query Match:	6.14%	Indels:	16
DB:	7	Gaps:	6

US-10-044-692-2 (1-1132) x CK392784 (1-619)

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Qy      209 GlnAlaGlyValProLeuGlyLeuProAlaProGlyAlaArgArgGlyLysAla 228
      3 GAAGACCGCAACCCCTGCGCTCGCATCTGAGGTACAAAGAGCATCTGATCC 62
Db
Qy      229 SerArgSerLeuProLeuProLysArgProArgArgGlyAlaAlaProGluProGluArg 248
      63 AGTACAAAGTGTCTTCAAGAGGACAGATCTGTCGAGAGTGAGGAG 122
Db
Qy      249 ThrProValGlyGlnGlySerThrAlaHisProGlyArgThrArgGlyProSerLysArg 268
      123 GGAACC-----CACAGCAGGTGCTACCAACCCCATCGGCACA 161
Db
Qy      269 GlyPheCysValValSerProAlaArg-----ProAlaGluGluLysThr 283
      162 TCATGG--GTGCCAAGTCTCTGCTGTCGCCCGAGGTGCTCATCTGAGAGAAATTTG 218
Db
Qy      284 SerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGlyArgGlnHis 303
      219 TCTTCAAGGAAAGAGTGTGACCTGAGTCTCTCT---GGGTGGGTGCTGTAAAC 275
Db
Qy      304 HisAlaGlyProProSerThrSerArgProProArgProTpmPmpThrProCysProPro 323
      276 AAGCCAGCTCCACATCTGCTGTCTGTCACCCCGCAAAATGCTTTCAGCTCAGGCCA 335
Db
Qy      324 ValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAsp---LysGluGlnLeuArg 342
      336 ---TTATTGAGACCAAGCATTTCTTACTCCAGGGAGAGTGGCAAGAGGCTTAAC 392
Qy      343 ProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeuValGlu 362
      393 CCTCATCTTCTACTGACCAACCTCCAGCTTAATTGACTGGGGCCAGGAGACTGTGGAG 452
Db
Qy      363 ThrL11PheLeuGlySerArgProTpmPmeProGlyThProArgArgLeuProArgLeu 382
      453 ATCATCTTCTGGGCTCAAGGCTTACGACATCAAGACCACTCTGCAAGACACACCTCA 512
Db
Qy      383 ProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHisAlaGln 402
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/db xref="taxon:9031"
/clone="CHST151a12"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQC.H18"
/notes="Organ: small intestine; Vector: pluscript II
KS(+); Site 1: EcoRI; Site 2: NotI; Modification of
pluscript II KS(+); (Stratagene) vector to accommodate
cDNA produced with the T-trimmed protocol (Construction of
unit-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pluscript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor
containing BspI and BamHI sites
[5'ggcgcgtgcagcccgacccgaaacgaag]
[5'aattcttttttcgataccg99gctgcacgc]"

```

ORIGIN

Alignment Scores:

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Pred. No.: 6,26e-14 Length: 875
Score: 348.50 Matches: 105
Percent Similarity: 53.46% Conservative: 34
Best Local Similarity: 40.38% Mismatches: 90
Query Match: 5.85% Indels: 32
DB: Gaps: 9

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US-10-044-692-2 (1-1132) x BU122597 (1-875)

```

QY 4 AlaProArgGysArgAlaValArgSerLeuArgSerHis----- 17
Db 38 GCTCCGGAATGACCGCGGAGAGACCTTCGCCGCTCGGCGCGCGCGCGCTG 97
QY 18 TyrArgGluValLeuProLeuAlaThrPheValArg-----ArgLeuGlyProGlnGly 35
Db 98 TAGCCGAGGCGACGCGCGTGCAGAGCCTTCGCCGCGCGCTGCAGAG-GGTGCACCGGG 156
QY 36 TyrArgLeuValGlnArgGlyAspProAla---AlaPheArgAlaLeuAlaGlnCys 54
Db 157 GAGGTGAGGTGCTGCAGAGCGAGCGCTCAGTCTACCGAGCTTCGTCGCGAGTGC 216
QY 55 LeuValCysValProTyrPaspAlaArgProProProAlaAlaProSerPheArgGlnVal 74
Db 217 GTGGTTCGCGTCCCGCGGTGCTCGCGCATCCCGCGCCATCTGCTTCAGCAGTTA 276
QY 75 SerCysLeuGluLeuValAlaArgValLeuGlnArgLeuGlyGluArgGlyAlaVal 94
Db 277 TCCAGTCAGAGCGAAGTCATCAAGAAATCGTTCAGAGGCTGTGTGAAGAAAGAG 336
QY 95 AsnValLeuAlaPheGlyPheAlaLeuLeuAspGlyAlaArgGlyGlyProGluAla 114
Db 337 AAGATCTTCGCGTATGATCTCTCTGATGATGAGAAAGTGTCACTTCAGAGTTTG 396
QY 115 PheThrThrSerValArgSerTyrLeuProAsnThrValThrAspAlaLeuArgGlySer 134
Db 397 CCATCTTCGTGATATACAGCTATCTGTCAATCTCTAACAAGAAAGATTCGGATCAGT 456
QY 135 GlyAlaTyrPglyLeuLeuLeuArgArgValGlyAspAspValLeuValHisLeuLeu-Al 154
Db 457 GGCCTCTGGAGATATCTCTAGATGATGATGAGGAGCGAGTATGATGATCTCTGAG 516
QY 154 AArgCysAlaLeuPheValLeuValAlaProSerCysAlaTyrGlnValCysGlyProPr 174
Db 517 CACGCTGCTCACTTCATGCTGCTTCGCCAAGTAACTGTTACAGAGGTCTCGGCGAAGC 576
QY 174 OLeuTyrGlnLeuGlyAlaAlaThrGlnAlaArg-ProProProHisAlaSerGlyProA 194
Db 577 AATTATATGAATCT---ATTTCGCTAACCGTATGCGCCATCCCA-----GGTTTGTTA 627
QY 194 ArgArgArgLeuGlyCysGluArgAlaTyrAsnHisSer-----ValArg 209
Db 628 GACGACGGTACTCA-----AGGTTTAAACATATATAGCTTCTTACTATATGCGCA 678

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```

QY 209 lualaglyValProLeuGlyLeuProAlaProGlyAlaArgArgArgGlySerAla 229
Db 679 AAGGTGCTGTTTCACAGGACATATCTTTCAGT-----CCCATGTGTGAAGTGCAG 732
QY 229 eArgSerLeuProLeuProLysArgProArgArgGlyAlaAlaProGluProGlu 247
Db 733 GCCAGAA-----CGTCAGAGTCTGTCTCCAGCAGGAG 767

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RESULT 42

CO014076

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..930

/organism="Coccidioides posadasii"

/mol_type="mRNA"

/strain="C735"

/db_xref="taxon:199306"

/clone="CIRC236"

/dev_stage="spherules"

/lab_host="E. coli DH10B, T1 phage resistant"

/clone_lib="Coccidioides posadasii spherule cDNA library, 0.4 to 2.3 kb"

/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV; Coccidioides posadasii spherule cDNA library, 0.4 to 2.3 kb"

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ORIGIN
Alignment Scores:
Pred. No.: 6.87e-14 Length: 930
Score: 348.50 Matches: 104
Percent Similarity: 50.16% Conservative: 55
Best Local Similarity: 32.81% Mismatches: 121
Query Match: 5.85% Indels: 37
DB: Gaps: 11

```

US-10-044-692-2 (1-1132) x CO014076 (1-930)

```

QY 605 GluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg----- 620
Db 4 GAGGTAGAGGAAGAAAGCGCGCAGG-----ATCTGTCTGAGAGAGACCTCGGCTAC 57
QY 621 -----LeuArgPheLeuProLysProAspGlyLeuArgProAlaAsnMet----- 636
Db 58 GGCACCTTCGATGCTCCCAAGCGCACCGAGGCTCGCCATCGTTAACTTGAGAAAG 117
QY 637 AspTyrValValGlyAlaArgThrPheArgArgGluValArgAlaGluArgLeuThrSer 656
Db 118 CGCGCATCGTCAAGTCAAGGTGAATGAGAGATGAGCTGGGCGACAGTCCCAACAG 177
QY 657 ArgValLysAlaLeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeu 676

```

```

Db      178 CTACTTCACCCGTTTTCAGGNGCTTAATTGTGAAAGAGCTTCGAAAGTCGGGCTCTC 237
Qy      677 GYIAlaserValleuGlyLeuAspIleHISArgAlaITrPArgThrPheValleuArg 696
Db      238 GGTGGGTGATGATTCCTCGTGGGACATGATCGTTTCGACTGAAAGAGGTTCCGGGAAAGA 297
Qy      697 -----ValArgAlaGlnAspProProGluIleuLeuPheValIysVal 711
Db      298 CTGTATCAGAGGGGAAATCAGCAGAAAGATCCG-----CTGTATTTGTGTAACCTT 348
Qy      712 AspValIThrGlyAlaITyrAspThrIleProGlnAspArgLeuThrGluValIleAlaSer 731
Db      349 GACGTGACAGGCTTGCTTGTATCCATCTCAGAAAGCGACTGCTGCGTTGGTGTACGGC 408
Qy      732 ILeIleYrProGlnAspThrITyrCysValArgArgTyrAlaValIle----- 747
Db      409 TTGATCTCC--GAGATGAATACCGGTGACAGATGACGGAGAGGTGGGGCTTACAC 465
Qy      748 GlnIysAlaAlaHISglYHIS-----ValArgIys 757
Db      466 CAGCGGGGTCTCCCGGCGCAGGAGCAAGATGAGGAGACAGCAAGCAACCCGTGAAAG 525
Qy      758 AlaPheYsSerHISValSerThrLeuThrAspLeuGlnProTyrMetArgIlnPheVal 777
Db      526 ---TTTGTCCTCCAGGGCGCTCCGCTGAGACTTAAAGAT---GCATACGACTTCGTC 579
Qy      778 AlaHISLeuGlnGluThrSerProLeuArgAspAlaValIleGluIlnSerSer 797
Db      580 GTGAGCGCAGCAAGAAAGTACGAAAGAAACCGTGTGTTCACACGGGGAAACGAG 639
Qy      798 LeuAsnGluAlaSerSerITyLeuPheAspValPheLeuArgPheMetCysHISAla 817
Db      640 AAACGGCAGCAGAGCCGACACTTTCGCGGCGCTTTCGACAGACACTGGGAAACAACCTG 699
Qy      818 ValArgIleArgGlyIysSerITyValGlnCysGlnGlyIleProGlnIysSerIleu 837
Db      700 GTGAAGATCGGAGAGATATTTTCGACAGAAAGAGGATCCCGAGGGCTCGGTTGTG 759
Qy      838 SerThrLeuLeuCysSerITyArgIysAspMetGluAsnIysLeu-----PheAla 855
Db      750 TCACATCTCTGTGCAATTTCTTACGGCGAGCAGCAAGCAGCGAGCTTGCGCTTCTTG 819
Qy      856 GlyIleArgArgAspGlyLeuLeuLeuArgValAspAspPheLeuLeuValThrPro 875
Db      820 GCGCGCGATGAAGATCGCTCTGCTGCTGATGACGACTCACTGCTTATCACACGAG 879
Qy      876 HIsLeuThrHISAlaIysThrPheLeuArgThrLeuValArgGlyValPro 892
Db      880 AAGGAGAGCAGCAGCAGCGGTTTCTACGGGTGATGCTGAAAGGGGGCCA 930

RESULT 43
LOCUS      CO028055      983 bp      mRNA      linear      EST 10-JUN-2004
DEFINITION EST066439 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
ACCESSION  CO028055
VERSION     CO028055.1  GI:48558725
KEYWORDS    EST.
SOURCE      Coccidioides posadasii
ORGANISM    Coccidioides posadasii
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE   1  (bases 1 to 983)
AUTHORS     Gardner,M.J. and Cole,G.T.
TITLE       Analysis of gene expression in Coccidioides posadasii mycelia and
            spherules via expressed sequence tags
JOURNAL     Unpublished (2003)
COMMENT     Other ESTs: EST806440
            Contact: Gardner MJ
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301 838 3519
            Fax: 301 838 0208

```

```

FEATURES             Email: gardner@igr.org.
            source      Location/Qualifiers
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            /organism="Coccidioides posadasii"
            /mol_type="mRNA"
            /strain="C735"
            /db_xref="taxon:199306"
            /clone="CIPA039"
            /dev_stage="spherules"
            /lab_host="B. coli DH10B, T1 phage resistant"
            /clone_11b="Coccidioides posadasii spherule cDNA library,
            0.5 to 5.3 kb"
            /note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
            Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
            kb"

ORIGIN
Alignment Scores:
Pred. No.:      1.87e-11      Length:      983
Score:          314.00      Matches:      88
Percent Similarity: 48.90%      Conservative: 45
Best Local Similarity: 32.35%      Mismatches: 115
Query Match:    5.27%      Indels:      24
DB:              Gaps:      8

US-10-044-692-2 (1-1132) x CO028055 (1-983)
Qy      827 GlnCysGlnGlyIleProGlnIysSerIleLeuSerThrLeuLeuCysSerITyArg 846
Db      974 CAGAAAGACGGGATCCCGAGGGCTCGTGTGTGACAGATCTGTGCAATTTCTTTCAC 915
Qy      847 GlyAspMetGluAsnIysLeu-----PheAlaGlyIleArgArgAspGlyLeuLeu 864
Db      914 GCGGAGCAGCAAGCAGCGGAGCTTGCTTGGCGCGGAGTGAAGAAATCGTCTGCTG 855
Qy      865 ArgLeuValAspAspPheLeuLeuValIThrProHISLeuThrHISAlaIysThrPheLeu 884
Db      854 CGTGTGATGACGACTACCTGCTTATCACAGAGAGAGAGCAGCAGCGGCTTCTCA 795
Qy      885 ArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeuArgIysThrVal 904
Db      794 CGGTGATGTGGAAGGGGCGCAGAGATATGGGATCTCGTGACTCCGCGCAAGACGTTG 735
Qy      905 ValAsnPheProValGluAspGluAlaLeuGlyIleThrAlaPheValGlnMet----- 922
Db      734 GTCAACTTTGAAGTTGAC-----GTGGCGGTTACGACATCCGGCGCTGGCGCAG 684
Qy      923 ProAlaHISGlyLeuPheProTyrCysGlyLeuLeuAspThrArgThrLeuGluVal 942
Db      683 TCGTGCAGAGACATTTCCATCTGCGGGAACCTTATCGATACAGAGCGCTGGCGATC 624
Qy      943 GlnSerAspTyrSerSerITyAlaArgThrSerIleArgAla-----SerLeuThrPhe 960
Db      623 AGCAAGATCGGACCGCGCAGCAGCAGATCTCCACGTGTGCGACTCGCTCACGGCTT 564
Qy      961 AsnArgGlyPheIysAlaGlyArgAsnMetArgArgIysLeuPheGlyValLeuArgLeu 980
Db      563 GAGCTGAGAGAGACCCCGAGAGGGGTTTACCCGAAATCTGTGTATGTTAAACTA 504
Qy      981 IysCysHISerLeuPheLeuAspLeuGlnValAsnSerLeuGlnIThrValCysThrAsn 1000
Db      503 CAGCGGCAACGGATTTCTTCGACGTGAACGACATTCGCGAGGGTGTGCTGGCGGCT 444
Qy      1001 ILeITyIlsLeuLeuLeuGlnAlaITyrArgPheHISAlaCysValLeuGlnLeuPro 1020
Db      443 GTATATACCGCGCTTCTGACTGTGCGATGAGAGATATGCTATCTGGCGTCTTCG 384
Qy      1021 PheHISGlnGlnValITrPlysAsn-----ProThrPhePheLeuArg 1034
Db      383 CCGCGGCGAGGAGACCGCGAGGTGAGAGGTTCTTGATGAGACATGCTCACCCGC 324
Qy      1035 ValIleSerAspThrAlaSerLeuCysITySerIleLeuIysAla-----LysAsnAla 1052

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Db 323 ACCATCGGGGCTCATCGACTACGCGGTGCGCTGATCCGCTCTCGACGAGAGCTCC 264
 Qy 1053 GJymeSerLeuGlyAlaValysGlyAlaValysGlyProLeuProSerGlyAla----- 1069
 Db 263 GGGGGTACGACGCGC--GAGGGCAGAGTGGGACAGACAGTAATATGCTTATTACA 207
 Qy 1070 -----ValGlnTrpLeuCyshGlnAlaPhe 1078
 Db 206 AGGGTGCAGATCCAGTGGTGGCGTGCAGCGCTTC 171

RESULT 44
 C0024489/c 1023 bp mRNA linear EST 10-JUN-2004
 LOCUS EST802873 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
 DEFINITION kb Coccidioides posadasii cDNA clone CIFA132 3' end, mRNA sequence.
 ACCSSION C0024489
 VERSION C0024489.1 GI:48551589
 SOURCE EST.
 KEYWORDS Coccidioides posadasii
 ORGANISM Coccidioides posadasii
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; mitosporic Onygenales; Coccidioides.
 1 (bases 1 to 1023)
 REFERENCE Gardner, M.J. and Cole, G.T.
 ANALYSIS of gene expression in Coccidioides posadasii mycelia and
 spherules via expressed sequence tags
 Unpublished (2003)
 OTHER STRS: EST802874
 CONTACT: Gardner MJ
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@ligr.org.
 FEATURES
 source
 1. 1023
 /location=Qualifiers
 /organism="Coccidioides posadasii"
 /mol_type="mRNA"
 /strain="C735"
 /db_xref="taxon:199306"
 /clone="CIFA132"
 /dev_stage="spherules"
 /lab_host="E. coli DH10B, T1 phage resistant"
 /clone_lib="Coccidioides posadasii spherule cDNA library,
 0.5 to 5.3 kb"
 /note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV.
 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
 kb"

ORIGIN
 Alignment Scores:
 Pred. No.: 6,08e-11 Length: 1023
 Score: 307.00 Matches: 92
 Percent Similarity: 49.12% Conservative: 47
 Best Local Similarity: 32.51% Mismatches: 120
 Query Match: 5.15% Indels: 26
 Gaps: 8
 DB: 7

US-10-044-692-2 (1-1132) x C0024489 (1-1023)

Qy 816 HIsAlaValArgIleAlaGlyLysSerTyValGlnCysGlnGlyIleProGlnGlySer 835
 Db 1001 CACCTTGTGAAGATCGGAGAAAGATTTCGA-CAGAGAAACGGGATCCCGCAGGGCTCG 943
 Qy 836 IleLeuSerThrLeuLeuCySerLeuCySTyTyrGlyAspMetGluAsnLysLeu----- 853
 Db 942 GTTGTGTCAAGCATCTGTGCAATTCTTCTACGGCGAGCAGACGAGCGGA-GCTGGC 884
 Qy 854 PheAlaGlyIleAlaGlyAspGlyLeuLeuAlaGlyValAspAspPheLeuLeuVal 873
 Db 883 TTTCTGGGGCGCATGAAGATGCTCTCGCTGCGCTGATGACGACTACTGCTTATC 824
 Qy 874 ThrProHleuThrHisAlaLysThrPheLeuArgThrLeuValArgGlyValProGlu 893

Db 823 ACCACAGAGAGAGACGACAGAGAGCGGTTTCTACCGGTATGCTGGAGAGGGGCCAGAG 764
 Qy 894 TyrGlyCysValValAsnLeuArgLysThrValValAsnPheProValGlnAspGlyAla 913
 Db 763 TATGAGATCTCGGTGACTCCCGGCAAGACGTTGGTCAACTTGAAGTTAG----- 713
 Qy 914 LeuGlyGlyThrAlaPheValGlnMet-----ProAlaHisGlyLeuPheProTyrCys 931
 Db 712 GTGGCGGTTACGACATCCGCGCGCTGGGACATCGTCGAGAGAGAAATTTCATCTCG 653
 Qy 932 GJyLeuLeuAspThrArgThrLeuGluValGlnSerAspTyrSerSerTyAlaAsp 951
 Db 652 GGAAACCTTATCGATACACAGACGCTGCGCATCAGCAAGATCGACCCGCCAGACAGAC 593
 Qy 952 ThSerIleArgAla-----SerLeuThrPheAsnArgGlyPheValAlaGlyAsn 969
 Db 592 GACGATCTCCACGTGTCGACTCGCTCAGCTTGAGCTGAGAGAGACCCGCCAGCGGG 533
 Qy 970 MetArgArgLysLeuPheGlyValLeuArgLysCysHisSerLeuPheLeuAspLeu 989
 Db 532 TTCTACCGCAATCTCTGTCTATGTTTAACTACAGCGCAGCGATGTTCTTCGACGTG 473
 Qy 990 GlnValAsnSerLeuGlnThrValCysThrAsnIleTyrIleLeuLeuGlnAla 1009
 Db 472 AAGCACAATTCGCGAGCGGTGCTGCGGGGTATATACCGCTTCTCGACTGTGCG 413
 Qy 1010 TyrArgPheHisAlaCysValLeuGlnLeuProPheHisGlnValTyrLysAsn--- 1028
 Db 412 ATGAGATGATGTCGATCTGATCTGCGCTCTCGGGGGCGAGCAGCGAGAGGTG 353
 Qy 1029 -----ProThrPheLeuArgValIleSerAspThrAlaSerLeuCys 1043
 Db 352 AGAGATCTCGATGACGACATGCTCACCCGCACTCGGGGGGCTCARTGACTACCGC 293
 Qy 1044 TyrSerIleLeuLysAla-----LysAsnAlaGlyMetSerLeuGlyAlaValysGlyAla 1061
 Db 292 GTGGCGCTGATCCGCTCTCGACGAGAGCTCCGGGGTGCACAGCGC--GAGGGCAGG 236
 Qy 1062 AlaGlyProLeuProSerGlyAla-----ValGlnTrpLeuCyshHis 1075
 Db 235 AGTGCACAGACAGTAATATGCTTATTACAAGGGTGACAGATCCAGTGGTGGCGGTG 176
 Qy 1076 GlnAlaPhe 1078
 Db 175 CAGCGCTTC 167

RESULT 45
 CF547484 774 bp mRNA linear EST 22-SEP-2003
 LOCUS AGENCOURT_15568263 NICHD_XGC_Kid1 Xenopus laevis cDNA clone
 DEFINITION IMAGE:7009014 5', mRNA sequence.
 ACCSSION CF547484
 VERSION CF547484
 KEYWORDS EST.
 SOURCE CF547484.1 GI:34884316
 ORGANISM EST.
 Xenopus laevis (African clawed frog)
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus; Xenopus.
 1 (bases 1 to 774)
 REFERENCE NC1-GenAP <http://www.ncbi.nlm.nih.gov/ncicgaf>.
 NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP);
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute, MD 20892
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaops-remail.nih.gov
 Tissue Procurement: Dr. Igor Dawid
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)

	290	GAGGAG---TATCAGCTCCAGGTTTACGTTAACCGTGACGAGAGCAGATCGGACCGACT	346
	756	ArgLySAlaPheIySerHisValSerThrLeuThrAspLeuGlnProIyrrMetArgGln	775
	347	GGCTGTCCAAAGAGGAGGAGCCATCTCATGTGCATACGAGGTGAGCATTTTCAATGCTCAG	406
Qy	776	PheValAlaHisIeuGlnGluThrSerProLeuArgAspAlaValIleGlnIns	795
	407	TTGATT---CAGATGGCGCAGCATGGGAGAGATCAAGATCTATCTATTCATCAGGTT	463
Qy	796	SeSerIeuAsnGluIaSerSerGlyIeuPheAspValPheLeuArgPheMetCysHis	815
Db	464	CACACAGATTAAAGGTGACACCAAGAGACTTGTTCAGAGACTGACCAACATGTCATGGCT	523
Qy	816	HisAlaValArgIleArgGlyIySerTyrVal-GlnCysGlnGlyIleProGlnIySe	835
	524	GATGTATGTGAAGGTGGTGAAGTACTATTGTGGCGTCAGAGATGGCATTCATGAGGCTC	583
Qy	835	HisLeuSerThrIeuLeuIyCysSerIeuCysTyrGlyAspMetGluAsnIySleuPheAl	855
Db	584	CATTCTTCGTCCTTCTCTGCACTTCTTCTTAATGCTCACCTGGAGAGATGTAATCTCTC	643
Qy	855	agIyIleArgArgAspGlyIeuLeuIeuValGluValAsp	869
	644	AGATATGACCAAGAGGGCTGATGATGAGATGATTGATGATGAC	686
RESULT 47			
BU224024		813 bp	mRNA
LOCUS	6037963349P1	CSEQCCHN23	Gallus gallus cDNA clone CHEST765Bp13 5', mRNA
DEFINITION			sequence.
ACCESSION	BU224024		
VERSION	BU224024.1	GI:25458494	
KEYWORDS	EST.		
SOURCE	Gallus gallus (chicken)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
REFERENCE	1 (bases 1 to 813)		
AUTHORS	Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.		
TITLE	A Comprehensive Collection of Chicken cDNAs		
JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)		
MEDLINE	22335534		
PUBMED	12445392		
COMMENT	Contract: Simon Hubbard		
	Department of Biomolecular Sciences		
	University of Manchester Institute of Science and Technology		
	(UMIST)		
	PO Box 88, Manchester, M60 1QD, UK		
	Tel: 01612008930		
	Fax: 01612360409		
	Email: Simon.Hubbard@umist.ac.uk.		
FEATURES	Location/Qualifiers		
source	1..813		

ORIGIN

compatible sites of a custom modified MCS of the phagescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9248-9253 and Bonaldi et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

Alignment Scores:	1.57e-09	Length:	813
Pred. No.:		Matches:	74
Score:	284.50	Conservative:	55
Percent Similarity:	55.03%	Mismatches:	39
Best Local Similarity:	39.15%	Indels:	25
Query Match:	4.77%	Gaps:	6
DB:	5		

US-10-044-692-2 (1-1132) x BU224024 (1-813)

DQ
73 GlnValSerCysIleuNysGluLeuValAlaArgValLeuGlnArgLeuCysGluArgGly 92

DB
1 CAGTTATCCAGTCACAGCAAGTCATCACAGAAGATCGTTCAGGGCTGTGTGAAGAAGA 60

OY
93 AlaIysAsnValLeuAlaPheGlyPheAlaLeuLeuAspGlyValaArgGlyGlyProPro 112

DB
61 AAGAAAGAACATCTTCGGTGATGATACTCTTCCTGGATGAGAAACAGTTGCATTCCAGA 120

OY
113 GluAlaPheThrHisSerValArgSerTyrLeuProAsnThrValThraPheAlaLeuArg 132

DB
121 GTTTGGCATCTTCGTATATACAGTAATCTGCCAATCTGTACACAGAAACGATTGCG 180

OY
133 GlySerGlyAlaTrrPglYLeuLeuLeuLeuArgValGlyAspAspValLeuValHisLeu 152

DB
181 ATCGATGGCCCTCTGGAGATACTCTCTGATGATAGCATAGGGAGACAGCGATGATGATCCTG 240

OY
153 LeuAlaArgCysAlaLeuPheValLeuValaAlaProSerCysAlaTyrGlnValCysGly 172

DB
241 CTGAGAGCACTGGACACTCTTCATCTGGTTCGCCCAAGTAACTGTTCACAGTCTGGGG 300

OY
173 ProPoleuTyrGlnLeuGlyValAlaAlaThrGlnAlaArgProProPro----- 188

DB
301 CAACCAATTTATGAACTT--ATTTCGGGTAAAGTAGGGCCATCTCCAGGGTTTGTTAGA 357

OY
189 -----HisAlaSer-----GlyProArgArgArgLeuGly 198

DB
358 CCACGGTACTCAAGGTTTAAACATATATAGCTTGCTGTGACTATGTGCGAAAAGCGTTGTG 417

OY
199 CysGluArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAla 218

DB
418 TTTCACAGG-----CACTATGTTTTCCAACGATACACAGTGGTGAGAGTCAAGCGCG-- 465

OY
219 ProGlyAlaArgArgArgGlyGlySerAlaSerArg-----SerLeuProLeuPro 235

DB
466 -----AGACGTGAGGTCTGTCTTCACACAGAGAAAAACAGAAAGACCAATGAGAT 516

OY
236 LysArgProArgArgGlyValaAlaLaPro 244

DB
517 ACAAAAGCTTAGGTCTGTATACAGCT 543

RESULT 48	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
EX882610	EX882610	646 bp mRNA	EX882610	1	linear	EST 20-JUL-2004			
			EX882610		tcdb	Oncohyrnchus mykiss	CDNA	clone	tcdb0060c.h.01
					sequence.				5prim,
			EX882610.2	GI:42815406		EST.			
						Oncohyrnchus mykiss	(rainbow trout)		
						Oncohyrnchus mykiss			
						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
						Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
						Protacanthopterygii; Salmoniformes; Salmonidae; Oncohyrnchus.			
						1 (bases 1 to 646)			
						Govoroun, M., Guiguen, Y. and Le Gac, F.			

TITLE Construction and primary characterization of normalized cDNA libraries in rainbow trout, *Oncorhynchus mykiss*
JOURNAL Unpublished (2003)
COMMENT On Dec 18, 2003 this sequence version replaced gi:40127495.
Contact: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigena@portefeuille.inra.fr to obtain the chromatogram of this sequence.
Plate: 0060 row: h column: 1
Seq primer: M13R
Location/Qualifiers

FEATURES

source

1.646
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/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/note="Vector: pT7T3D-pac; AGENAE Rainbow trout multi-tissues - normalized + 2 subtractions; Clone distribution: AGENAE Resource centre, Francois PUMI, Francois Pluim@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LRBG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"

ORIGIN

Alignment Scores:

Pred. No.: 1.4e-09 Length: 646
Score: 283.00 Matches: 61
Percent Similarity: 60.31% Conservative: 18
Best Local Similarity: 46.56% Mismatches: 52
Query Match: 4.75% Indels: 0
DB: 5 Gaps: 0

US-10-044-692-2 (1-1132) x BX882610 (1-646)

QY 1000 AenlietYrYsIlLeuLeuLeuGlnAlaTYrArGpHeHsAlaCyseValLeuGlnLeu 1019
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QY 1080 LeuYsLeuThrArHsArGValThrTYrValProLeuLeuGlySerLeuArGThrAla 1099
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DEFINITION BX315053 tcay *Oncorhynchus mykiss* cDNA clone tcay0029b.n.21 5prim, mRNA sequence.
ACCESSION BX315053
VERSION BX315053.2 GI:42620226
KEYWORDS EST.
SOURCE *Oncorhynchus mykiss* (rainbow trout)
ORGANISM *Oncorhynchus mykiss*

REFERENCE
AUTHORS Govoroun,M., Guiguen,Y. and Le Gac,F.
TITLE Construction and primary characterization of normalized cDNA libraries in rainbow trout, *Oncorhynchus mykiss*
Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29595698.
Contact: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigena@portefeuille.inra.fr to obtain the chromatogram of this sequence.
Plate: 0029 row: n column: 21
Seq primer: M13R.
Location/Qualifiers

FEATURES

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ORIGIN

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Best Local Similarity: 46.56% Mismatches: 52
Query Match: 4.75% Indels: 0
DB: 5 Gaps: 0

ORIGIN

US-10-044-692-2 (1-1132) x BX315053 (1-731)
QY 1000 AenlietYrYsIlLeuLeuLeuGlnAlaTYrArGpHeHsAlaCyseValLeuGlnLeu 1019
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QY 1020 PropHeHsGlnGlnValTrrYsAsnProThrPheHeLeuArGValIleSerAspThr 1039
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DEFINITION animal Clona intestinalis cDNA clone cima830013 5', mRNA sequence.
ACCESSION  BM363763
VERSION     BM363763.1 GI:4775564
KEYWORDS    EST
SOURCE      Clona intestinalis
ORGANISM    Clona intestinalis
REFERENCE   1 (bases 1 to 651)
AUTHORS     Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
TITLE       Expressed genes in Clona intestinalis (2004)
JOURNAL     Unpublished (2004)
COMMENT     Contact: Yutaka Satou
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4095
            Fax: 81-75-705-1113
            Email: yutaka@ascidian.zool.kyoto-u.ac.jp.
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FEATURES
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US-10-044-692-2 (1-1132) x BM363763 (1-651)
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Search completed: October 28, 2004, 20:46:57
 Job time : 7891 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 29, 2004, 08:05:49 : Search time 1214 Seconds

(without alignments)
4781.256 Million cell updates/sec

Title: US-10-044-692-2

Perfect score: 5961
Sequence: 1 MPRAIRCAVSLRSHYRE.....TALAAANPALPSDKITLD 1132

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Ygapop 10.0 , Ygapext 0.5
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Searched: 3413475 seqs, 2563800928 residues

Total number of hits satisfying chosen parameters: 6826950

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	5961	100.0	3399	17 US-10-384-339C-28	Sequence 28, Appl
3	5961	100.0	4015	9 US-09-733-294A-3	Sequence 3, Appl
4	5961	100.0	4015	9 US-09-990-080-1	Sequence 1, Appl
5	5961	100.0	4015	9 US-09-843-676-224	Sequence 224, App
6	5961	100.0	4015	9 US-09-953-052-1	Sequence 1, Appl
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9	5961	100.0	4015	14 US-10-054-295-224	Sequence 224, App
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ALIGNMENTS

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; Sequence 32, Application US/09749728B
; Parent No. US20020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihito
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTES
; FILE REFERENCE: 00766.000043
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US/09/749,728B
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741

PRIOR FILING DATE: 2000-11-02
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver.2.0
SEQ ID NO 32
LENGTH: 3396
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
OTHER INFORMATION: (1)..(3399)
US-09-749-728B-32

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Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
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US-10-044-692-2 (1-1132) x US-09-749-728B-32 (1-3396)

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QY 201 ArgAlaTyrAsnHisSerValArgGlyValAlaGlyValProLeuGlyLeuProAlaProGly 220
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Db 1381 GTGTAGGCTGT 1440
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QY 541 LeuAlaValPheLeuHisTyrLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db 1621 CTGCGCAAGTCTGCACTGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db 1681 TTTTATGTACGAGAGCGAGTTTCAAAAGAACAGGCTTTTCTTCAACGGAAGTGT 1740
QY 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu 600
Db 1741 TGGAGCAAGTGTGAAGCATTTGGAATCAGACGACTTAAAGAGGTGTGAGCTGCG 1800
QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 CTGTGGAAGCAGAGGTGTGAGGAGCATCGGGAAGCGAGCGCGCTGTGTGAGCTCAGA 1860

QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
DB 1061 CTCGGCTTCATCCCAACCTGAGCGGCTGGCCGATTTGTAACATGACTCTGTC 1920
QY 641 GlyAlaArgThrPheArgArgGlyIleValArgAlaGluArgLeuThrSerArgValIleVal 660
DB 1921 GGAGCGAACAAGCTTCGAGAGAAAGAGGCGCGCTCTCACTCAAGGATGAAAGCA 1980
QY 661 LeuPheSerValIleLeuAsnTyrGluArgAlaArgAspProGlyLeuLeuGlyValAspVal 680
DB 1981 CTGTTACCGGCTCACTACAGCGGCGCGCGCCCTCTGAGGCGCTCTGTC 2040
QY 681 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
DB 2041 CTGGGCTCGAGAGATTCACAGGCGCTGGCGCACTTCGTCTCTGCTGGGCGCCAG 2100
QY 701 AspProProGlyLeuTyrPheValIleValAspValThrGlyValArgThrIle 720
DB 2101 GACCGCGCGCTGAGCTGACTTGTCAAGGTGATGACGGGCGGTACAGACCATC 2160
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
DB 2161 CCCAGGACAGGCTCAGAGGTCACTCGCAGCATCATCAACCCAGAACCGTACTGC 2220
QY 741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgGlyAlaPheLys 760
DB 2221 GTGCTCGGTATGCGGTGTCAGAGGCGCGCCCATGGGCACTCGCAAGGCTTCAAG 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
DB 2281 AGCAGCTCTCACTTGACAGACTCCAGCGGTACATGACAGATTCGTGCTCAGCTG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerLeuLeuGln 800
DB 2341 CAGGAGACAGCGCCCTGAGGATGCGGTGTCATGAGCAAGCTCTCTGTAATG 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
DB 2401 GCCAGCACTGCGCTTTCAGACTCTTCTCAAGCTTCATGTGCACACAGCGCTGCGCATC 2460
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
DB 2461 AGGGGCAAGTCTTACGTCAGGCGGAGATCCGAGAGGCTCCATCTCTCCAGCGCTG 2520
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluLeuValPheValGlyIleArgArgAsp 860
DB 2521 CTCTGACAGCTGTGCTACGCGCAGATGAGAACAGCTGTGCGGGATTTGCGCGGAC 2580
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
DB 2581 GGGCTGCTCTGCGTTGTGTGATGATTTCTTGTGTGTGACACCTCACTCCACCGCG 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
DB 2641 AAAACCTTCTCAGAGCCCTGTGTCGAGGTGTCCTGATAGGCTGCGTGAACCTTG 2700
QY 901 ArgGlyThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
DB 2701 CGGAAGACAGTGTGAATTCCTCTGTAAGAAGCAGGCGCTGTGGCGCACGCGCTTTGTT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
DB 2761 CAGATGCGGCGCCAGGCTTATTCCTGTGTGTGCGCTCTGCTGATACCCGAGACCTTG 2820
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
DB 2821 GAGGTGACAGAGGAGTACTCCAGCTATGCGCGAGCTCATAGAGCGAGTCTACCTTC 2880
QY 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgGlyLysLeuPheGlyValLeuArgLeu 980
DB 2881 AACCCCGGCTTCAAGGCTGTGGAGAACATGCGTCCGAAACTCTTTGGGGCTTTCGCGCTG 2940
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000

DB 2941 AAGTGTACACCTGTTCTTGGATTGAGGTGAACACCTTCAGACGCTGTGCACCAAC 3000
QY 1001 TLeTyrIleLeuLeuLeuGlnAlaIleTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
DB 3001 ATCTACAAGATCTCTGCTCTCAGCGGTACAGGTTTACGATGTGTCTGCACTCCCA 3060
QY 1021 PheHisGlnGlnValATrPLeAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
DB 3061 TTTCATCAGCAAGTTTGGAAGAACCCCATTTTTCCTGCGCGATCATCTGACACGGCC 3120
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValLysGly 1060
DB 3121 TCCCTCTCTACTCCATCTGAAAGCCAAAGCAGAGGATGTGCTGGGCGCCAAAGGCGC 3180
QY 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
DB 3181 GCGCGCGCGCTCTGCTCTCGAGGCGGTGAGTGTGCTGTCACCAAGCATTCCTGCTC 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
DB 3241 AAGCTGACTCAGACCGGTGTACCTACCTGACCTCTGGGGTCACTCAGACACGCCAG 3300
QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
DB 3301 ACGCAGCTGAGTCGGAAGCTCCCGGGAGACGAGCTGACTGCGCTGAGAGCGCACCAAC 3360
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
DB 3361 CCGGCACTGCGCTCAGACTTCAGACCATCTTGAC 3396

RESULT 2
US-10-384-339C-28
; Sequence 28, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GEN
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 3399
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: telomerase reverse transcriptase
; PATENT DOCUMENT NUMBER: AF015950
US-10-384-339C-28

Alignment Scores:
Pred. No.: 0 Length: 3399
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-044-692-2 (1-1132) x US-10-384-339C-28 (1-3399)
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGln 20

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Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
Db 61 GTGCTGCCCTGCTCCAGCGTTCCGTGGCCCTTGGGAGCCCGAGGCTGGCGCTGGTGAG 120
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db 121 CCGCGGGAGCCCGCGCTTCCGCGGCTGTGGCCAGTGCCTGGTGGCTGTGCCCTGG 180
Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLeuGlyLeu 80
Db 181 GAGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Qy 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyValAlaCysValLeuAlaPheGly 100
Db 241 GTGGCCCGAGTGTGCAGAGCTGTGCAGCGCGCGGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
Db 301 TTGCGCTGTGTGACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Qy 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTyrGlyLeu 140
Db 361 AGCTACCTGCTCCCAACGCGTACCGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Qy 141 LeuArgArgValGlyAspAspValLeuValAlaLeuLeuAlaArgCysAlaLeuPheVal 160
Db 421 CTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
Qy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db 481 CTGTGTGCTCCCACTGCGCTGACGAGTGTGGCGCGCGCGCGCGCGCGCGCGCG 540
Qy 181 AlaThrGlnAlaArgProProProAlaSerGlyProArgArgArgLeuGlyCysGln 200
Db 541 GCCACTAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Qy 201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 601 CGGCGCTGGAACCATACGCTGACGAGGAGCGCGGCTCCCTGGCGCGCGCGCGCG 660
Qy 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
Db 661 GCGGAGGCGCGCGGAGTGCACGCGAGCTTGGCGTGGCCCAAGAGGCCCAAGCCT 720
Qy 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTyrAlaHisProGly 260
Db 721 GGCGCTGCGCTGAGCGCGAGCGAGCGCGCGCTGGGCGAGGAGTCTGGGCCACCC 780
Qy 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGln 280
Db 781 AGGAGCGCTGACCGAGTGCAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Qy 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 841 GAGGCCACTCTTGTGAGGAGTGCCTCTCTGCAAGCGCCTCCACCCCATCTCGTGG 900
Qy 301 ArgGlnHisAlaGlyProProSerThrSerArgProProAlaArgProTyrAspThrPro 320
Db 901 CGCCGACACACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Qy 321 CysProProValTyrAlaGlnThrHisPheLeuTyrSerSerGlyAspLeuGlnGln 340
Db 961 TGTCCCGCGGTAGCGCGAGACCAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCT 1000
Qy 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1021 CTGGCGCGCTCTTCTTACTGAGCTCTGAGGCGCGAGCTGAGCTGCGGCGCTCG 1080
Qy 361 ValGlnThrTlePheLeuGlySerArgProTyrPheProGlyThrProArgArgLeuPro 380

Db 1081 GTGGAGACCATCTTCTGTGGTTCCAGCGCCGTGATGCCAGGACATCCCGCAGGTTGCC 1140
Qy 381 ArgLeuProGlnArgTyrTyrPrgLysMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
Db 1141 CGCTGCGCCAGCGCTACGTGGCAAAATGCGGCCCTGTTCTTGTGAGCTGCTTGGAAACAC 1200
Qy 401 AlGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
Db 1201 GCGGAGTGCCTTACGCGGGTGTCTCTCAAGACGACATGCGCGCGTGCAGCTGCGGTACAC 1260
Qy 421 ProAlaAlaGlyValCysAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGln 440
Db 1261 CCAGCAGCGCGTGTGTGTGCGCGAGAGAGCCCGAGGAGCTGTGTGTGTGTGTGTGTGT 1300
Qy 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
Db 1321 GAGGACAGAGACCCCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrPrgLys 480
Db 1381 GTGTACGCTTCTGTGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
Qy 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheHisSerLeuGlyLysHis 500
Db 1441 AGGCACACACAGACCGCTTCTTCAAGAACACCAAGAGTTCTATCTCTCTGCGGAGACAT 1500
Qy 501 AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
Db 1501 GCCAAGCTCTGCTGTGAGAGCTACGTTGAGAGATGAGCGGAGCGGAGCTGCTTGGCTG 1560
Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisAspGlyLeuArgGlnGln 540
Db 1561 CGCAGAGACCCAGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
Qy 541 LeuAlaLysPheLeuHisTyrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db 1621 CTGGCCAACTTCTGTGACATGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
Qy 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db 1681 TTTTATGTACGAGAGACACAGCTTTCAAAAGAGCGCTTTTCTTCAACCGAAGAGTGT 1740
Qy 581 TrpSerLysLeuGlnSerLysLysLysLysLysLysLysLysLysLysLysLysLys 600
Db 1741 TGGAGCAAGTTGCAAAAGATTGAATCAGACAGCATTTGAAGAGGTGCACCTGCGGAG 1800
Qy 601 LeuSerGlnAlaGlyValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 CTGTGGAAGCAGAGGTACAGCAGCATCGGAGAGCCAGGCGCGCTGCTGACGTCCAGA 1860
Qy 621 LeuArgPheLeuProLysProAspGlyLeuArgProLysLysMetAspTyrValVal 640
Db 1861 CTCGCGTTCATCCCAAGCGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
Qy 641 GlyAlaArgThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAla 660
Db 1921 GAGAGCAAGACGTTCCGAGAGAAAGAGGCGCGAGCGTCTACCTCGAGGCTGAAGGCA 1980
Qy 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 1981 CTGTTCAGCGTGTCAATACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTG 2040
Qy 681 LeuGlyLeuAspAspLysHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
Db 2041 CTGGCGCTGACCAATTCACAGGCGCTGCGGACCTTGTGTGTGTGTGTGTGTGTGT 2100
Qy 701 AspProProGlnLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrTle 720
Db 2101 GACCGCGCGCTAGCTGTACTTGTCAAGGTGAGTGAAGCGCGCGCTGACCAACATC 2160
Qy 721 ProGlnAspArgLeuThrGlnValLysLysLysLysLysLysLysLysLysLysLys 740
Db 2161 CCCAGAGCAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAGTACTGC 2220
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QY 741 ValArgArgTyrAlaValAlaGlnIleValAlaIleSGLYHisValArgIleValAlaPheLeu 760
 Db 2221 GTGGCTGGATGATGCGGTGCTGAGAAAGCCGCCCATGGCACTCCGCAAGCCCTTTCAG 2280
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaIleLeu 780
 Db 2281 AGCCAGCTCTGACCTTGAACACCTCCAGCGGTACATGACGACAGTGGTGGCTCACCTG 2340
 QY 781 GlnGlnThrSerProLeuArgAspAlaValAlaIleGlnIleSerSerSerLeuAsnGln 800
 Db 2341 CAGGAGACCAAGCCCGCTGAGGATCCGTCATCGACAGCAAGCTCCCTCTGATGAG 2400
 QY 801 AlasSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
 Db 2401 GCCACGATGGCTCTTGCACGCTCTTCAACCTTCAATGTCACCAAGCCGCTGGCATC 2460
 QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnIleSerIleLeuSerThrLeu 840
 Db 2461 AGGGGCAAGTCTTACGTCAGTGCAGGGGATCCGCAAGGGCTCCATCTCTCCAGCGTG 2520
 QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnIleLeuPheAlaGlyIleArgArgAsp 860
 Db 2521 CTCTGCAAGCTGTGCTACCGGCAATGAGAACAGCTGTTCGGGGATTCGGCGGGAC 2580
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 Db 2581 GGGCTGCTCTGCGCTTGGTGATGATTTCTTTGGTGATGACACCTCACTTCCACCGCG 2640
 QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAlaAsnLeu 900
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 Db 2761 CAGATGCGCGCCAGCGCTTATCCCTGATGCGGCTGCTGCTGATACCCGAGCCCTG 2820
 QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 Db 2821 GAGGTGCAAGAGGACACTCCAGCTATGCGGACCTTCATCAGAGCCAGTCTTCACTTC 2880
 QY 961 AsnArgGlyPheLeuAlaGlyArgAspMetArgGlyLeuPheGlyValAlaLeuArgLeu 980
 Db 2881 AACCGCGCTTCAAGGCTGGGAGAAACATGCGTCCGAACTCTTGGGGTCTTGGCGCTG 2940
 QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAlaAspSerLeuGlnThrValCysThrAsn 1000
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 QY 1001 IleTyrIleValLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
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 QY 1021 PheHisGlnGlnValIleTyrIleAspProThrPhePheLeuArgValIleSerAspThrAla 1040
 Db 3061 TTTCATCAGCAAGTTTGGAAAGAACCCACATTTTCTCGCGCTCATCTCAACACGGCC 3120
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 Db 3121 TCCCTCTGCTACTCCATCTTGAAGCCAAAGACGAGGATGTGCTGGGGGCGCAAGGGC 3180
 QY 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTyrLeuCysHisGlnAlaPheLeuLeu 1080
 Db 3181 GCGCGCGGCGCTCTGCGCTCCAGAGCGCTGCAAGTGGCTGTGCCAACCAATTCCTGCTC 3240
 QY 1081 LysLeuThrArgHisArgValIleThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db 3241 AAGCTGACTCGACACCGTGTCACTTACGTGCCACTCTCGGGGTCACTCAGGACAGCCGAG 3300

QY 1101 ThrGlnLeuSerArgIleLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
 Db 3301 AGCCAGCTGAGTCCGAACTCCCGGGAGACAGCGTGACTGCTTGAGGCGGCAAGCAAC 3360
 QY 1121 ProAlaLeuProSerAspPheLeuThrIleLeuAsp 1132
 Db 3361 CCGGCACTGCCCTCAGACTTCAGACATCCTGGAC 3396

RESULT 3

US-09-733-294A-3
 ; Sequence 3, Application US/09733294A
 ; Patent No. US20020045588A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: William M. Gaarde
 ; APPLICANT: Susan M. Preler
 ; APPLICANT: Edward V. Wanciewicz
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
 ; FILE REFERENCE: ISPH-0527
 ; CURRENT APPLICATION NUMBER: US/09/733,294A
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR FILING DATE: 2000-05-16
 ; NUMBER OF SEQ ID NOS: 108
 ; SEQ ID NO 3
 ; LENGTH: 4015
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (56)...(3454)
 US-09-733-294A-3

Alignment Scores:
 Pred. No.: 0 Length: 4015
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-044-692-2 (1-1132) x US-09-733-294A-3 (1-4015)

QY 1 MetProAlaGlnProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGln 20
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 Db 116 GTGCTGCGGCTGGCCACGCTTGGCGGCGGCTGGGGCCCGAGGCTGGCGCTGGTGCAG 175
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 Db 176 CCGGGGAGCCCGCGGCTTTCGCGCGCTGGTGGCCAGTGGCTGTGTGCTGCTGG 235
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 Db 236 GAGGACGCGGCGCCCGCGCGCCCTTCTCCGCAAGTGTCTGCTGAAGAGCTG 295
 QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaValAsnValLeuAlaPheGly 100
 Db 296 GTGGCGCGAGTCTCAGAGGCTGTGCGAGCGCGCGGGAAGAGTGTGCTTGGC 355
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 QY 121 SerTyrLeuProAspThrValThrAspAlaLeuArgGlySerGlyValATrpgIleLeuLeu 140
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 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160

Db 476 CTGCGCCGCTGGGGGACGACGCTGCTGCTCACTGCTGGCACTGCTGGCGCTCTTTGTG 535
Qy 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyValA 180
Db 536 CTGGTGGCTCCCAAGCTGCGCTTACCAAGGTGTGGGGCCGCCCTGTACCAAGCTGGCGCT 595
Qy 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db 596 GCACACTCAAGCCCGGGCCCGCCCACTAGTGGACCCCGAAGCGCTGTGGATGCCAA 655
Qy 201 ArgAlaTTPAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
Db 656 CGGCGCTGGAACCAATGCGTCAGAGAGCGGGGTCCCTGGGCTGCCAGCCCGGGT 715
Qy 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProGlyArgProArgArg 240
Db 716 GCGAGAGAGCGCGGGGGGAGTGCACGCCAAGTCTGCGTGGCCCAAGAGGCCAGCGCT 775
Qy 241 GlyAlaAlaProGluProGluProGluProGluProGluProGluProGluProGluProGlu 260
Db 776 GCGCGTGGCTTGGAGCGGAGCGGAGCGGCGGCTGGGAGCGGCTGGGAGCGGAGCGGAGC 835
Qy 261 ArgThrArgGlyProSerArgProArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
Db 836 AGGACGGGTGACCGAGTACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
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Qy 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyLysArgGluGln 340
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Db 1136 GTGAGAACCATCTTCTGGGTTCAGAGCCCTGGAATGCCAGGACTCCCGCAGATTTGCC 1195
Qy 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyLysAsnHis 400
Db 1196 CGCGTGGCCCGGCTACTGCAATGCGGCCCTGTCTGTGAGCTGTGGAGAACAC 1255
Qy 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
Db 1256 GCGAGTCCCTTCAAGGGGTCTCTCAAGAGCACTGCGCGCTGCGAGCTGGGTACC 1315
Qy 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGlu 440
Db 1316 CCAGAGCCGGGTGTGTGTGCGCGGAGAAAGCCCAAGGCTCTGTGGCGGCCCGAGAG 1375
Qy 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db 1376 GAGGACACAGACCCCGCTGCTGTGTGAGCTGTGCGCGAGCAAGAGCCCTGTGAG 1435
Qy 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
Db 1436 GTGTACGGCTTGTGCGGGCTCTGCTGCGCGGCTGGTGGTCCCGAGGCTCTGGGGCTCC 1495
Qy 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysPheLysSerLeuGlyLysHis 500
Db 1496 AGGCAACAAGACGCGCTTCTCTCAGGAACACCAAGAGTTCATCTCCCTGGGAGAGCAT 1555
Qy 501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgArgCysAlaThrLeu 520
Db 1556 GCCAAGCTCTCGCTCAGAGAGCTGACGTGGAGATGAGCGTGGGACTGTGGCTTGGCTG 1615

Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgPheArgGluGlu 540
Db 1616 GCGAGAGGCCAGGGGTGGT 1675
Qy 541 LeuAlaLysPheLeuHisThrLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db 1676 CTGGCCAAAGTTCCTGCACCTGGCTGATGAGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1735
Qy 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db 1736 TTTTATGTCAACGAGACACAGTTCACAAAGAACAGGCTTTTCTTCAACGAGAGTGTCT 1795
Qy 581 TrpSerLysLeuGlnSerIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGlu 600
Db 1796 TGGAGCAAGTTGCAAGACATTTGAAATGACAGACTGTAAGAGGGGTGAGCTGGCGGAG 1855
Qy 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1856 CTGTGGAAGCAGAGTCAAGCAGCATCGGGAAGCGCGCCCGCTGTGAGCTCCAGA 1915
Qy 621 LeuArgPheLysProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db 1916 CTGCGCTTCATCCCAAGCTGACGGGCTGGCGCCATTTGTGAACATGACTAGTGTGTG 1975
Qy 641 GlnAlaArgThrPheArgArgGluLysArgAlaGlnArgLeuThrSerArgValLysAla 660
Db 1976 GAGCGCAAGAGTTCGCGAGGAAGAGGGCGAGCGTCACTCAGAGGGTGAAGCA 2035
Qy 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyValaSerVal 680
Db 2036 CTGTTCAAGCTGTCTCACTTACAGAGCGGGCGGGCGCCCGCTCTGGGGCGCTTGTGTG 2095
Qy 681 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
Db 2096 CTGGGCTGTGAGATATTCACAGGGCCCTGGCGCACTTGTGTGTGTGTGTGTGTGTGTGTGT 2155
Qy 701 AspProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
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Qy 721 ProGlnAspArgLeuThrGluValIleAlaSerIleLysProGlnAsnThrTyrCys 740
Db 2216 CCCAGAGACGGCTCAGAGAGTCAATGCCAGCATCATCAAAACCCAGAACAGTACGCTC 2275
Qy 741 ValArgArgTyrAlaValValGlnLysAlaHisGlyHisValArgLysAlaPheLys 760
Db 2276 GTGCGTGGTATGCCGTGGTCCAGAAAGCGGCCCATGGGCACTGCCAAGGCTTCAAG 2335
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
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Qy 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGlu 800
Db 2396 CAGAGACCAAGCCCGCTGAGGATGCCGTGTCATCGAGAGAGCTCTCCCTGATGATGAG 2455
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaAlaValArgIle 820
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Qy 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
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Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
Db 2576 CTCTGACGCTGTGTACCGCGCAGCATGAGGAACAAGCTGTGTGGCGGATTTGGCGGGATC 2635
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2636 GGGCTGCTCTGCGT 2695

QY	301	ArgGlnHisIaIaGlyProProSerThrSerArgProProArgProThrAspThrPro	320
Db	956	CGCGAGACACACCGGGGCCCCCATCACATCCGGGACACAGTCCCTGGGACAGCCT	1015
QY	321	CyAProProValIyrrIaGluThrLysHisIaPheLeuTySerSerGlyAspLysGluGln	340
Db	1016	TGTCCTCCCGGTGTCAGCCGAGACCAAGACACTTCTTACTCTCAGAGGACAAAGGAGCAG	1075
QY	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
Db	1076	CTGGGGCCTCTCTTCACTCAGCTCTGAGGCCAGCTGACTGCTGGCCCTGGAGGCTTC	1135
QY	361	ValGluThrLysPheLeuLysSerArgProTyrMetProGlyThrProArgArgLeuPro	380
Db	1136	GTGAGAGCAACATCTTCTGAGTTCAGGACCTTGATGCCAGGAGACTCCCGCAGTTGGCC	1195
QY	381	ArgLeuProGlnArgTyrrTrpGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis	400
Db	1196	CGCTGGCCCCAGGGCTACTGGCAAAATCGGGCCCTGTGTTCTGGAGCTGTTGGGAACAC	1255
QY	401	AlaGlnCysProTyrrGlyValIleLeuLeuThrHisGlySerProLeuArgAlaAlaValThr	420
Db	1256	GCGCAGTGGCCCCCTACGGGGGTCTCTTAAGACGACGCTCCGGCTGGAGCTCGGTCACC	1315
QY	421	ProAlaIaGlyValCysAlaArgGluLysProGlnLysSerValAlaAlaProGluGln	440
Db	1316	CCAGAGCGGGTGTCTGTGGCCCGGAGAGGCCAGGAGCTCTGGGGGGCCCCCGAGGAG	1375
QY	441	GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProThrPgn	460
Db	1376	GAGGACACAGACCCCCGTGGCTGTGATGCTGCTCGGCAGACACAGACACCCCTGGACAG	1435
QY	461	ValTyrrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrPglYser	480
Db	1436	GTGTCGGCTTCGTGCGGGCTTGCCTGGCCGGCTGGTGGCCCCCAGGCTCTGGGGCTCC	1495
QY	481	ArgHisaGlnIuArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
Db	1496	AGGCACACAGAACCGCGCTTCCCTCAGAGAACACCAAGAAATTCATCTCCCTGGGAGAACAT	1555
QY	501	AlaIysIeuSerLeuGlnGluLeuThrTrpLysMetSerValAArgAspCysAlaTrpLeu	520
Db	1556	GCCAAGCTCTCGCTCAGAGGTGACGGAGATGACGTCGGGACTGCGCTTGGCTG	1615
QY	521	ArgArgSerProGlyValGlyCysValProAlaIaGlnHisArgLeuArgGluGlnIle	540
Db	1616	CGCAGAGGCCAGGGGTTGGCTGTGTTCCGGCCCGAGAGCACGCTGCTGGAGAGATC	1675
QY	541	LeuAlaLysPheLeuHisIleTrpLeuMetSerValTyrrValAlaGluLeuLeuArgSerPhe	560
Db	1676	CTGGCCCAATTCCTCACACTGGGTGATGAGTGTACGTGTCAGAGCTGCTCAGTCTTTC	1735
QY	561	PheTyrrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrrArgLysSerVal	580
Db	1736	TTTTATGTACCGAGAACACACGTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTCTC	1795
QY	581	TrpSerLysLeuGlnSerIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGln	600
Db	1796	TGGAGCAATGTCAAAGCATTTGAAATCAGACGCACTTGAAGAGGGTGCACACTCGGAG	1855
QY	601	LeuSerGluAlaGlyValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
Db	1856	CTGTCCGAAGCAGAGGTACAGGACGATCCGGAAGCCAGGCCCGCTGCTCAGCTCCAGA	1915
QY	621	LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrrValVal	640
Db	1916	CTCCGCTCATCCCAAGCCTGACGGGCTGCGGCGCATTTGAGACATGACATGACGTGTC	1975
QY	641	GlyAlaIaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
Db	1976	GGAGCCAGAACGTTCCGACAGAAAGAGGCGCAGCGCTCCTCACTCCAGGCTGAAGCA	2035

QY	661	LeuPheSerValLeuAsnTyrGluArgAlaArgPheProGlyLeuLeuGlyAlaSerVal	680
Db	2036	CTGTTCAGCCTGTCTCAACTACAGACGGGGGGCGGCGCCCTCTCTGAGGCGCTCTGTG	2095
QY	681	LeuGlyLeuAspAspIleHisArgAlaTAPArgThrPheValLeuArgValArgAlaGln	700
Db	2096	CTGGGCGCTTGACATATCCACAGGCGCTGGCCACCTTGTGTCTCGTGTGGGGGCCAG	2155
QY	701	AspPheProProGluLeuTyrPheValIysValAspValThrGlyAlaTyrAspThrIle	720
Db	2156	GACCCGCGCGCTGAGCTGACTTGTTCAGAGTGGAATGTGACAGGGCGGCGATCAACACATC	2215
QY	721	ProGlnAspArgLeuThrGluValIleIleAspSerIleIleLeuProGlnAsnThrTyrCys	740
Db	2216	CCCGAGACAGGCTCACAGAGATCATCCGACGATATCAAAACCCAGAACACGATACGCG	2275
QY	741	ValArgArgTyrAlaValValGlnIysAlaIleHisGlyHisValArgIysAlaPheLys	760
Db	2276	GTGGGTGCGATATGGCCGTGTCCAGAAAGGCGGCCCATGGGACAGTCCGACAGGCGCTTCAAG	2335
QY	761	SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	780
Db	2336	AGCACAGCTCTTACTTTCAGACAGCTTCACGCCATCATGCGACAGTTCGTGGCTACCTG	2395
QY	781	GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu	800
Db	2396	CAGAGAACAGACCCGCTGAGGAGATGCCGTGTATCAGACAGAGAGCTCTCCCTCGAATGAG	2455
QY	801	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	820
Db	2456	GCCAGCAATGGCGCTTTCGAGGCTTCTCAAGCTTCAATGTCACACACCGCGTGGCGATC	2515
QY	821	ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	840
Db	2516	AGGGGCAAGTCTTAAGTTCACAGTGCACAGGGATCCCGAGGGCTCCATCTCTCCACGCTG	2575
QY	841	LeuCysSerLeuCysTyrGlyAspMetGluAsnIysLeuPheAlaGlyIleArgAspArg	860
Db	2576	CTCTGCACCGCTGTGCTACGGCGGACATGAGAAACAAGCTGTTTCGGGGATTCGGCCGAGAC	2635
QY	861	GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
Db	2636	GGGCGTCTCTCGGCTTGTGTGTGAGATTTCTTGTGTGTGACCTCACCTCACCCACGCG	2695
QY	881	IysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
Db	2696	AAAACTTCTTCACAGGACCTCTGTCCGAGGTGTCTCTAGATATGCTGTGGTGGTGAACCTTG	2755
QY	901	ArgLysThrValValAsnPheProValGluAspGlnAlaLeuGlyGlyThrAlaPheVal	920
Db	2756	CGAAGACAGTGTGTAACTTCCCTGTAGAGACAGAGCCCTGGGTGACAGGCTTTGT	2815
QY	921	GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu	940
Db	2816	CAGATGCCGCGCCACAGGCTCATATCCCTGCGCGGCTGTGCTGTGGATACCCGACCTG	2875
QY	941	GluValGlnSerAspTyrSerSerSerTyrAlaArgHisSerIleArgAlaSerLeuThrPhe	960
Db	2876	GAGGTGCAGAGGACTACTCCAGCTATGCCGGAACCTTCATCAGAGCAGCTCACTTCC	2935
QY	961	AsnArgGlyPheLysAlaGlyArgAsnMetArgArgIysLeuPheGlyValLeuArgLeu	980
Db	2936	AACCGCGGCTTCAAGGCTGGAGGAACATGCGTGCAGAACTCTTGGGGGTCTTGGCGCTG	2995
QY	981	IysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
Db	2996	AAGTGTCAACAGGCTGTCTTGTGATTTGAGGTGAACAGCTTCCAGACGGGTGTGACCAAC	3055
QY	1001	IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
Db	3056	ATCTTACAATACTCTCTGTGTGAGGCGATCAAGGTTTACGCGATGTGTGTGCACACTCCA	3115
QY	1021	PheHisGlnGlnValIrrPylAsnDroThrPhePheLeuArgValIleSerAspThrAla	1040

Db 776 GGCCTGCCCCCTGAGCCGAGCGGACGCCCTTGGGCAAGGGGTCTGGGCCCAACCCGGGC 835
Qy 261 ATGTHrArgIyProSezAspArgIyPheCyValIalSerProAlaArgProAlaIglu 280
Db 836 AAGAGCGCGTGAACCGAGTACCGTGGTTCTGTGTGTGTCTGACCTGCGACAGACCCGCCAA 895
Qy 281 GluAlaThrSerLeuGluIyAlaLeuSerGlyThrArgHisSerHisProSerValIglu 300
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Qy 301 ArgGlnHisAlaIgluProProSerThrSerArgProArgProIleThrAspThrPro 320
Db 956 CGCCAGACCAACCGGGCCCCCATTCACATCGCGGCACACGCTCCCTGGGACAGCCCT 1015
Qy 321 CysProProValIyAlaIgluThrIyHisPheLeuTySerSerGlyAspIyAspIgluIln 340
Db 1016 TGTCCCCCGGTGACCCGAGACCAAGCACTTCTCTACTCTCTCAGGCAACAGAGACG 1075
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Db 1076 CTGCGGCCCTCTCTCTACTCAAGCTCTGAGGCCAGCTGACTGCGCTCGAGAGCTC 1135
Qy 361 ValIgluThrIlePheLeuGlySerArgProIlePheProGlyThrProArgArgLeuPro 380
Db 1136 GTGGAGACCATCTTCTGTGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGTTGCC 1195
Qy 381 ArgLeuProGlnArgIyTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400
Db 1196 CGCCTGCCCCAGCGCTACTGCAATGCGGCCCTCTTCTGTGAGTGTGTGGAAACAC 1255
Qy 401 AlaGlnCysProIyArgIyValIleLeuLeuIyThrHisCysProLeuArgAlaAlaIln 420
Db 1256 GCGCAGTCCCTTCAGGGGTGCTCTCAAGCCACTGCCCGCTGGAGTGGCGTCAAC 1315
Qy 421 ProAlaIgluIyAlaIyAlaArgIyIlePheProGlnIySerValAlaIleProIgluIln 440
Db 1316 CCAGCACCGGTGTCTGTGCCCGGAGAACCCCGAGGCTCTGTGGCGGCCCGGAGAG 1375
Qy 441 GluAspThrAspProArgArgLeuValIleLeuLeuArgIlnHisSerSerProIlePgn 460
Db 1376 GAGACACAGACCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1435
Qy 461 ValTyArgIyPheValIleArgAlaCysLeuArgArgLeuValIleProIgluIleTySer 480
Db 1436 GTGTACGGCTCTGTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1495
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Db 1496 AGGCACAACGAAACCCGCTCTCTCAGGAACACCAAGAGTTCACTCTCTGGGGAGCAT 1555
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Db 1676 CTGGCAAGTCTGTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1735
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Db 1736 TTTTATGTACGAGACCAAGCTTTTCAAAAGAACAGCTTTTCTACCGAAGAGTCT 1795
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Db 1796 TGGACCAAGTTCAAGCACTTGAATCAGACAGCACTTGAAGAGGTGTCACTCGGGAG 1855
Qy 601 LeuSerGluAlaIgluValArgIlnHisArgIlnAlaArgProAlaLeuLeuThrSerArg 620
Db 1856 CTGTGGAGAGCAGAGTCAAGGATCGAGGACAGGCGCCCTGTCTACGTCCAGA 1915

Qy 621 LeuArgPheIleProIySerProAspGlyLeuArgProIleValAsnMetAspTyValIle 640
Db 1916 CTGCGCTTATCCCAAGCTGTACGGGCTGTGGCCGATTTGAACTGACTACGTCTGTG 1975
Qy 641 GlyAlaArgThrPheArgArgGlyIyAspAlaGluArgLeuHisSerArgValIleAspAla 660
Db 1976 GAGCCAGAAAGTTCCTCCAGAGAAAGAGGGCGAGGTGTCACTCGAGGTGAAGGCA 2035
Qy 661 LeuPheSerValLeuAsnTyArgIlnArgAlaArgArgProIyLeuLeuGlyAlaSerVal 680
Db 2036 CTGTTACGGTCTCAACTACAGCGGGCCGGCGCCGCGCTCTGGGCGCTCTGTGT 2095
Qy 681 LeuGlyLeuAspAspIleHisArgAlaIleArgArgThrPheValIleArgValAlaGln 700
Db 2096 CTGGGCGCTGAGCATATTCACAGGGCTGTGGCACTTCTGTGTGTGTGTGTGTGTGTGT 2155
Qy 701 AspProProProGluLeuTyTrpPheValIyAspValIlnThrGlyAlaTyAspThrIle 720
Db 2156 GACCGCGCGCTGAGCTGTACTTGTCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2215
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Db 3356 ACGCAGCTGAGTGGAGAGCTCCCGGGGACGACGCTGACCTGAGGCGCCGACGCCAAC 3415
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3416 CCGGCACTGCGCTCAGACTTCAAGACCATCTGAC 3451

RESULT 6

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TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 72

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

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INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4015 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 56..3454

OTHER INFORMATION: /product= "human telomerase reverse transcriptase (hTERT)"

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-953-052-1

Alignment Scores:

Pred. No.: 0

Score: 5961.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 9

Gaps: 0

US-10-044-692-2 (1-1132) x US-09-953-052-1 (1-4015)

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QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
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QY 81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlyAlaLysAsnValLeuAlaPheGly 100
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QY 861 GlyLeuLeuLeuValArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
DB 2636 GGGCGCTCCCTGGCTTTGGTGGATGATTTCTTTGGTGACACTCACCCTCACCACGGG 2695
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValLeuLeu 900
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QY 961 AsnArgGlyPheLeuValGlyValArgAsnMetArgGlyValPheGlyValLeuLeuLeu 980
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QY 1021 PheHisGlnGlnValThrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
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RESULT 7

US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Inagner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00293005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product="hTERT"
/note="human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224
Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-044-692-2 (1-1132) x US-10-053-758-224 (1-4015)
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DB 56 ATGCGCGCGGCTCCCGGCTGCGAGACCGTGCCTCCCTGCGAGCAGACATACCGCGAG 115
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
DB 116 GTGCTGCGGCTGCGCACGTTCTGTGGCGGCTGGGAGCCCAAGGCTGGGCGCTGGTGAG 175
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 176 CCGGCGGAGCCCGCGGCTTTCCGCGCGCTGCTGTGGCCAGTGCTGTGTGCGTGCCTGG 235
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80
DB 236 GACGACAGCGCGCCCGCGCGCGCTCTCCCTCCGAGTGTCTGCTGAGAGAGAGCTG 295

QY	81	ValAlaArgValLeuGlnArgLeuCySeGluArgGlyAlaLysAsnValLeuAlaPheGly	100
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Db	356	TTGGCGGTGTGGAGCGGGGCCCGGGGGGGCCCCCGAGGGCTTCACACACAGCTGGCC	415
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Db	416	AGCTACTGTGCCAACACAGGTGACCGACGCACTCGGGGGAGCGGGCGTGTGGGCTGTG	475
QY	141	LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
Db	476	CTGGCGCGGTGGCGCAGCAGGTGTGTTCACCTGTGGACAGCTCGCGCTCTTTG	535
QY	161	LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
Db	536	CTGGTGGCTCCAGACTCGGCTTACAGATGTGGGGCGCGCGCTGTACAGCTCGGGCT	595
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QY	321	CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
Db	1016	TGTCCCCCGGTGTGACCGAGACCAAGACTCTCTTACTCTTCAAGCGACCAAGACAG	1075
QY	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
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QY	361	ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
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QY	381	ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
Db	1196	CGCCTGCCCCACAGCTTACTGGCAAAATGGCGCCCTGTTTCTGGAGCTGTCTTGGGAACAC	1255
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[illegible]


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Db      2516  AGGGGCAAGTCTTACGTCAGTGCAGGGGATCCGCAAGGGCTCATCTCTCCACGCTG 2575
Qy      841  LeuCysSerLeuCysTyrGlyAspMetGluAsnIleuPheAlaGlyIleArgArgAsp 860
Db      2576  CTCTGCACCTCTGTGTACGCGACATGAGAACAAAGCTTTTGGGGGATTCGGGGGAGC 2635
Qy      861  GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db      2636  GGGCTGCTCTGCGCTTGGTGGATGATTTCTTGTGGTACACTCACCCTCACCCAGCGG 2695
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Db      2696  AAAACCTTCTCAGAGACCTGTGCGAGGTGTCTGTGATGAGCTGCGTGTGAACCTTG 2755
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Db      2876  GAGGTGCAGAGGACTACTCCAGCTATGCGGACCTCCATCAGACGCTCTCACCTTC 2935
Qy      961  AsnArgGlyPheLeuAlaGlyValArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db      2936  AACCGCGCTTAAGGCTGGAGGAACATGCTCGCAACTTTTGGGGTCTTGGGGCTG 2995
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Db      2996  AAGTGTCAACAGCTGTTCTGTGATTTGACGTGAACAGCCTCCAGCGGTGGCAAC 3055
Qy      1001  IleTyrIleIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnIleuPro 1020
Db      3056  ATCTACAAAGATCTCTCTGTGACAGGCTACAGGTTTCAAGCATGTGTGTGACGCTCCA 3115
Qy      1021  PheHisGlnGlnValTyrPheAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
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Qy      1121  ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db      3416  CCGGCACTGCGCTCAGACTTCAAGACCATCTGTGAC 3451

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; APPLICANT: Genon Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE REFERENCE: 015389-003500PC
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-044-692-2 (1-1132) x US-10-208-243-1 (1-4015)
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RESULT 8
US-10-208-243-1
; Sequence 1, Application US/10208243
; Publication No. US20030044394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.

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DB 1616 CGCAGAGAGCCAGGGGTGTGCTGTGTCCGCGCCAGAGCACTCTGCTGAGAGATC 1675
QY 541 LeuAlaLysPheLeuHisTyrLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
DB 1676 CTGGCCAAAGTTCGCACTGAGTGTATGATGATGATGATGATGATGATGATGATGAT 1735

QY 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1736 TTTTATGTCAGGAGACCAACGTTTCAAAAGAACGGCTCTTTTCTACCGGAAAGATGTC 1795
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DB 1796 TGAGCAAGTGTGCAAGAGCATTTGAATCAGACAGCATTTGAAGAGGTGCACCTCGGAG 1855
QY 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
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QY 621 LeuArgPheLeuProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
DB 1916 CTGCGCTTCAATCCCAACCTGACGGGCTGCGCCGATTTGAACATGACATGATGCTGT 1975
QY 641 GAlaAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValAla 660
DB 1976 GGAGCCAGAGAGTTCGCGAGAAAGAGGCGAGGCTCTCACCTCGAGGGGTGAAGCA 2035
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DB 2036 CTGTTCAGCGTGTCACTACAGAGGCGGCGCGGCGCCCGCTCTGAGGCGCTCTGTG 2095
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DB 2096 CTGGGCGCTGAGAGATATCACAGGGGCTGGCGCACTTCTGATGCGTGTGGGCGCCAG 2155
QY 701 AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
DB 2156 GACCCGCGCTGAGCTGTACTGTCAAGGTGATGTGAGGGGCGCTGACAGACACATC 2215
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
DB 2216 CCCAGAGACAGCTACAGAGGTATCCCGACATCATCAAAACCCAGAACATGATGTC 2275
QY 741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
DB 2276 GTGCGTGGGTATGCGGTGTCCAGAGGCGCGCCCATGTGGCACAGTCCGAGAGCTTCAAG 2335
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; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linguist, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054, 295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
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; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product="hTR"
; /note="human telomerase reverse
; transcriptase (hTR) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
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Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
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Db 116 GTGCTGCCGCTGGCCACCTTCGTGCGGCGCTGCGGCGCCAGGGCTGGCGGCTGCGAG 175
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Db      2936 AACCGCGGCTTAAAGGCTGGAGAAACATGCTCCGAACTTTGGGGTCTTTCGGCGCTG 2995
QY      981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db      2996 AAGTGTACAGGCTGTGTTCTGGATTGGCAGGTGAACAGCCTCAAGCAGGTGTGACCAAC 3055
QY      1001 IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
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QY      1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
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QY      1041 SerLeuCySerLeuLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaLysGly 1060
Db      3176 TCCCTCTGTACTCATCTGAAAGCAAGCAAGGATGCGTGGGGGCAAGGCGC 3235
QY      1061 AlaAlaGlyProLeuProSerGluAlaValGlnThrPheCysHisGlnAlaPheLeuLeu 1080
Db      3236 GCCGCCGCGCTCTGCTCCGAGGCGCTGAGTGTGCTGTCACCAACCATTTCTGCTC 3295
QY      1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db      3296 AAGCTGACTGCAACCGGTGACCTAGCGCACTCTGGGGTCACTGAGACAGCCGAG 3355
QY      1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db      3356 ACGGAGCTGAGTCGGAAGCTCCCGGGGAGAGAGCGCTGACCTGTGAGGCGCCAGCAAC 3415
QY      1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
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RESULT 11
US-10-105-963-1

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; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; TITLE OF INVENTION: Recombination

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; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION:
US-10-105-963-1

Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-044-692-2 (1-1132) x US-10-105-963-1 (1-4015)
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QY      21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPargLeuValGln 40
Db      116 GTGCTGCCCTGCGCCACGTTGCTGCGCGGCTGGGGGCCCGAGGCTGCGGCTGTGACG 175
QY      41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
Db      176 CGCGGGAGACCGCGCGCTTTCGCGCGCTGTGCGCCAGTGTGCTGTGTGCTGTGCTGTG 235
QY      61 AspAlaArgProProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu 80
Db      236 GACGACGCGCGCGCGCGCGCGCGCGCGCTTCTTCTGCGAGGTGCTGCTGAAAGAGCTG 295
QY      81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 100
Db      296 GTGGCCCAAGTCTCTCAAGGCTGTGCGAGCGCGCGGAGAAAGTGTGCTGTGCGC 355
QY      101 PheAlaLeuLeuAspGlyAlaArgGlyLysProProGluAlaPheThrThrSerValArg 120
Db      356 TTGCGGCTGTGAGAGGGGCGCGGGGGGCGCGCGCGCGCGCGCTTCAACACAGCGTGGC 415
QY      121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaThrGlyLeuLeu 140
Db      416 AGCTACCTGCGCCCAACAGGTGACCACTGCGCGGAGAGCGGGGCGCTGGGGGCTGTGCT 475
QY      141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db      476 CTGGCGCGGGGGGAGAGCGGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 535
QY      161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
Db      536 CTGGTGGCTCCCAAGTGTGCGCTTCAAGGTTGCGGGGCGCGCTGTGACCAAGCTGGCGCT 595
QY      181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
Db      596 GCCACTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGGAAGGCTGTGGA 655
QY      201 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
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Db	716	GCGAGGAGCGCGGGGCACTGCGCCAGCCGAAGTCTCCGTTGCCCAAGAGGCCAGGCT	775
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Db	776	GGCGCTCCCTCGTAGCCGAGCGGACCGCCGTTGGGAGGGGTCTGGGGCCACCCGGGC	835
Qy	261	ArgThrArgGIYProSerAspArgGIYPhGcYValValSerProAlaArgProAlaGIY	280
Db	836	AGGAGCGGTGACCGAGTACCGTGTGTTCTGTGTGTGTCTGACCTGCGAGACCCGCCGA	895
Qy	281	GIuAlaThrSerLeuGIuGIYAlaLeuSerGIYThrArgHisSerHisProSerValGIY	300
Db	896	GAAGCCACTCTTTTGAAGGGTGCCTCTGTGACGCGGCACATCCACCCATCCGTGGGC	955
Qy	301	ArgGIuHisHisAlaGIYProProSerSerThrArgProProArgProTrpAspThrPro	320
Db	956	CGCCAGCACCCAGCGGGGCCCCCATCCAGCAATCGGGCCACCAAGTCTCTGGAGACGCT	1015
Qy	321	CysProProValTYrrAlaGIuThrThyHisPheLeuTYrSerSerGIYAspLysGIuGIY	340
Db	1016	TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTTACTCTTAGCGCAAGAGGACAG	1075
Qy	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGIYAlaArgArgLeu	360
Db	1076	CTGGCGCCCTCTCTTACTCAGCTCTCTGAGGCCAGCCGTGATGGCGGTGGAGGCTC	1135
Qy	361	ValGIuThrTIIepheLeuGIYSerArgProTrpMetProGIYThrProArgArgLeuPro	380
Db	1136	GTGAGACCAATCTTTCTGGGTTCAGAGCCCTCGAATGCCAGGACATCCCCGAGTTGCC	1195
Qy	381	ArgLeuProGIuArgTYrTTrpGIuMetArgProLeuPheLeuGIuLeuLeuGIYAsnHis	400
Db	1196	CGCTCGCCCAAGCGCTACTCGCAATATGGCGCCCTGTGTTCTGGAGCTGCTGGGAACAC	1255
Qy	401	AlaGIuCysProTYrGIYValLeuLeuLeuYThrHisCysProLeuArgAlaAlaValThr	420
Db	1256	GCGAGTGCCTCTACGGGGGTGCTCTCTCAAGACGACTGCCGCTGCGAGCTGGCGTACC	1315
Qy	421	ProAlaAlaGIYValCysAlaArgGIuLysProGIuGIYSerValAlaAlaProGIuGIY	440
Db	1316	CCAGCAGCGCGGTGTGTGTGCCGGGAGAAGCCCAAGGCGCTGTGTGGCGGCCCCGAGAG	1375
Qy	441	GIuAspThrAspProArgArgLeuValGIuLeuLeuArgGIuHisSerSerProTrpGIY	460
Db	1376	GAGGACACAGACCCCGTGTGTGTGTGTGAGCTGCTCGCCAGCAAGACGCCCTTGCGAG	1435
Qy	461	ValTYrGIYPhGcValArgAlaCysLeuArgArgLeuValProProGIYLeuTrpGIYSer	480
Db	1436	GTGTACGGTTCGTGGGGCGCTGTGGCGCGGTGTGTGCCGCCAGGCTCTGGGGCTTC	1495
Qy	481	ArgHisAsnGIuArgArgPheLeuArgAsnThrLysLysPheIISerLeuGIYIleHis	500
Db	1496	AAGGACACAGAACCGCGCTTCTTCAGGAACACAAAGAAATTCATCTCTTGAGAAAGAT	1555
Qy	501	AlaLysLeuSerLeuGIuGIuLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520
Db	1556	GCCAACTCTTCGCTGAGAGCTGACGTGAGAGATGAGACGTGCGGAGATGGCGCTTGGCTG	1615
Qy	521	ArgArgSerProGIYValGIYCysValProAlaAlaGIuHisAspLeuArgGIuGIuIle	540
Db	1616	CGGAGAGCCCAAGGGGT	1675
Qy	541	LeuAlaLysPheLeuHisTrpLeuMetSerValTYrValValGIuLeuLeuArgSerPhe	560
Db	1676	CTGGCCAAAGTCTCTGACGTGGGTGAGATGTGTACGTGTGTGTGTGTGTGTGTGTGT	1735
Qy	561	PheTYrValThrGIuThrPheGIuLysAsnArgLeuPhePheTYrArgLysSerVal	580
Db	1736	TTTTTAATGTCACGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTGT	1795
Qy	581	TrpSerLysLeuGIuSerIISerLysIISerLeuGIuHisIISerLysArgValGIuLeuArgGIY	600
Db	1796	TGAGAGCAAGTTGCAAGCAATGTGAATCAACAGCACTTGAAAGAGGTGTGAGCTGGGGAG	1855

QY	601	LeuSerGIuAlaGIuValArgGIuNIaArgGIuAlaArgProAlaLeuLeuThSerArg	620
Db	1856	CTGTGGAGAACAGAGGGTCAGAGCGAGCTCGAGAAAGCCAGGCCCTGGTCGTACGTCACGA	1915
QY	621	LeuArgRheLIeProIysProaEArgIYLeuAuArgProLIeValaAsmMeaAspTYrValaVal	640
Db	1916	CTCCGGCTTCATCCCCAAAGCTGACGGGGCTGCGGCCGATTGTAAACATGGACTACACGTCGG	1975
QY	641	GIYAlaArgThrPheaArgArgIuLYbArgAlaGIuArgLeuThSerArgValIysAla	660
Db	1976	GGAGCCCAAGAACTGTCCCGACAGAAAGAAAGAGGCGAGACCGTCACTCAAGGGGTGAAGGCA	2035
QY	661	LeuPheSerValIleuAsnTYrGIuAArgAlaArgArgProGIYLeuLeuGIYAlaSerVal	680
Db	2036	CTGTTCAGCGGTCTCACTACAGAGCGGGCGCGGCCGCCGCTCTGGGGCCCTCTGTGG	2095
QY	681	LeuGIYLeuAspAspLIeNIaArgAlaATrPArgThrPheValIleuArgValaArgAlaGIu	700
Db	2096	CTGGGGCCTCGACGATATCCACAGGGCCTGGACGACCTTCGTGTGTGTGGGGGCCAG	2155
QY	701	AspProPProPogIuLeuTYrPheValIysValaAspValaThrGIYAlaTYrAspTRTLe	720
Db	2156	GACCCGCGCGCTGAGCTGACTTGTGTCAAGTGAGATGACGGGCGCGTACAGACACATTC	2215
QY	721	ProGIuAspArgLeuThrGIuValaLIeAlaSerLIeIleLYbProGIuAsnThTYrCYs	740
Db	2216	CCCCAGACAGAGCTCACAGAGGTATCGCAGCATATCAAAACCCAGAAACAGTCACTCG	2275
QY	741	ValaArgArgTYrAlaValaValaGIuLYbAlaAlaNIaGIYNIaValaArgLYbAlaPheLYs	760
Db	2276	GTGCTCGCGTATGGCGGTGTCCAAAGAGCCGCATAGGAGCATTCGCAAGGCTTCACAG	2335
QY	761	SerNIaValaSerThrLeuThrAspLeuGIuProTYrMeaArgGIuNIaPheValaNIaIleu	780
Db	2336	AGCCACGCTCTTACTTGACAGACCTTCACACCGTACATGCAAGTTGCGGTCACTCAGT	2395
QY	781	GIuGIuThrSerProLeuArgAspAlaValaLIeGIuGIuNIaSerSerLeuAsnGIu	800
Db	2396	CAGGAGACCAACCCGCTGAGGGAGATGCGGTGTATCAAGACAGAGCTTCCTCCGAATGAG	2455
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Db	2456	GCCACAGAGGGCTCTTGACGCTCTTCTTCAAGCTTATGTGCCACACAGCGCGTGGCATTC	2515
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Db	2516	ACGGGCAAGTCTTACGTCAAGTGCACAGGGGATCCGACAGGGCTCAATCTTCACAGCTG	2575
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Db	2696	AAAAACCTTCTCAGGACCTCGGTCCGAGAGTCCCTGATGGCTCGTGGTGTGTAACCTTG	2755
QY	901	ArgLYbThrValaValaAsnPheProValaGIuAspGIuAlaLeuGIYGIYThrAlaPheVal	920
Db	2756	CGGAAACAGTGTGAATCTTCCCTGTAAACACAGGCCCTGGGTGGCAAGGCTTTGTT	2815
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QY 1041 SerLeuCysIySerIleLeuIyAlaIyAsnAlaIyMetSerLeuGlnValIyAlaIyGly 1060
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QY 1061 AlaAlaIyProLeuProSerGlnIleValIleGlnITrIlePheCysHisGlnAlaPheLeu 1080
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RESULT 12
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; Sequence 1, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lininger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hTERT"
; /note= "human telomerase reverse
; transcriptase (hTERT) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-692-1
; US-10-044-692-1 (1-1132) x US-10-044-692-1 (1-4015)
Alignment Scores:
Pred. No.: 0 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 14 Gaps: 0
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Db 236 GTGGCGCCAGTGTCTCAGAGGCTGTGCGAGCGCGCGGAGAAAGTGTGTGCTGCGC 355
QY 101 PheAlaLeuLeuAspGlyAlaITrArgIyGlyITrProGlnIleAlaPheITrITrSerValArg 120
Db 356 TTGGCGCTGTGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTACACACGCTGCGC 415
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1436 GTGTACGGCTTGT 1495
481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheLysSerLeuGlyLysHis 500
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501 AlaLysLeuSerLeuGlnLysLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
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521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlnLeu 540

1616 CGCAGAGCCAGAGGTTGGCTGTCTCCGCGCCAGAGACCGCTGTGCTGAGAGATC 1675
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1796 TGGAGCAAGTTGCAAGAGATTGAAATCAGACAGCACTTGAAGAGGCTGCGCTCGGAG 1855
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1856 CTGTGGAAGCAGAGGTGAGGACAGATCGGAGACCGAGCCCGCTTGTGACGTCCAGA 1915
621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
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641 GlyAlaArgThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAla 660
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681 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
2096 CTGGGCTCGAGAGATCACAGAGGCTGGCGCACTTGTGTGTGTGTGTGTGTGTGTGTGT 2155
701 AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
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RESULT 13
US-10-044-539-1
Sequence 1, Application US/10044539
Publication No. US2003010093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTrr"
/note= "human telomerase reverse
transcriptase (hTrr) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-539-1
Alignment Scores:
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Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
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Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTrpArgLeuValGln 40
Db 116 GTGCTGCGGCTGCGCAGCTTGTGCGGCGCTGCGGCGCCAGGCGTGGCGGCTGTGCG 175
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTTrp 60
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Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeu 80
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QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
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QY 321 CysProProValTyrArgGluThrArgHisPheLeuTyrSerSerGlyValAspGluGln 340
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QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
Db 1076 CTGCGGCTCTCTTCTTACTCACTGACTCTGTAGGCGCAAGCTGTACTGTGGCGTGGAGGCT 1135
QY 361 ValGluThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
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Db 1196 CGCTCTCCCGAGGCTACGTGGCAATGCGGCTCTTCTTGTGGAGTGTCTGGGAACCAAC 1255
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Db 1256 GCGCACTGCCCTTACGCGGGTGTCTCTCAAGACCACTGCGCGCTGTGAGCTGGGTGACCC 1315
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValaAlaAlaProGluGln 440
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Db 1796 TGGACAAAGTTGCAAAAGCATTTGATCAAGACACTTGAAGAGGCTGCAAGCTGCGGAG 1855
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Db 2096 CTGGGCTGTGACGATATTCACAGGCGCTGTGCGCACTTGTGTGTGTGTGTGTGTGTGTGTG 2155
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RESULT 14
US-10-325-810-1

Sequence 1, Application US/10325810
Publication No. US20030204069A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.

Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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LOCATION: 56..3454
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component"
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US-10-325-810-1

Alignment Scores:

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Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-044-692-2 (1-1132) x US-10-325-810-1 (1-4015)

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Db GTGCTCCCGCTGGCGAGTTCGTGGCGCGCTGGGGCCCAAGGGCTGGCGCTGGTGCAG 175
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 ; APPLICANT: Ralph, Brandenberger
 ; APPLICANT: Joseph, Gold D.
 ; APPLICANT: John, Irving
 ; APPLICANT: Mandalam, Ramkumar
 ; APPLICANT: Mok, Michael
 ; APPLICANT: Shelton, Dawne
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	3396	4	AAH48235
2	5961	100.0	3396	4	AAH49601
3	5961	100.0	3396	4	AAH44366
4	5961	100.0	3396	12	ADG70113
5	5961	100.0	3399	6	ABV78144
6	5961	100.0	3399	6	ABZ35720

7	5961	100.0	3399	6	ABX09963	Abx09963 Human tel
8	5961	100.0	3399	6	ABL91685	Ab191685 Human pol
9	5961	100.0	3399	12	ADG90598	Adg90598 Human TER
10	5961	100.0	3798	2	AAV27876	Aav27876 Human tel
11	5961	100.0	3955	2	AAV22379	Aav22379 Human tel
12	5961	100.0	4015	2	AAZ00724	Aaz00724 Human tel
13	5961	100.0	4015	2	AAZ20279	Aaz20279 Human tel
14	5961	100.0	4015	2	AAZ30154	Aaz30154 CDNA enco
15	5961	100.0	4015	4	AAH45901	Aah45901 Human hTE
16	5961	100.0	4015	6	AAH46821	Aad46821 Human tel
17	5961	100.0	4015	6	ABA97534	Abag97534 Cancer ce
18	5961	100.0	4015	8	ACC57552	Acc57552 Human tel
19	5961	100.0	4015	8	ABZ22474	Abz22474 Human tel
20	5961	100.0	4015	8	ACC44482	Acc44482 Human tel
21	5961	100.0	4015	8	ABX18391	Abx18391 Group III
22	5961	100.0	4015	10	ACC58039	Acc58039 Human tel
23	5961	100.0	4015	12	ADG85223	Adg85223 Human tel
24	5961	100.0	4015	12	AD182171	Ad182171 Human cat
25	5961	100.0	4042	2	AAV72117	Aav72117 Human cat
26	5961	100.0	4070	6	ABL53711	Ab153711 Human tel
27	5956	99.9	4015	2	AAZ08150	Aaz08150 Human tel
28	5954	99.9	3396	2	AAH18266	Aax18266 Telomeras
29	5954	99.9	3964	2	AAH18254	Aax18254 Human tel
30	5954	99.9	4023	2	AAV60320	Aav60320 Human tel
31	5954	99.9	4027	2	AAH89424	Aax89424 Human EST
32	5954	99.9	4027	3	AAZ29388	Aaz29388 hEST2, a
33	5954	99.9	4027	10	ADCA47060	Adc47060 Human TER
34	5954	99.9	4027	20	ADBA4081	Ada4081 Human tel
35	5952	99.8	3457	8	ABZ76217	Abz76217 Human TER
36	5952	99.8	4037	2	AAV22428	Aav22428 Human tel
37	5952	99.8	3766	6	AAH46790	Aad46790 pGRN145 p
38	5925	99.4	8742	6	AAH46793	Aad46793 pWGB5A p1
39	5903	98.7	3500	2	AAH18375	Aax18375 Telomeras
40	5882	98.7	3918	2	AAH18269	Aax18269 Telomeras
41	5882	98.7	3918	2	AAH18278	Aax18278 Telomeras
42	5871	98.5	3543	8	ABZ69628	Abz69628 Plasmid c
43	5871	94.5	3203	2	AAH18268	Aax18268 Altered C
44	5601	94.0	3323	2	AAH18277	Aax18277 Altered C
45	5593.5	93.8	3855	2	AAV22382	Aav22382 Human tel

ALIGNMENTS

RESULT 1	AAH48235	AAH48235	standard; DNA; 3396 BP.
ID	AAH48235	standard; DNA; 3396 BP.	
XX	AAH48235		
AC	AAH48235		
XX			
DT	21-SEP-2001 (first entry)		
XX			
DE	Heart muscle cell differentiation related DNA SEQ ID NO: 32.		
XX			
KW	Heart muscle cell; human; cell differentiation; heart disease; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200148151-A1.		
XX			
PD	05-JUL-2001.		
XX			
PF	27-DEC-2000; 2000MO-JP009323.		
XX			
PR	28-DEC-1999; 99UP-00372826.		
XX			
PR	28-FEB-2000; 2000MO-JP001148.		
XX			
PR	02-NOV-2000; 2000MO-JP007741.		
XX			
PA	(KYOM) KYOMA HAKKO KOGYO KK.		
XX			
PI	Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;		
XX	Yamada Y;		
XX			
DR	WPI; 2001-425656/45.		

QY LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
 Db CTGTGGAGACAGAGAGTCAAGGAGCATGGGAAGCCAGGCCCTGCTGACGTCACCA 1860
 QY LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 Db CTCCGCTTCATCCCAAGGCTGACGGGCTGCGCGCATGTGAACATGGACTACGTCGG 1920
 QY GlyAlaAspThrPheArgArgGluLysArgAlaGluValGluLeuThrSerArgValLysAla 660
 Db GGAGCGCAAAACGTTCCGACAGAAAAGAGGCGGAGCGCTCACCTCGAGGGTGAAGGA 1980
 QY LeuPheSerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyValAsnSerVal 680
 Db CTGTTCAAGGCTCTCAACTACAGAGCGGCGCGCGCCGCGCTCTGGGCCCTCTGTG 2040
 QY LeuGlyLeuAspAspIleHisArgAlaIlePheArgThrPheValLeuArgValArgAlaGln 700
 Db CTGGGCTGAGAGATATCCACAGGGGCTGGGCACTTGTGTGCTGCTGCTGGGCGCCAG 2100
 QY AspProPheProGluLeuTyrPheValLysValAspValThrGlyValIleArgPheThrIle 720
 Db GACCCGCGCGCTGACGCTGACTTTGTCAAGGTGATGTGACGGGCGCGCTGACACACATC 2160
 QY ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
 Db CCCCGAGACAGGCTCAAGAGGATCCGACACATCATTAACCCCAAGAACGATATCTCC 2220
 QY ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
 Db GTGGCTCGGTATGCGGTGTCCAGAAAGCGCCCATGGGCACTGCGCAAGGCGCTTCAAG 2280
 QY SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
 Db AGCCACGCTCTACCTTGCACAGACCTCCAGCCGTCATCCGACAGTTCCTGCTCAACCTG 2340
 QY GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
 Db CAGGAGACCAAGCCCGCTGAGGAGTCCGTGCTGATGACACAAAGCTCTCTCTGAAATGAG 2400
 QY AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
 Db GCCACAGATGGGCTCTTGGACGCTTCCATACGCTTATGTGCACACAGCCGCGGCAATC 2460
 QY ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 Db AGGGGCAAGTCTTACGTCAGTCCAGGCGGATCCGCGAGGGCTCCATCTCTCCACGCTG 2520
 QY LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
 Db CTCTGACGCTGTGCTACGGGCAATGGAAACAGAGCTTTGGCGGGATTTGGCGGGAGC 2580
 QY GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
 Db GGGCTGCTCTCTGCTTGGTGGATGATTTCTTGTGTGACACCTACCTACCCACGCG 2640
 QY LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
 Db AAAACCTTCTCAGGAGCCTGTGTCGAGGTGTCTCCGATATGCTGCTGTGGAACTTG 2700
 QY ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrPheValPheVal 920
 Db CGAAAGACAGTGTGAATCTTCCCTGAGAGAGAGAGGCGCTGGGTGGCAAGGCTTTTGT 2760
 QY GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
 Db CAGATGCGCGCCACGCGCTATTCCTCTGTGTGGCTCTCTGTGATACCGGAGACCTG 2820
 QY GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 Db GAGGTGACAGAGACTACTCCAGCTATGCCGAGACCTCATCAGAGCCAGTCTCACTTC 2880

QY AsnArgGlyPheLysAlaGlyValArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
 Db AACCGGCTTCAAGGCTGGGAGGAACAGGTGCAAACTCTTTGGGGTCTTGGCGCTG 2940
 QY LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 Db AAGTGTCAAGCTGTCTTCTGATTTGGATTTGACAGGTGAACACCTCCACAGCGTGTGACCAAC 3000
 QY IleTyrLysIleLeuLeuLeuGlnAlaIleTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 Db ATTTCAGATCTCTCTGCTGACAGCGTACAGTTCACGATGTGTCTGACAGCTCCCA 3060
 QY PheHisGlnGlnValIleTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 Db TTTCATCAGCAAGTTTGGAAAGAACCCCAATTTTCTGCGGGTATCTCTGACACGGCC 3120
 QY SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaLysGly 1060
 Db TCCCTCTGCTACTCATCTCATCTGAAAGCCAAAGACGAGGAGATGCTGTGGGGCCAAAGGC 3180
 QY AlaAlaGlyProLeuProSerGluAlaValGlnTyrLeuCysHisGlyAlaPheLeuLeu 1080
 Db GCGCGCGGCTCTGCTCTCCAGGCGCTGACAGTGTGTGCTGCTGACCAAGCATCTCTGCTC 3240
 QY LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db AAGTCATCTGACACACGATGTACCTACAGTGCACCTCTGGGGTCACTCAGACAGCCGAC 3300
 QY ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
 Db ACGCAGCTGAGTCGGAACCTCCGGGAGACGACGTGACTGCTGCTGAGGCGCGACAGCAAC 3360
 QY ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 Db CGGCACTGCTCTCACTTCAAGACATCTCGAGC 3396

RESULT 2
 ID AAH49601
 ID AAH49601 standard; DNA; 3396 BP.
 AC AAH49601;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Human coding sequence #2.
 XX
 KW Angiogenesis; cardiant; cell differentiating agent; bone marrow;
 KW heart muscle cell; heart disease; human; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200148149-A1.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-FEB-2000; 2000WO-JP001148.
 XX
 PR 28-DEC-1999; 99JP-00372826.
 XX
 PA (KYOM) KYOMA HAKKO KOGYO KK.
 XX
 PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;
 XX
 DR WPI, 2001-418252/44.
 DR P-PSDB; AAG64329.
 XX
 PT New adult bone marrow-originated cells capable of differentiating into
 PT heart muscle cells, applicable as remedies for various heart diseases
 PT particularly with damaged heart muscle accompanying degeneration.
 XX
 PS Disclosure; Page 134-142; 158pp; Japanese.
 XX
 CC The present invention relates to cells isolated from bone marrow, which

CC are capable of at least differentiating into heart muscle cells. The
 CC cells are applicable as remedies for various heart diseases particularly
 CC with damaged heart muscle accompanying degeneration. The present sequence
 CC was used to illustrate the present invention

XX Sequence 3396 BP; 549 A; 1157 C; 1088 G; 602 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3396
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-044-692-2 (1-1132) x AAH49601 (1-3396)

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Qy 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTrpArgGlu 20
Db 1 ATGCGCGCGCTCCCGCTCCAGCGCTGCTCCCTGCTGCGACGCGCTACCGCGGAG 60
Qy 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
Db 61 GTGCTGCGCGCTGCGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 120
Qy 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
Db 121 CGCGGGAGCGCGCGCTTCCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 180
Qy 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGln 80
Db 181 GAGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Qy 81 ValAlaArgValLeuGlnArgLeuGlyValArgGlyValAlaValAsnValLeuAlaPheGly 100
Db 241 GTGCGCGCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 300
Qy 101 PheAlaLeuLeuAspGlyValArgGlyValProProGlnAlaPheThrTrpSerValArg 120
Db 301 TTGCGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Qy 121 SerTrpLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATrGlyLeuLeu 140
Db 361 AGCTACTGCGCGCAACAGCGTGAACGCACTGCGCGCGCGCGCGCGCGCGCGCG 420
Qy 141 LeuArgArgValGlyAspArgValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
Db 421 CTGCGCGCGCGCGCGCGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 161 LeuValAlaProSerCysAlaTrpGlnValCysGlyProProLeuTrpGlnLeuGlyAla 180
Db 481 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Qy 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
Db 541 GCCACTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Qy 201 ArgAlaTrpAsnHisSerValArgGlyValGlyValProLeuGlyLeuProAlaProGly 220
Db 601 CGGCGCTGGAACCAATGAGTGAAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 660
Qy 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysTrpArgArg 240
Db 661 GCGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Qy 241 GlyAlaAlaProGluProGluArgTrpProValGlyGlnGlySerTrpAlaHisProGly 260
Db 721 GGCCTGCTGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Qy 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
Db 781 AGGAGCGCTGAGCGAGTGAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
  
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Qy 281 GluAlaThrSerLeuGlnGlyValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
Db 841 GAGGACACTTTTGGAGGGGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Qy 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTrpAspTrpPro 320
Db 901 CGCCAGCACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Qy 321 CysProProValAlaValAlaGluThrLysHisPheLeuTrpSerSerGlyAspLysGln 340
Db 961 TGTCCCGCGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
Qy 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyValArgArgLeu 360
Db 1021 CTGCGCGCGCTCTCTACTGAGCTCTGTGAGCGCGCGCGCGCGCGCGCGCGCG 1080
Qy 361 ValGluThrTrpPheLeuGlySerArgProTrpMetProGlyTrpProArgArgLeuPro 380
Db 1081 GTGGAGACCATCTTTCTGGTTCCAGCGCTGTGATGCCAGGAGACTCCCGGAGTTGCC 1140
Qy 381 ArgLeuProGlnArgTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis 400
Db 1141 CGCTGCGCGCGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCG 1200
Qy 401 AlaGlnCysProTrpGlyValLeuLeuLysThrHisCysProLeuArgAlaValThr 420
Db 1201 GCGCAGTGCCTCTCAGGGGTGCTCTCAAGACGCACTCCCGCTGCGAGCGCGTCA 1260
Qy 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGlu 440
Db 1261 CCAGAGCGCGGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
Qy 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
Db 1321 GAGGACACAGACCCCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
Qy 461 ValTrpGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
Db 1381 GTGTACGGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440
Qy 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysPheHisSerLeuGlyLysHis 500
Db 1441 AGGACACAGAGCGCGCTTCTCAGAGACACAGAGATTCATCTCTGGGAGAGCAT 1500
Qy 501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
Db 1501 GCCAAGCTTCTGCTGAGAGGCTGACGTGAGATGAGGTGCGGAGACTGCCCTTG 1560
Qy 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGlu 540
Db 1561 CGCAGAGCGCGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
Qy 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTrpValValGluLeuLeuArgSerPhe 560
Db 1621 CTGCGCAAGTCTCTGACTGCTGATGACTGTGATGCTGTGAGAGTGTCTTTC 1680
Qy 561 PheTrpValTrpGluThrThrPheGlnLysAsnArgLeuPhePheTrpArgLysSerVal 580
Db 1681 TTTTATGTCAGGAGACACGTTTCAAAAGAACAGGCTCTTTTTCACCGGAGAGTGT 1740
Qy 581 TrpSerLysLeuGlnSerLysGlyLysArgGlnHisLeuLysArgValGlnLeuArgGlu 600
Db 1741 TGGAGCAAGTGTGAAGCATTTGGAATCAACAGCATTTAAGAGGGTGAAGCTCGCG 1800
Qy 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
Db 1801 CTGTGGAAGCAGAGGTGACGAGCATCGGGAAGCAGCGCGCGCGCGCGCGCG 1860
Qy 621 LeuArgPheLysProLysProAspGlyLeuArgProLysValAsnMetAspTrpValVal 640
Db 1861 CTCGCTTATCCCGCAAGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
Qy 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGluArgLeuThrSerArgValAla 660
  
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Db      1921 GGAGCCAGAAAGCTCCGACGAGAAAGAGGGCCGAGCGCTCACCTCGAGGGGTGAAGCA 1980
Qy      661  LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db      1991 CTGTTACAGCGTGTCAACTACGAGCGGGCGCGCCCGCTCTGGGCGCCCTCTGG 2040
Qy      681  LeuGlyLeuAspAspIleHisArgAlaTTPArgThrPheValLeuArgValArgAlaGln 700
Db      2041 CTGGGCTCTGAGAGATATCCACAGGGGCTGGCGCACTTGCTGCTGCTGGGCGCCAG 2100
Qy      701  AspProProGlyLeuLeuTyrPheValIysValAspValThrGlyAlaTyrAspThrIle 720
Db      2101 GACCCGCGGCTGAGCTGTAATTTGTCAAGGTGATGTGACGGGCGCGTACACACACATC 2160
Qy      721  ProGlnAspArgLeuThrGluValIleAlaSerIleIleIysProGlnAsnThrTyrCys 740
Db      2161 CCCCGAGACAGGCTCAGGAGGTGATCCGACATCATCAACCCCAAGAACAGTATGTC 2220
Qy      741  ValArgArgTyrAlaValAlaGlnIysAlaAlaHisGlyHisValArgIysAlaPheIys 760
Db      2221 GTGCTCGGTATGCGGTGTCCAGAAAGCCGCCCATGGCAGCTCCGCAAGGCTTCAG 2280
Qy      761  SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db      2281 AGCCAGCTCTTCACTGACAGACCTCCAGCCGTACATGCGACAGTGTGGGTCACTG 2340
Qy      781  GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuGlnGlu 800
Db      2341 CAGGAGACACAGCCGCTGAGGGATGCGTCTCATGCAAGCAAGCTCCCTCTGATGAG 2400
Qy      801  AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
Db      2401 GCCAGAGTGGCTCTTCAAGCTCTTCAAGCTTTCATATGTCACACACCGCTGGCATC 2460
Qy      821  ArgGlyIysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db      2461 AGGGGCAAGCTCTTCAAGTCAAGTCCAGGGGATCCGCAAGGCTCATCTCTCCACGCTG 2520
Qy      841  LeuCysSerLeuCysTyrGlyAspMetGluAsnIysLeuPheAlaGlyIleArgArgAsp 860
Db      2521 CTCTGACGCTGTGCTTACGCGACATGAGAAACAAGCTTTTGGGGGATTCGGCGGGAC 2580
Qy      861  GlyLeuLeuLeuLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db      2581 GGGCTGCTCTCTCGTTGGTGAATGATTTCTTGGTGAACCTCACTCACCCACGCG 2640
Qy      881  LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db      2641 AAAACCTTCTCAGACCTGTGTCGAGGTGTCTGAGTATGGCTGCGGTGAACCTTG 2700
Qy      901  ArgIysThrValValAsnAspProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db      2701 CGGAAGACAGTGTGAATCTTCCCTGTAGAAGACGAGGCTGGGTGGCAAGGCTTTGTT 2760
Qy      921  GlnMetProAlaHisGlyLeuPheProTyrPyrGlyLeuLeuLeuAspThrArgThrLeu 940
Db      2761 CAGATGCCGCGCCACGCGCTATTCCTCTGTGGCTGCTGCTGTGATACCCGACCTCG 2820
Qy      941  GluValAlaGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db      2821 GAGGTGACAGAGCACTACTCCAGCTATGCCCCGAGCTTCATCAGACCCAGTCTCACCTTC 2880
Qy      961  AsnArgGlyPheIysAlaGlyArgAsnMetArgArgIysLeuPheGlyValLeuArgLeu 980
Db      2881 AACCGCGGCTTCAAGGCTGGAGAGAACATGCGTCCGAACTTTTGGGGCTTGGCGGTG 2940
Qy      981  LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db      2941 AAGTGCACAGCGCTTTCTGTGATTGCAAGGTAAACAGCTCCAGACGCGTGTCCACCAAC 3000
Qy      1001  IleTyrIysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020

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Db      3001 ATCTAACAGATCTCTCTGAGCGGTACAGGTTTCAAGCATGTGTGCTGCACTCCA 3060
Qy      1021  PheHisGlnGlnValIleThrIysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db      3061  TTTCTATCAGCAGTTTGGAGAAGACCCACATTTTCTCTGCGGTATCTCTACAGCGGC 3120
Qy      1041  SerLeuCysTyrSerIleLeuIysAlaIysAsnAlaGlyMetSerLeuGlyValIysGly 1060
Db      3121  TCCCTCTGCTACTTCATCTGAAAGCAAGAACGAGGAGTGTCTGCTGGGCGGCAAGGGC 3180
Qy      1061  AlaAlaGlyProLeuProSerGluAlaValGlnTyrPleuCysHisGlnAlaPheLeuLeu 1080
Db      3181  GCCGCGGCGCTCTCTCCAGAGCGGTGACAGTGTGTGTGACCAAGCATTTCTGTCTC 3240
Qy      1081  LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerIleuArgThrAlaGln 1100
Db      3241  AAGCTGACTGACACCGGTGTCACTTACGTGACACTCTGAGGATCACTCAGGACAGCCAG 3300
Qy      1101  ThrGlnLeuSerArgIysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db      3301  ACGCAGCTGAGTCGGAAGCTCCCGGGAGCAGACGCTGACTGCTGGAGGCGCAGCAAC 3360
Qy      1121  ProAlaLeuProSerAspPheIysThrIleLeuAsp 1132
Db      3361  CCGGCACTGCTCTCAGACTTCAAGACCAATCTTGAC 3396

RESULT 3
AAH44366
ID      AAH44366 standard; cDNA; 3396 BP.
XX
AC      AAH44366;
XX
DT      26-SEP-2001 (first entry)
XX
DE      Human telomerase nucleotide sequence SEQ ID NO:32.
XX
KW      Differentiation; heart muscle cell; cytokine; transcription factor;
KW      proliferation; surface antigen; heart disease; cardiomyocyte;
KW      bone marrow; umbilical blood cell; heart muscle degeneration;
KW      myocardial infarction; ss.
XX
OS      Homo sapiens.
XX
PN      MO200148150-A1.
XX
PD      05-JUL-2001.
XX
PF      02-NOV-2000; 2000MO-JP007741.
XX
PR      28-DEC-1999; 99JP-00372826.
XX      28-FEB-2000; 2000MO-JP001148.
XX
PA      (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI      Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
PI      Yamada Y;
XX
DR      MPI; 2001-425655/45.
XX      P-PSDB; AAB99930.
XX
PT      Cells capable of differentiating into cardiomyocytes and originating in
PT      bone marrow or umbilical blood cells for study of cardiomyocyte
PT      differentiation and treatment of heart disease.
XX
PS      Disclosure; Page 141-147; 187p; Japanese.
XX
CC      The present invention describes cells originating in bone marrow or
CC      umbilical blood cells which are capable of differentiating into
CC      cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
CC      differentiation of the cells; (2) a method for carrying out the
CC      differentiation into cardiomyocytes, regulated by a promotional and/or
CC      inhibitory factor; (3) a method for the differentiation of the cells into
CC      cell types other than cardiomyocytes; (4) drug compositions promoting the

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CC Formation of heart muscle and regeneration of heart tissue which contain
CC the cells; (5) a method for the production of antibodies which recognise
CC the cells; especially antibodies which recognise a surface antigen on the
CC cells; (6) a method for screening factors which promote the proliferation
CC of the cells; (7) a method for immortalising the cells by expressing
CC telomerase in them; (8) drug compositions for the treatment of heart
CC disease which contain the immortalised cells; and (9) cell-free
CC supernatant from the culture of the cells and its use in promoting their
CC differentiation into cardiomyocytes. The cells are used in the treatment
CC of diseases involving heart muscle degeneration, such as myocardial
CC infarction and in the study of cardiomyocyte differentiation. AAH44351 to
CC AAH44309 and AAB99915 to AAB99915 represent sequences used in the
CC exemplification of the present invention

XX Sequence 3396 BP; 549 A; 1157 C; 1088 G; 602 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3396
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-044-692-2 (1-1132) x AAH44366 (1-3396)

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QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTrpArgGlu 20
DB 1 ARGCCGCGGCTCCCGCTGCGAGCCGTCGCTCCCTGCTGGCAGCACAACCGCGAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln 40
DB 61 GTGCTGCGCCCTGCGCCAGTTCGTCGCGCCGCTGGGCGCCCAAGGCGTGGCGTGCAG 120
QY 41 ArgGlyAspProAlaIlePheArgAlaLeuValAlaGlnCysLeuValCysValProTrp 60
DB 121 CGGGGGAGCCCGCGGCTTCGCGCGCTGGTGGCCAGAGCTGGTGGCGGCTTGG 180
QY 61 AspAlaArgProProProAlaIleProSerPheArgGlnValSerCysLeuArgGluLeu 80
DB 181 GAGCGACGCGCGCGCCCGCCCTCTTCGCGCAGGTGTCGCTGAGAGAGCTG 240
QY 81 ValAlaArgValIleGlnArgLeuCysGluArgGlyValAlaLysAsnValLeuAlaPheGly 100
DB 241 GTGGCCCGAGTGTGCGAGGCTGTGCGAGCGCGCGCAGAAACCTGCTGGCGCTTGGCG 300
QY 101 PheAlaLeuLeuAspGlyValArgGlyValProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGCGCTGTGGAGCGGGGCGCGGGGGCGCCCGGAGGCTTCAACACAGCGTGGC 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValaTrpGlyLeuLeu 140
DB 361 AGCTACCTCCCAACACGCGTGAACGACGACGCTGGGGGAGCGGGGCGTGGGGCTGCTG 420
QY 141 LeuAlaArgValAlaGlyAspValIleValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGGCGCGGCTGGGCGACGACGCTGCTGCTCACTCTGACGCTGCGCGCTCTTTGG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 CTGGTGGCTTCCAGCTGCGCTTACAGAGTGTGGGCGCGCGCTGTACACGCTGGCGCT 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 541 GCCACCTCAGGCGCGCGCCCGCAGCAGCTAGTGAACCCGAGAGGCTCTGGGATCGGA 600
QY 201 ArgAlaTrpAsnHisSerValArgGlyValaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGGCGCTGAGACCATGTGCTCAGGAGGCGCGGGGTCCCTGGGCTGCGACGCCCGGT 660
QY 221 AlaArgArgArgGlyValSerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GGAGGAGGCGCGGGGCGAGTGCACGCCAGAGTCTGCTGCTGCCAAGAGGCCCAAGCGGT 720
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QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly 260
DB 721 GCGGCTGCCCTTCCAGCGGAGGAGGAGCGCCCTTTGGGCGAGGGTCTCGGGCCACCGGGGC 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 781 AGGAGCGGTGGACCGAGTACCGGTGTCTGTGGTGTCACTTCCGAGACCGCGCGGA 840
QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyTyrArgHisSerHisProSerValGly 300
DB 841 GAAGCCACTCTTTGGAGGAGTGGCTCTTGGCAGCGCCACTCCACCCATCCGTGGGC 900
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro 320
DB 901 CGCAGACACACGCGGGGCGCCCATTCACATCGCGGCGCACAGTCCCTGGGACAGCGCT 960
QY 321 CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln 340
DB 961 TGTCCCGCGGTGTACGCGCAGACCAAGCACTTCTCTACTCTCAGGCGCACAAGAGCAG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1021 CTGGGCGCTTCTCTCTACTCAAGCTCTTGAAGGCCAGCTTACTGCGCGCTGGAGGCTC 1080
QY 361 ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro 380
DB 1081 GTGAGACCATCTTTCTGGGTTCAGGCGCTGATGCGAGGAGTCCCGCGAGTGGCC 1140
QY 381 ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGlnLeuGlnHis 400
DB 1141 CGCTGCGCCCGACGCGTACTCGGCAATGCGCGCCGTGTTGAACTGCTGGGAACAC 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrLysCysProLeuArgAlaAlaValThr 420
DB 1201 GCGCAGTGCCTTACGGGGTCTCTCAAGACGCACTGCCGCTCGAGCTCGGTCAAC 1260
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440
DB 1261 CCAGACGCGGTGTGTGTCGCGGAGAAAGCCCAAGGCTGTGGCGGCGCCCGAGAG 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln 460
DB 1321 GAGGACACAGACCGCCGTCGCTGTGACGCTCTCCGACACACAGCGCCCTGGCAG 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer 480
DB 1381 GTGTACGCTTGTGTGGGCTGTGCTGCGCGCGCTGGTGGTCCCGCAGGCTCTGGGGCTTC 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
DB 1441 AGGCAACAAGAACGCGGCTTCTCAGAGAAACCAAGAACTCATCTCCCTGGGGAAGCAT 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
DB 1501 GCCAAGCTTCTGCTCAGAGAGTGAAGTGAAGAGTGGAGGAGCTGCGCTTGGCTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGluIle 540
DB 1561 CGCAGAGGCCAGGGGTTGCTGTGTTCCGCGCGCAGAGACCGTCTGCTAGAGAGATC 1620
QY 541 LeuAlaLysPheLeuHisIleTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
DB 1621 CTGGCCAACTTCTCGACACTGCTGATGAGTGTGATGCTGTGAGACTGCTGAGTCTTTC 1680
QY 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1681 TTTTATGTCAACGAGACACGTTTCAAAAGAACAGCTCTTTTCTTACCGGAAGGTGTC 1740
QY 581 TrpSerLysLeuGlnSerIleGlyTyrLeuArgGlnHisLeuLysArgValGlnLeuArgGlu 600
DB 1741 TGAAGCAAGTTCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGTTGACCTTGGCGGAG 1800
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QY LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
 Db CTGTGGAGACGAGGTGACGAGCATCGGAAAGCCAGGCCCTGTGTGACGTCCAA 1860
 QY LeuArgPheIleProIysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 Db CCCCCCTTCATCCCAAGCCTGACGGGCTGCGGCCCATGTGTGAACATGACATCACTGCGTG 1920
 QY GylAlaArgThrPheArgArgGlyLysAspArgAlaGluArgLeuThrSerArgValLysAla 660
 Db GGAGCCAGAACGCTTCGCGAGAAAGAGAGGCCGACGCTCCACCTCGAGAGGTGAAGGCA 1980
 QY LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
 Db CTGTTCAAGGTCTCACTACACAGAGGGGCGCGGCCCTCTGTGGCGCGCTGTG 2040
 QY LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
 Db CTGGGCTGTGAGATTCACAGAGCGCTGCGCACCTTGCTGCTGCTGCGGCGCCAG 2100
 QY AspProProGluLeuTyrPheValLysValAspValThrGlyValTyrAspThrIle 720
 Db GACCCGCGCTGAGCTGATCTTGTCAAGGTGATGACGGGCGCGTACACACCATC 2160
 QY ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
 Db CCCCAGAGACGGCTCCGAGAGGTCACTGCGACAGTATCAACCCAGAACAGTACTG 2220
 QY ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
 Db GTGGCGTGGTATGCCGTGTCCAGAGGGCGGCCCAAGGCGCACCTCGCAAGGCTTCAAG 2280
 QY SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
 Db ACCCAGCTCTTCACTTGAACAACCTCCAGCGGTACATGACAGTTCGGTGCCTCCG 2340
 QY GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
 Db CAGAGAACAGCCCGGTGAGGATGCCGTGTCATGACAGACAGCTCTCCCTGAAATGAG 2400
 QY AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValAlaGly 820
 Db GCACAGAGTGGCTCTTCGACGCTTCTCAACGCTTATGTGCCACACCGCGCGCATC 2460
 QY ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 Db AGGGGCAAGTCTTACCTCCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTG 2520
 QY LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
 Db CTCTGCAAGCTGTGCTACGCGCAATGAGAACAGCTGTTGCGGGGATTCGCGCGGAC 2580
 QY GlyLeuLeuLeuArgLeuValAspAspPheLeuValThrProHisLeuThrHisAla 880
 Db GGGCTGCTCTCGTGGTGGATGATTTCTTGTTGTGACACCTCACCTCACCCACGCG 2640
 QY LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
 Db AAAACCTTCTTCCAGGACCTGTGCTCCAGAGTGTCCCTGAGATATGGCGGTGGAACTTG 2700
 QY ArgLysThrValAlaAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
 Db CGGAAGACAGTGTGAATCTTCTGTGAAGACAGAGCCCTGGGTGGCACGCGCTTTGTT 2760
 QY GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
 Db CAGATCCCGGCCCAACGCGCTATTCCTCGTGGCGGCTGCTGTGATACCGGACCTCG 2820
 QY GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 Db GAGGTGCACAGGACATCTCCAGCTATGCGCGGACCTTCATCGAACCGATCTCACCTTC 2880
 QY AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980

Db ||||| 2881 AACCGCGCTCAAGGCTGGAGAGAAACATGCTCCCAAACTCTTGGGCTTGGCGGCTG 2940
 QY ||||| 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 Db ||||| 2941 AAGGTCAACAGGCTTCTTCTGTGATTTGAGGTGAACAGCTCCAGACGGGTGTGCACCAAC 3000
 QY ||||| 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 Db ||||| 3001 ATCTACAGATCTCTCTGCTGAGGCGTACAGTTCACGACATGTGTGTCAGCTCCCA 3060
 QY ||||| 1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 Db ||||| 3061 TTTCATCAGCAAGTTTGGAAAGAACCCACATTTTCTCGGCGGTATCTTCACACGGGCC 3120
 QY ||||| 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValLysGly 1060
 Db ||||| 3121 TCCCTCTGCTACTCCATCTGAAAGCCAAAGCAGAGGATGTGCTGGGGGCGCAAGGGCC 3180
 QY ||||| 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
 Db ||||| 3181 GCGCGCGGCTCTGCTGCTCCAGAGCGGTGACGTGCTGTGCACCAACATTCCTGCTC 3240
 QY ||||| 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db ||||| 3241 AAGCTGACTCGACACCGTGTCACTACGTGCCACTCTCGGGGTCACTCAGACAGCCAG 3300
 QY ||||| 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnLysAlaAsn 1120
 Db ||||| 3301 ACGCAGCTGAGTGGAAAGCTCCGGGGAGCAGACGTGACTGCTGTGAGGGCCGACGCCAAC 3360
 QY ||||| 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 Db ||||| 3361 CCGGCACTGCTCTCAGACTTCAAGACATCTTGAC 3396

RESULT 4
 ADG70113
 ID ADG70113 standard; DNA; 3396 BP.
 AC ADG70113;
 XX 11-MAR-2004 (first entry)
 DT 11-MAR-2004 (first entry)
 DE hTERT coding sequence.
 KW ds; gene; cytosolic; gene therapy; reverse transcriptase-inhibitor;
 KW HIV-1; reverse transcriptase; human telomerase reverse transcriptase;
 KW hTERT; chimeric; catalytic site; unregulated cellular growth; cancer;
 KW tumor.
 OS Homo sapiens.
 XX
 PN WO2003095605-A2.
 XX
 PD 20-NOV-2003.
 XX
 PF 14-APR-2003; 2003WO-EP003874.
 XX
 PR 08-MAY-2002; 2002US-0378820P.
 XX
 PA (PHMA) PHARMACIA ITAL SPA.
 XX
 PI Moll J, Schumacher A, Stouten P;
 XX
 XX MPI; 2004-012095/01.
 DR P-PSDB; ADG70114.
 XX
 PT New HIV-1 Reverse Transcriptase and human Telomerase Reverse
 PT Transcriptase proteins and nucleic acids, useful in gene therapy or for
 PT treating or preventing unregulated cellular growth, e.g. cancer cell or
 PT tumor growth.
 XX
 PS Example 1; SEQ ID NO 3; 141bp; English.

XX The invention relates to the isolation of compounds that bind and inhibit
 CC the activity of HIV-1 reverse transcriptase (RT) or human telomerase
 CC reverse transcriptase (hTERT). The method involves determining these
 CC compounds using a HIV-1 RT/hTERT chimeric construct containing the
 CC catalytic sites of each enzyme. The nucleic acid is useful for treating
 CC or preventing unregulated cellular growth, including cancer cell and
 CC tumor growth. It is also useful in gene therapy. Compounds that inhibit
 CC telomerase activity can be used to treat cancer. The vectors of the
 CC invention can be used to amplify DNA or RNA encoding HIV-RT/hTERT and/or
 CC express DNA which encodes HIV-RT/hTERT. This sequence corresponds to a
 CC coding sequence for the human TERT protein.

XX Sequence 3396 BP; 549 A; 1157 C; 1088 G; 602 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3396
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-044-692-2 (1-1132) x ADG70113 (1-3396)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
 Db 1 ATGCCCCGGGCTCCCGCTGCGAGCCGAGCGCTCCCTGCTGCGAGCCACTACCGCGAG 60
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPheValGln 40
 Db 61 GGTCTCCGCTGGCGACAGTTCGTGCGCGCTGCGGCGCCCGAGGGCTGGCGGCTGTGCAG 120
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 Db 121 CGGGGGAGACCGCGGCTTCCGCGCGCTGTGTGCCAGTGGTGTGCGGCTTGG 180
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGlnLeu 80
 Db 181 GAGCGACG 240
 QY 81 ValAlaArgValLeuGlnArgLeuCysGlyArgGlyAlaAlaLysAsnValLeuAlaPheGly 100
 Db 241 GTGGCCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGAGAACCTGTGCTTGGC 300
 QY 101 PheAlaLeuLeuAspGlyValArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 Db 301 TTCGCGCTGTGGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
 Db 361 AGCTACCTCCCAACACGCGTGAACCGACGCTGCGGGGAGCGGGGCTGTGGGCTGTG 420
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 421 CTGGCGCGCGGTGGGCGACACGCTGCTGTACCTGTGCACTGCGCGCTCTTTTGG 480
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 Db 481 CTGGGTGGCTCCAGAGCTGCGCTACAGGTGTGGGGCGCGCGCTGTACAGCTCGGCGCT 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 Db 541 GGCACACAGGCG 600
 QY 201 ArgAlaTyrAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 601 CGGGCTGTGACACCTAGCTTCAAGGAGCGCGGGGCTCCCTGTGGCTGTCCACCGCGGT 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 Db 661 GCGAGGAGGCGCGGGGCGAGTCCAGCGCGAGCTGTGCGCTTCCCAAGAGCGCGCGGT 720

QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerThrAlaHisProGly 260
 Db 721 GGGCGTGGCTTGGAGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 Db 781 AGAGCGCGTGAACCGAGTACCGTGGTCTGTGTGTGTGTACCTGCGAGACCGCGCGAA 840
 QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyTyrThrArgHisSerHisProSerValGly 300
 Db 841 GAAGCCACTCTTGTGAGGGTGGCTCTGTGACGCGCGCACTCCACCCACTCCGTGGGC 900
 QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
 Db 901 CGCGAGACACAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
 QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
 Db 961 TGTCCCCCGTGTAGCGCGAGACCAAGCACTTCTTACTCTTCAAGCGACCAAGAGCAG 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 Db 1021 CTGGGCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
 QY 361 ValGlnThrLeuPheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
 Db 1081 GTGAGACCATCTTTCTGGGTTCCAGGCCCTGTGATGCCAGGAGACTCCCGGAGGTGGCC 1140
 QY 381 ArgLeuProGlnArgTyrTyrGlnMetLysProLeuPheLeuGlnLeuLeuGlyAsnHis 400
 Db 1141 CGCTGCGCCAGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
 Db 1201 GCGAGTGGCGCTTACGGGGTGTCTTCAAGAGCACTGCGCGCTGCGAGCTGGCTTACC 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGlu 440
 Db 1261 CCAGCAGCGCGGTGTGTGCGCGGAGAACCCCGAGGCTGTGTGGCGCGCGCGAGAG 1320
 QY 441 GlnAspThrAspProArgArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
 Db 1321 GAGGACACAGACCCCGTGTGCTGTGTGAGCTGTGCTCCCGACACAGACGCGCGGAG 1380
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
 Db 1381 GTGTACGCTTGTGTGCGGGCTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440
 QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheLeuSerLeuGlyLysHis 500
 Db 1441 AGGCACACAGAACCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1500
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
 Db 1501 GCGAAGCTCTGCTGACAGAGCTGACGTGAAGAGACGCGGAGACTGTGGCTTGGCTG 1560
 QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluLe 540
 Db 1561 CGCAGAGACCCAGGGGTTGGCTGTGTTCGCGCGCGCGAGACACCTGTCTGCGAGAGATC 1620
 QY 541 LeuAlaLysPheLeuHisTyrPheLeuMetSerValTyrValAlaGlnLeuLeuArgSerPhe 560
 Db 1621 CTGGCCAAGTTCCTGCACTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
 QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
 Db 1681 TTTTATGTCAAGAGACACAGCTTTCATAAAGAACAGGCTTTTTCATCCGGAAGAGTTC 1740
 QY 581 TyrSerLysLeuGlnSerLysGlyLysArgGlnHisLeuLysArgValGlnLeuArgGln 600
 Db 1741 TGGAGCAAGTTGCAAAAGATTGGAATCAGACAGCACTTTGAAGAGGTGTGACCTCGGAG 1800
 QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620

1801 CTGTGGAAAGCAGAGGTGAGGAGCATCGGAGAGCCGCGCTGTGACGTCCAGA 1860
621 LeuAArgPhe11eProlyseProaspGlyLeuAArgPro11eValAsnMetLaspTyrVal1 640
1861 CTCCGCTTCATCCCAAGGCTGACGGGCTGCGCGCATTTGTGAACATGGACATCAAGCTCGTG 1920
641 GlyAlaArgThrPheAArgArgGlyLysAArgAlaGlyAArgLeuThrseryArgValLysAla 660
1921 GGAGCCAGAACCTTCGCGAGAGAAAGAGGCGCGAGCTCTCACTTCGAGGGTGAAGGA 1980
661 LeuPheSerValLeuAsnTyrGlyLysAArgAlaAArgArgProGlyLeuLeuGlyAlaSerVal 680
1981 CTGTTCAAGGTGCTCAACTACAGAGCGGCGCGCGCTCTGAGCGGCTCTGAG 2040
681 LeuGlyLeuAAspAsp11eHisAArgAlaTTPAArgThrPheValLeuAArgValAArgAlaGln 700
2041 CTGGGCTGTGGAGATATCCACAGGGGCTGGCGCATCTGTGTGTGTGGCGGCCAG 2100
701 AAspProProGlyLeuTyrPheValLysValAspValThrGlyAlaTyrAspThr11e 720
2101 GACCCGCGCTGAGCTGATCTTTGTCAAGGTGATGTGAAGGCGCGCTGACACCATTC 2160
721 ProGlnAspArgLeuThrGlyLysAlaSer11eLysProGlnAsnThrTyrCys 740
2161 CCCAGAGACAGGCTACCGAGGTCATCGCCAGATCATCAACCCAGAACAGTATCTGC 2220
741 ValAArgArgTyrAlaValAlaGlyLysAlaHisGlyHisValAArgLysAlaPheLys 760
2221 GTGGCTCGGTATGCGGTGTCCAGAGGCGCGCCATGGGCGACGTCCGCAAGGCTTCAAG 2280
761 SerHisValSerThrLeuThrsAspLeuGlnProTyrMetArgGlnPheVal1AHisLeu 780
2281 ACCACGCTTCTAAGCTTGACAGACCTCCAGCCGTACATGACAGAGTTGAGTCTACCTG 2340
781 GlnGlnThrsSerProLeuAArgAspAlaVal11eGlnGlnSerSerSerLeuAsnGln 800
2341 CAGAGAGACAGCCGCTGAGGATGCGTCGTATGACAGACAGGCTCTCCCTGATGATAG 2400
801 AlaSerSerGlyLeuPheAspValPheLeuAArgPheMetCysHisHisAlaValAArgGle 820
2401 GCCACAGAGGCGCTCTTCACAGCTCTTCATCGCTTCATGTGCACACCCGCGGCCATTC 2460
821 ArgGlyLysSerTyrValGlnCysGlnGly11eProGlnGlySer11eLeuSerThrsLeu 840
2461 AAGGGGCAAGTCTTACCTCCAGTGCAGGGGATCCCGAGGGCTCCATCTCTTCACAGCTG 2520
841 LeuCysSerLeuCysTyrGlyAspMetGlyAsnLysLeuPheAlaGly11eAArgArgAsp 860
2521 CTCTGAGGCTGTGCTGACCGGACATGAGAACAGCAAGCTTTTGGGGGATTCGGCGCGAGC 2580
861 GlyLeuLeuLeuAArgLeuValAspAspPheLeuLeuValThrsProHisLeuThrsHisAla 880
2581 GGGCTGCTCTCTCGTTGGTGTGATTTCTTGTGGTGAACCTCACTCACTCCACCGCG 2640
881 LysThrPheLeuAArgThrLeuValAArgGlyValProGlnTyrGlyCysValValAsnLeu 900
2641 AAAACCTTCTTAAGGACCTTGCGCGAGGTGTCCCGAGATGAGCTGCGGGGAACTTG 2700
901 ArgLysThrValValAsnPheProValGlyAspGlyAlaLeuGlyGlyThrsAlaPheVal 920
2701 CGGAAGACAGTGTGTAATCTTCCTGTAGAAAGAGAGCCCTGGGTGGCAAGGCTTTGT 2760
921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrsArgThrLeu 940
2761 CAGATGCCCGGCCACCGCTATTCCTCTGTGCGGCTCTGTGTGATACCGCGAACCTTG 2820
941 GlnValGlnSerAspTyrSerSerTyrAlaArgThrSer11eAArgAlaSerLeuThrsPhe 960
2821 GAGGTGACAGGACACTACCTACGATAGCCGAGCTTCATCAAGACAGTCTCAACCTTC 2880
961 AsnAArgGlyPheLeuValAArgAspMetArgArgLysLeuPheGlyValLeuAArgLeu 980

2881 AACCGCGCTTCAAGCTGGAGAGAACATGCGCTCCGCAACTCTTTGGGGTCTTGGCGGCTG 2940
981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrsValCysThrAsn 1000
2941 AAGGTGACAGGCTGTCTTGTGATTTGGATTTGAGTGAACAGCTTCAAGACGGTGTGCACCAAC 3000
1001 IleTyrLys11eLeuLeuLeuGlnAlaTyrAArgPheHisAlaCysValLeuGlnLeuPro 1020
3001 ACTTCAAGATCTCTCTGTGAGCGGTACAGGTTTCAAGCATGTGTGTGTGAGCTCCCA 3060
1021 PheHisGlnGlnValTTPlysAsnProThrPhePheLeuAArgVal11eSerAspThrAla 1040
3061 TTTTCATCGCAAGATTGGAAAGAACCCCATTTTCTCGCGGTATCTTCAACAGCGGC 3120
1041 SerLeuCysTyrSer11eLeuLysAlaLysAsnAlaGlyMetSerLeuGlyVal1AArgGly 1060
3121 TCCCTGTCTACTCCATCTGAAAGCAGAACGAGGATGTGCTGTGGGGGCCAAGGCC 3180
1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTyrLeuCysHisGlnAlaPheLeuLeu 1080
3181 GCGCGCGGCTCTGCTCCGAGGCGGTGAGTGGCTGTGCAACAGCATTCCTGCTC 3240
1081 LysLeuThrsArgHisAArgValThrsTyrValProLeuLeuGlySerLeuAArgThrAlaGln 1100
3241 AAGCTGACTCGACACCGTGTCACTTACGTGCCACTCTGGGGGTCACTCAGAGACAGCCCG 3300
1101 ThrGlnLeuSerArgLysLeuProGlyThrsThrLeuThrsAlaLeuGlnAla1AAsn 1120
3301 ACGCAGCTGAGTGGAAAGCTCCGGGAGACGACGTGACTGCTGTGAGGCGCCAGCAAC 3360
1121 ProAlaLeuProSerAspPheLysThr11eLeuAAsp 1132
3361 CCGGCACTGCCCTCAGACTTCAAGACATCTCTGAGC 3396

RESULT 5
ABV78144
ID ABV78144 standard; DNA; 3399 BP.
XX
AC ABV78144;
XX
XX 15-NOV-2002 (first entry)
DT
XX
XX
DE Human telomerase reverse transcriptase DNA SEQ ID NO 28.
XX
XX RNA inhibition; dERNA1; gene expression inhibitor; oncogene; cytostatic;
KM virucide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
PN MO200255693-A2.
PD
XX 18-JUL-2002.
PF
XX
PF 09-JAN-2002; 2002WO-EP000152.
PR
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055289.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
PA
XX (RIBO-) RIBOPHARMA AG.
XX
XX Kreutzer R, Limmer S, Roost S, Hadwiger P;
XX
XX WPI; 2002-590671/63.
XX
XX Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
XX Claim 10; Page 129-130; 203pp; German.
XX
XX The invention relates to inhibiting expression of a target gene (I) in a

cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (i) and at least one end of dsRNA1 has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. In humans, also genes in plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of a gene related to the invention

XX Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3399
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-044-692-2 (1-1132) x ABV78144 (1-3399)

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QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 1 ATGCCGCGGCTCCCGCTGCGAGCGCGTCCCTGCTGCGAGCCACTACCGCGAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrArgLeuValGln 40
DB 61 GTCGTCGCGCGCCAGCTTCGTCGCGCGCGCCGCGCGCCGCGCGCGCGCGCGCG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CCGCGGGAGCCCGCGGCTTCCGCGCGCTGTCGCGCCAGCTGCTGTCGCGCTG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
DB 181 GAGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGlyArgGlyAlaAlaAsnValLeuAlaPheGly 100
DB 241 GTGGCCCGAGGTGTGAGAGGCTGTGCGAGCGCGCGAGCAAGACCTGCTGCGCTT 300
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTCGCGCTCTGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValAlaTyrGlyLeuLeu 140
DB 361 AGCTACCTGCCCAACACGCGTGAACGCGAGCTGCGGGGAGCGGGGCGTGGGCTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGGCGCGGTGGGCGACACGCTGTGCTTCACCTGTGACGCGCGCTCTTTTGG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 CTGGTGCTCTCCAGCTGCGCGCTACACAGCTGTGGGGCGCGCGCTGACACGCT 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
DB 541 GCCACTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 201 ArgAlaTyrAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGGGCGCTGAGACCATAGCTCAGAGAGGCGCGGGGTCCTCGCGCTGCGACCGCG 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCGAGAGAGCGCGCGGGGCGAGTGCACGCGCAAGCTCTCCCTCCCAAGGCGCG 720
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260

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DB 721 GCGCTGCGCGCTGAGCGGAGCGAGCGCGCGCTGGGCGAGGGCTCTGGGCGCACCGCGG 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
DB 781 AGAGCGGTGAGCCAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyTyrArgHisSerHisProSerValGly 300
DB 841 GAAAGCACTCTTTGGAGGGTCCGCTCTGTGCAAGCGCGCACTCCACCAACCGGGGC 900
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
DB 901 CCGCAGACACAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 321 CysProProValTyrAlaGlnThrThrHisPheLeuTyrSerSerGlyAspArgGlnGln 340
DB 961 TGTCCCGCGGTGTAGCGCCAGACCAAGCACTTCTCTCACTCTCAAGGCGCAAGAGCAG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyValaArgArgLeu 360
DB 1021 CTGGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 361 ValGlnThrIlePheLeuGlySerArgProTyrMetProGlyTyrThrProArgArgLeuPro 380
DB 1081 GTGAGACCATCTTCTGAGGTTCCAGCGCGCTGATGCCAGGAGACTCCCGCAGTTGCC 1140
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlnHis 400
DB 1141 CGCTTCGCCCGAGCGCTACTCGGAAATGGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB 1201 GCGAGTGCCTCTTACGCGGTGTCTCTCAAGAGCACTGCCGCTCGAGCTCGGCTCAC 1260
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu 440
DB 1261 CCAGCAGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
QY 441 GluAspThrAspProArgArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB 1321 GAGGACACAGACCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
DB 1381 GTGTACGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis 500
DB 1441 AGGCACAAAGAAAGCGCGCTTCTCTCAGAAACACCAAGAAATTCATCTCCCTGGGAA 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
DB 1501 GCCAAGCTCTCGCTCAGAGGCTGACGTGAAGAGAGGTGCGGAGACTGCGCTTGGCTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluLeu 540
DB 1561 CGCAGAGAGCCAGGGGTTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
QY 541 LeuAlaLysPheLeuHisTyrLeuMetSerValTyrValGlnLeuLeuArgSerPhe 560
DB 1621 CTGGCGCAAGTCTCTCAGCTGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGT 1680
QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1681 TTTTATGTACGGAACACCGTTTCAAAAGAACAGGCTCTTTTGTACCGGAAGGTGT 1740
QY 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGln 600
DB 1741 TCGAGCAAGTTCACAAAGCATTTGGAATCAGACGACTTGAAGAGGTGCACTGCGGAG 1800
QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620

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Db 1801 CTGTCGAGACAGAGGTCCAGCATCCGAGAACCCGCGCTCGTGCATGTCACA 1860
 Qy 621 LeuArgPheIleProIysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
 Db 1861 CTCGGCTTATCCCAAGACCTGACGGGCTGCGCCCATTTGTGAACATGACATACGTCG 1920
 Qy 641 G1yAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
 Db 1921 GGAAGCCAGAACGTTCCGACAGAAAGAGAGCCGACGCTCACTCCAGAGGGTGAAGCA 1980
 Qy 661 LeuPheSerValLeuAsnTyrGluValArgAlaArgArgProGlyLeuLeuGlyLysSerVal 680
 Db 1981 CTGTTACAGGCTGCTCAACTACGACGGGCGCGCGCTCGCTCGGCGCTCTGTG 2040
 Qy 681 LeuGlyLeuAspAspIleHisArgAlaTProArgThrPheValLeuArgValArgAlaGln 700
 Db 2041 CTGGGGCTGACGATATCCACAGGGCTGCGCACCTTGCTGTGGTGTGGCGGCCAG 2100
 Qy 701 AspProProGluLeuTyrPheValLysValAspValThrGlyValTyrAspThrIle 720
 Db 2101 GACCCGCGCCCTGAGCTGACTTTGTCAAGGTGATGTACGGGCGCGCTACACACCATC 2160
 Qy 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
 Db 2161 CCCACAGACAGGCTCACGAGGTCATCGCCAGCATCATCAACCCAGAACAGTACTCG 2220
 Qy 741 ValArgArgTyrAlaValAlaGlnLysAlaHisGlyHisValArgLysAlaPheLys 760
 Db 2221 GTGGCGGTATGCCGTGTCCAGAAAGCGCCGCAAGGCGACGTCGCAAGGCTTCAAG 2280
 Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
 Db 2281 ACCCAGCTCTTACCTTGACACAGCTCCAGCCGTCATCGACAGCTTCGTGGCTCACTCG 2340
 Qy 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
 Db 2341 CAGGAGACACAGCCCGCTGAGGATGCCGTGCATGACAGACAGCTCTCCCTGATGAG 2400
 Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValAlaGlie 820
 Db 2401 GCCAGACGTGGCTCTTCACAGCTTCCTACAGCTTCATGTGCACACCCGCGCCATC 2460
 Qy 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 Db 2461 AGGGGCAAGTCTTACCTTCCAGTGCACAGGAGATCCGCAAGGCTCATCTCTCCACGCTG 2520
 Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
 Db 2521 CTCTGCAGGCTGTGCTACGCGCATGAGAACAAAGCTGTTGCGGGGATTCGGCGGAG 2580
 Qy 861 GlyLeuLeuLeuValAspAspPheLeuValThrProHisLeuThrHisAla 880
 Db 2581 GGGCTGCTCTCGTTGTGTGATGATTTCTGTTGTGTACACCTCACTCACCCACGCG 2640
 Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
 Db 2641 AAAACCTTCTCAGAACCTGTGTCGAGGTGTCTCGATATGCTGCTGCTGTGAACCTTG 2700
 Qy 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
 Db 2701 CGGAAGACAGTGTGAACTTCCCTGTGAGAAAGACGAGGCTCGGTGGACAGGCTTTGTT 2760
 Qy 921 GlnMetProAlaHisGlyLeuPheProTyrGlyLeuLeuLeuAspThrArgThrLeu 940
 Db 2761 CAGATGCCGCGCCACAGCTATTTCCCTGTGGGCTCTCTGTGTGATCCCGGACCTCG 2820
 Qy 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 Db 2821 GAGGTGCAGAGGACCTACCTCCAGCTATGCCCGGACCTCATCAGACCGAGTCTACCTTC 2880
 Qy 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
 Db 2881 AACCGCGGCTTCAAGGCTGGAGAAACATGCGTCAACTCTTGGGGCTTGGCGGCTG 2940

Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 Db 2941 AAGTGTACAGGCTGTTCTGTGATTTGACAGTGAACAGCTTCCAGACGCTGTGACACAA 3000
 Qy 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 Db 3001 ACTTCAAGATCTCTCTGTGTGACAGGCGTACAGCTTTCACGACATGTGTGTGACAGCTCCA 3060
 Qy 1021 PheHisGlnGlnValTTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 Db 3061 TTTTCAATCAGCAAGTTTGAAGAAACCCCATTTTCTGCGGTGATCTCTACACAGCGGC 3120
 Qy 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValLysGly 1060
 Db 3121 TCCCTGTGCTACTCCATCTGAAGCCAAAGACGAGGATGTGCTGGGGGCAAGGGGC 3180
 Qy 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTProLysCysHisGlnAlaPheLeuLeu 1080
 Db 3181 GCGGCGGCGCTCTGCGCCCTCGAGGCGGTGACGTGGTGTGCAACACATTCCTGCTC 3240
 Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db 3241 AAGCTGACTCGACACCGTGTCACTACGTGCCACTCTGGGGGTCACTCAGGACAGCCGAG 3300
 Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
 Db 3301 AGCAGCTGAGTGGAAAGCTCCGGGAGACGAGGCTGAGCTGCGCTGTGAAGCCGACCAAC 3360
 Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 Db 3361 CCGGCACTGCCCTCAGACTTCAAGACATTCCTGGAC 3396

RESULT 6
 ABZ35720
 ID ABZ35720 standard; DNA; 3399 BP.
 XX
 AC ABZ35720;
 DT 07-FEB-2003 (first entry)
 DE Human elomerase reverse transcriptase polynucleotide SEQ ID NO 28.
 XX
 KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytosolic; virocid; protozoicide; gene expression; antisense; tumour; infection; plasmidium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
 OS Homo sapiens.
 XX
 PN DE10100588-A1.
 PD 18-JUL-2002.
 XX
 PF 09-JAN-2001; 2001DE-01000588.
 PR 09-JAN-2001; 2001DE-01000588.
 XX
 PA (RIBO-) RIBOPHARMA AG.
 XX
 PI Kreutzler R, Limmer S, Roost S, Hadwiger P;
 XX
 DR WPI; 2002-683450/74.
 XX
 PT Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target.
 PT
 PS Claim 13; Page 25-26; 100pp; German.
 CC
 CC The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligonucleotides (dsRNAi and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide

CC pairs. At least part of one strand (S1, S2) of the ds structures in each
CC of dsRNA1 and II are complementary to regions in the target gene. The
CC method uses antisense inhibition of gene expression using double stranded
CC RNA inhibition (RNAi). The method is particularly used to treat tumors
CC or infections, especially by Plasmidum or viruses/viroids (pathogenic on
CC humans, animals or plants). The method provides more effective inhibition
CC of expression than known methods using a single dsRNA, even at very low
CC concentrations. When dsRNA has at least one unpaired nucleotide at the
CC end, stability (and thus effective concentration in the cell) is improved
CC and efficiency can be increased further by pretreating the cells with
CC interferon. The present sequence is that of a target DNA of the invention
XX

Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:

Seq. No.:	2,38e-218	Length:	3399
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-044-692-2 (1-1132) x AB235720 (1-3399)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 1 ATCCCGGGCGCTCCCGCTGCGAGCGGTGGCTCCCTGCTGCGAGCCACTACCGCGAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
DB 61 GTGCTGCGCTGCGACGTTTCGTGCGCGCTGCGGCGCCCGAGGCGCTGCGCGGTGCGAG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CGCGGGAGACCGGGGCGCTTTCGCGCGCTGCGCGCCAGCTGCTGCTGCTGCGCGCTG 180
QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuGluLeu 80
DB 181 GAGCGACGGCGCGCGCGCGCGCGCGCTTCTCGCGACGAGTGTCTGCGAGGAGCTG 240
QY 81 ValAlaArgValLeuGlnArgLeuGlyGluArgGlyValAlaGlnValLeuAlaPheGly 100
DB 241 GTGGCCCGAGTGTGCGAGGCGTGTGCGAGCGCGCGCGAGAACGTGCTGCGCTTGGC 300
QY 101 PheAlaLeuLeuAspGlyValArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGGCGCTGTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 121 SerTyrLeuProLeuThrValThrAspAlaLeuArgGlySerGlyAlaTTPGlyLeuLeu 140
DB 361 AGCTACTGCGCCAAACAGGTGACCGACGCTGCGGGGAGCGGGGCGGTGGGCTGCTG 420
QY 141 LeuArgArgValGlyAAspArgValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGGCGCGCGGTGCGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 CTGGTGTCTCCAGCTGCGCTGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCT 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 541 GCGCACTCAGGCG 600
QY 201 ArgAlaThrPheHisSerValArgGlyValAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGGGCGCTGAGAACCTACGCTGAGGAGCGCGGGGTCTCCCTGCGCGCTGCGAGCGCG 660
QY 221 AlaArgArgArgGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCGAGAGGCT 720
QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTTPAlaHisProGly 260

DB 721 GCGCTGCG 780
QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 781 AGGAGCGGTGAGCCAGAGGACCGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 281 GluAlaThrSerLeuGluGlyValaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAGGACCACTCTTTGGAGGGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTTPAspThrPro 320
DB 901 CGCGAGACCAACGCT 960
QY 321 CysProProValTyrAlaGluThrTyrHisPheLeuTyrSerSerGlyAspLysGln 340
DB 961 TGTCCCGGTGTAGCGAGACCAAGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB 1021 CTGGCGCGCT 1080
QY 361 ValGluThrTLePheLeuGlySerArgProTTPMetProGlyThrProArgArgLeuPro 380
DB 1081 GTGAGACCATCTTCTGTGGTTCCAGGCGCTGAGTGCAGGAGACCTCCCGAGGTGCGC 1140
QY 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGluLeuGlyValHis 400
DB 1141 CGCTGCG 1200
QY 401 AlaGlnCysProTyrGlyValaLeuLeuTyrHisCysProLeuArgAlaAlaValThr 420
DB 1201 GCGAGTGCCTCTACGGGGTGTCTCTCAAGACGACTGCGCGCTGCGAGCTGCGTCAAC 1260
QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGlu 440
DB 1261 CCAGAGCGCGGTGTGTGTGCGCGAGAACCGCGCGCGCTGTGTGTGTGTGTGTGTGT 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln 460
DB 1321 GAGGACACAGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTTPGlySer 480
DB 1381 GTGTAGGCTGT 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgPheThrTyrLysPheHisSerLeuGlyLysHis 500
DB 1441 AGGCACAAAGAACCGCGCTTCTCAAGAACACCAAGAAATCATCTCTCTGAGAGACAT 1500
QY 501 AlaLysLeuSerLeuGlnGluLeuThrTTPLysMetSerValArgAspCysAlaTTPLeu 520
DB 1501 GCCAGCTCTGCTGTAGAGAGCTGAGCTGAGAGTGAAGTGTGCGGGACCTGCGCTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGluGlu 540
DB 1561 CGCAGAGCGCCAGGGGT 1620
QY 541 LeuAlaLysPheLeuHisSerTTPLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
DB 1621 CTGGCCAAATCTCTGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
QY 561 PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
DB 1681 TTTTATGTACCGAGACACAGTTTCAAAGAAGACAGCTTTTCTACCGAAGAGTGT 1740
QY 581 TTPSerLysLeuGlnSerTTPGlyLysArgGlnHisLeuLysArgValGlnLeuArgGlu 600
DB 1741 TGGAGCAAGTTGCAAGCATTTGGAATCAGACGCACTTGAAAGAGGTGTGCGCGGAG 1800
QY 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620

Db 1801 CTGTGGAGCAGAGGTCAGGAGCATCGGAGAACCGGCCCTCTGTCATGCTCCAGA 1860
 QY LeuArgPheIleProlyProAspGlyLeuArgProIleValAsnMetAspTyrVal 640
 Db 1861 CTCCTGTTATCCCAAGCCTGACGGGCTGCGGCCCATTTGTGACATGACATGACGTCG 1920
 QY 641 G1yAlaArgThrPheArgArgGlyuysArgAlaGluArgLeuThrSerArgValIysAla 660
 Db 1921 GGAGCGAAGAACGTTCCGAGAGAAAAGAGGCGCGCTCACCTCGAGGGTGAAGGCA 1980
 QY LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
 Db 1981 CTGTTACAGCTGCTCAACTACAGACGGCGCGCGCCGCTCTCTGGAGCGCTCTGTG 2040
 QY LeuGlyLeuAspAspIleHisArgAlaTProArgThrPheValLeuArgValArgAlaGln 700
 Db 2041 CTGGGCTGGAGATATCCACAGGGCTGCGGACCTTGCTGTGTGTGTGTGTGTGTGTGT 2100
 QY AspProProGluLeuTyrPheValIysValAspValThrGlyAlaTyrAspThrIle 720
 Db 2101 GACCCGCGCGCTGAGCTGACTTTGTCAAGGTGGATGTACGGGCGCGTACGACATC 2160
 QY ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
 Db 2161 CCCGAGACAGGCTCAGGAGGTCATCGCAGCATCATCAACCCGAGAACAGTACTGC 2220
 QY ValArgArgTyrAlaValAlaGlnIysAlaHisGlyHisValArgIysAlaPheLys 760
 Db 2221 GTGGCGGTGATGCGCTGTCCAGAAAGCGCCGACGTCGTCGCAAGGCTTCAAG 2280
 QY SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
 Db 2281 AGCCAGCTCTCACTTACACAGACCTCCAGCGGTACATGACAGATTCGTGGCTCACCTG 2340
 QY GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerLeuAsnGln 800
 Db 2341 CAGGAGACCAAGCCGCTGAGGATGCGTGCATGACAGAGCTCTCCCTCGAATGAG 2400
 QY AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
 Db 2401 GCCAGAGTGGGCTCTTCAACGCTTTCATGCTTATGTGCCACACCGCGGCCATC 2460
 QY ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
 Db 2461 AGGGGGAATCTCTACTCCTCAGTCCAGGGGATCCCGAGGGCTCTCTCTCCAGCTG 2520
 QY LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
 Db 2521 CTCTGAGCCTGTGTACGGCGCATGAGAACAACTGTGGCGGGAATTCGGCGGAGC 2580
 QY GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
 Db 2581 GGGCTGTCTCTCGT 2640
 QY LysThrPheLeuArgThrLeuValArgGlyValProGlyTyrGlyCysValValAsnLeu 900
 Db 2641 AAAACCTTCTCAGACCTGTGTCGAGGTGTCCTCGAATATGCTGCTGTGTGTGTGTGT 2700
 QY ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyIleThrAlaPheVal 920
 Db 2701 CGGAAGACAGTGGTGAATTCCTCTGTAGAAGACGAGGCCCTGGGTGGCAGCGCTTGT 2760
 QY GlnMetProAlaHisGlyLeuPheProTProCysGlyLeuLeuLeuAspThrArgThrLeu 940
 Db 2761 CAGATGCGCGCCACGCGCTATTCCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2820
 QY GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 Db 2821 GAGGTGCAAGACGACTTCACGCTATGCGCGGACCTTCATCAGACCGACTCCTTC 2880
 QY AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
 Db 2881 AACCGCGGCTTCAAGGCTGGAGAACATGCGTGCAGAACTCTTGGGGTCTTGGCGGCTG 2940

QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 Db 2941 AAGTGTCAAGCTGTCTTCTGATTTTGACAGTGAACAGCTCTCAGACGGTGTGACCAAC 3000
 QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 Db 3001 ATCTACAAGATCTCTCTGTGTGAGGCGTACAGGTTTCAAGCATGTGTGTGTGTGTGTGT 3060
 QY 1021 PheHisGlnGlnValThrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 Db 3061 TTTCATCAGCAAGTTTGAAGAACCCCATTTTCTGTGCGGTATCTTGAACAGGGCC 3120
 QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValAlaLysGly 1060
 Db 3121 TCCCTCTGTACTTCATCTCTGAAGCAAGAACGAGGATGCTGTGGGGGCGCAAGGGC 3180
 QY 1061 AlaAlaGlyProLeuProSerGlnAlaValGlnTProLeuCysHisGlnAlaPheLeuLeu 1080
 Db 3181 GCCGCGGCGCTCTGCGCTCCGAGGCCGTGAGTGGCTGTGCCACCAACATTCCTGCTC 3240
 QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 Db 3241 AAGCTGACTGACACCGGTGACCTACGCTCACTCTGAGGTCATCTCAGACAGCCGAG 3300
 QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
 Db 3301 AGCGACTGATGTCGAAAGTCCCGGGAGCAGAGCTGACTGCTGTGAGGCGCCAGCAAC 3360
 QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 Db 3361 CCGGACCTGCTCTCAGACTTCAAGACATCTCGAGC 3396
 QY 3361 CCGGACCTGCTCTCAGACTTCAAGACATCTCGAGC 3396
 Db 3361 CCGGACCTGCTCTCAGACTTCAAGACATCTCGAGC 3396
 RESULT 7
 ABX09963
 ID ABX09963 standard; DNA; 3399 BP.
 AC ABX09963;
 XX
 DT 23-JAN-2003 (first entry)
 XX
 XX Human telomerase reverse transcriptase DNA fragment SEQ ID 28.
 DE
 XX Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
 KW
 XX
 OS Homo sapiens.
 XX
 PN DE10100587-C1.
 XX
 PD 21-NOV-2002.
 XX
 XX 09-JAN-2001; 2001DE-01000587.
 PF
 XX 09-JAN-2001; 2001DE-01000587.
 PR
 XX (RIBO-) RIBOPHARMA AG.
 PA
 XX Kreutzler R, Limmer S, Rost S, Hadwiger P;
 PI
 XX WPI; 2002-742209/81.
 DR
 XX
 XX Inhibiting expression of target genes, e.g. oncogenes, in cells, by
 PT introduction of complementary double-stranded oligoribonucleotide, after
 PT treating the cell with interferon.
 PS
 XX Disclosure; Page 30-31; 98p; German.
 CC This invention describes a novel method for inhibiting expression of a
 CC target gene by introducing into the cell that containing the target gene at
 CC least one oligoribonucleotide (dsRNA) that has a double-stranded (ds)
 CC structure of not more than 49 consecutive nucleotides (nt), where at
 CC least a segment of one strand of the ds structure is complementary with

CC the target gene and the cells are treated with interferon before
 CC introduction of dsRNA. The method is used to inhibit expression of
 CC target genes, particularly oncogenes, cytokine genes, id (not defined)
 CC protein genes, developmental or prion genes, or genes expressed in
 CC pathogenic organisms (particularly plasmoidal) or in viruses or viroids
 CC (pathogenic in humans, animals or plants). Treating the cells with
 CC interferon greatly increases the extent to which dsRNA can inhibit
 CC expression of the target genes, and the effect is even greater when dsRNA
 CC are modified to increase their stability. ABX0936-ABX10075 represent
 CC gene fragments used to illustrate the method of the invention
 CC
 XX
 SQ Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3399
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-044-692-2 (1-1132) X ABX09363 (1-3399)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
 Db 1 ATCCCGGCGCTCCCGCTGCCAGCGGTGCGCTCCCTGCTGCCAGCCACTACCGCGAG 60
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyThrArgLeuValGln 40
 Db 61 GTCTGCGCGTGGCCACGTTTCGTCCGGCGCTGCGGCGCCAGGCGGTGGCGGTGGCAG 120
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 Db 121 CCGGGGAGCCCGCGGCTTCCGCGCTGTGGCCAGTGCCTGTGTGTGGCGCTTG 180
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGluLeu 80
 Db 181 GAGCAGCGCGCGCGCGCGCGCGCGCGCTCTCCGCGCAGGTGTCTGCTGAGGAGCTG 240
 QY 81 ValAlaArgValLeuGlnArgLeuGlyValArgGlyValAlaValSerValLeuAlaPheGly 100
 Db 241 GTGGCGCGAGTGTGCGAGAGCTGTGCGAGCGCGCGCGAGAACGTGTGGCGCTTGCG 300
 QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 Db 301 TTGGCGGTGTGAGCGGGGCGCGCGGGGCGCGCGCGAGGCTTTCACCAACAGGTGCGC 360
 QY 121 SerTyrLeuProLeuThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
 Db 361 AGCTACCTGCCCAACAGGTGACCGAGCACTGCGGGGAGCGGGGCGGTGGGCGTGTG 420
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db 421 CTGGCGCGCGGTGGCGAGCGAGTGTCTGCTGCTGCGAGCGCTGCGGCTCTTGTG 480
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 Db 481 CTGGTGGCTCCAGCTCGGCTACAGGTGTGGGGCGCGCGGTGTACAGCTCGGGCT 540
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
 Db 541 GCCCACTAGGCGCGCGCGCGCGCACAGCTAGTGAGCCCGAGAGGCTCTGGAGTGGAA 600
 QY 201 ArgAlaThrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 601 CCGGCGCTGGAGCACTAGGCTGAGGAGCGGGGTCCCTCTGGCGCTGCCAGCCCGGGT 660
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 Db 661 GCGAGAGGGCGCGGGGAGTGCAGCGCAAGTGTGCGTTGCCCAAGAGGCCAGCGCT 720
 QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrAlaHisProGly 260

Db 721 GCGCTGCCCTGTAGCCCGAGCGAGCGCGCTTGGGCGAGGGGTCTTGAGCCACCGGGC 780
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 Db 781 AGGAGCGGTGAGCCAGTGAACCGTGTGTTCTGTGTGTGTACCTGCCAGACCCGCCAA 840
 QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 841 GAAAGCACTCTTTTGAAGGGTGGCTCTGTGGCAGGCCCACTCCACCACTCCGTGGGC 900
 QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
 Db 901 CCGCAGCACACGCGCGCGCGCCCATCCATCGCGGCCACACAGTCTCGGAGCAGCGCT 960
 QY 321 CysProProValTyrAlaGlnThrThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
 Db 961 TGTCCCCGCGTGTAGCCGAGACCAAGCACTTCTCTACTCTTCAGGGGAGCAAGAGCAG 1020
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 Db 1021 CTGGCGCGCTCTCTCTACTAGCTCTGAGGCCAGCGCTGAGCGCTGGAGGCTC 1080
 QY 361 ValGlnThrThrPheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
 Db 1081 GTGGAGACCATCTTCTGTGGTTCAGGCCCTGTGATGCCAGGACTCCCGCAGGTGGCC 1140
 QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
 Db 1141 CCGCTGCCCAACGCTACTCGGCAATGGCGCCCTGTCTGGACTGTGGAAACAC 1200
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuAlaAlaValThr 420
 Db 1201 GCGCAGTGCCTCTAGCGGGGTGTCTCTCAAGACGACCTGCCCTCGAGCTCGGTGAC 1260
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGlu 440
 Db 1261 CCAAGACCGGTGTGTGTGCGGAGAACGCCAGGGCTGTGTGGCGCCCGCAAGAG 1320
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
 Db 1321 GAGGACACAGACCCCGCTGTGGTGTGAGCTGTCCGCAACAGCAGCGCCCTGGCAG 1380
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
 Db 1381 GTGTAGCGCTGTGTGGCGGCTGTGCTGCCCGCGCTGTGTGCCCAAGCGCTTGGGGCTCC 1440
 QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysPheHisSerLeuGlyLysHis 500
 Db 1441 AGGCACACGAAAGCGCGCTTCTCAAGAACACCAAGAGTCACTTCCCTGGGAAAGCAT 1500
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaThrLeu 520
 Db 1501 GCCAAGCTCTCGGTGAGAGGTGACGTGAAGATGAGGTGCGGGATGCGCTTGCTG 1560
 QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlyGluLeu 540
 Db 1561 CCGAGAGGCCAGAGGGGTGTGTGTGTCGCGCGCAGACACCGTCTGGGTGAGGAGATC 1620
 QY 541 LeuAlaLysPheLeuHisThrPheLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
 Db 1621 CTGGCAAGTCTCTGACCTGAGCTGATGATGTGTACTGTGAGCTGTCAAGCTCTTTC 1680
 QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
 Db 1681 TTTTATGTACGAGAGCACAGTTTCAAAAGAACAGGCTCTTTTCTTACCGAAGAGTGT 1740
 QY 581 TrpSerLysLeuGlnSerLysIleGlyLysArgGlnHisLeuLysArgValGlnLeuArgGlu 600
 Db 1741 TGGAGCAAGTGTGAAAGCATTTGAAATCAGACAGCACTTAAAGAGGTGTGAGCTGGGAG 1800
 QY 601 LeuSerGluAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
 Db 1801 CTGTGGAGACAGAGGTCAAGGACATCGGAGAACAGGCGCGCGCTGCTGACGTCAAA 1860

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QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db 1861 CTCGGCTTCATCCCAAGCCTACCGGGCTGGCGCATTTGTGAACATGACATACGTCGTG 1920
QY 641 GlyAlaArgThrPheArgArgGlyLysArgAlaGlyLysLeuThrSerArgValLysAla 660
Db 1921 GGAGCCAGAACCTTCGCGAGAAAAGAGGGCGGAGCGCTCTCACTCGAGGCTGAAGGCA 1980
QY 661 LeuPheSerValLeuAsnTyrGlyLysArgAlaArgArgProGlyLeuLeuGlyLysVal 680
Db 1981 CTGTTACAGGCTCTCACTACACAGCGGGCGCGCGCGCTCTCTGGCGCTCTGTG 2040
QY 681 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
Db 2041 CTGGGCGCTGAGATATCCACAGGGCTGGCGCATCTTGTCTGCTGGTGTGGCGGCCAG 2100
QY 701 AspProProProGlyLeuLysPheValLysValAspValThrGlyValTyrAspThrIle 720
Db 2101 GACCCGCGCGCTGAGCTGACTTTGTCAAGTGATGTGACGGGCGCGTACGACACATTC 2160
QY 721 ProGlnAspArgLeuThrGlyValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
Db 2161 CCCAGGACAGGCTCACGAGGTCATCGCAGCATCATCAACCCCAAGAACATGATCTGC 2220
QY 741 ValArgArgTyrAlaValAlaGlyLysAlaHisArgLysHisValArgLysAlaPheLys 760
Db 2221 GTGCGTGGATATGCGCGTGTCCAGAGGCCCGCCCATGGGCACTCCGCAAGGCTTCAG 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValHisLysLeu 780
Db 2281 ACCCAGCTCTTACCTTACAGACGCTCCAGCGCTACATCATGACAGTTCGTGGCTCACTG 2340
QY 781 GlnGlnThrSerProLeuArgAspAlaValValIleGlnGlnSerSerSerLeuAsnGln 800
Db 2341 CAGGAGACAGGCGCGGTGAGGATGCGTGTATGACAGAGCTCCCTCGAATGAG 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
Db 2401 GCCAGCAGTGGCTCTTCAACGCTTCTTCAACGCTTATGTGCAACACCGCGCGCATC 2460
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2461 AGGGGGAAGTCTTACGTCAGTCCAGGGGATCCCGAAGGCTCATCTCTTCCAGCGTG 2520
QY 841 LeuCysSerLeuCysTyrGlyLysPheGlyLysAsnLysLeuPheAlaGlyIleArgArgAsp 860
Db 2521 CTCTGACGCTGTGCTACGCGCAATGAGAACACAGCTGTTCGCGGGAATTCGCGCGGAC 2580
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGGCTGCTCTCGTGTTGGTGGATGATTTCTTGTGTGTGAACACTCACTCACCCACGCG 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGlyTyrGlyCysValValAsnLeu 900
Db 2641 AAAACCTTCTCAGACGCTGTGTCGAGGTGTCCTCGAATAGGCGCGGTGAACCTTG 2700
QY 901 ArgLysThrValValAsnPheProValGlyAspGlyAlaLeuGlyGlyThrAlaPheVal 920
Db 2701 CCGAAGACAGTGTGAATCTTCCCTGTGAAGACGAGGCGCTGTGGCAACGCGCTTTTGT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAGATGCGCGCCACAGGCTATTCCTCTGTGCGGCTGTGTGTGTGATACCGGACCTTG 2820
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgLysSerLeuThrPhe 960
Db 2821 GAGGTGCAAGGCACTACCTACGCTATGCGCGGACCTCATGACGACGCTCACTTC 2880
QY 961 AsnArgGlyPheLysAlaGlyLysAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db 2881 AACCGGCGCTTACAGGCTGGAGGAACATGCGTCCGAAACTCTTTGGGCGCTTTCGCGCTG 2940

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QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db 2941 AAGTGTACAGGCTGTTCTTGATTTGACAGGTGAACAGCTCCACACGCTGTGACCAAC 3000
QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATCTACAGATCTCTCTGTGAGGCTGACAGTTTCACGATGTGTCTGACAGCTCCA 3060
QY 1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3061 TTTCATCAGCAGATTGGAAGAACCCACATTTTCTCTGCGGTATCTCTGACACGCGC 3120
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyValLysGly 1060
Db 3121 TCCCTGTGCTACTTCATCTCCTGAAGCAAGAACGAGGATGTCCTGGGCGCCCAAGGCG 3180
QY 1061 AlaAlaGlyProLeuProSerGlyAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
Db 3181 GCCGCGCGCTCTCTCCCTCCAGGCGCGTGCAGTGTGTGCACCAACATTCCTGCTC 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3241 AAGCTGACTGACACCGTGTACCTTACGCTTCTGCGGTCACTCAGACAGCCCG 3300
QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn 1120
Db 3301 ACGCAGCTGAGTGGAGAGCTCCCGGGAGACAGCTGAGCTGCCCTGGAGGCCGACGAC 3360
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3361 CCGGCACTGCCCTCAGACTTCAAGACATCTCGAGC 3396

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RESULT 8
ABL91685
ID ABL91685 standard; DNA; 3399 BP.
AC ABL91685;
XX
XX 28-MAY-2002 (first entry)
DT
XX
XX Human polynucleotide SEQ ID NO 28.
DE
XX
XX Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KM Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KW cytosolic; virulence; protozoan; antibacterial; ds.
XX
XX Homo sapiens.
OS
XX
XX DE10100586-C1.
PN
XX
XX 11-APR-2002.
PD
XX
XX 09-JAN-2001; 2001DE-01000586.
PF
XX
XX 09-JAN-2001; 2001DE-01000586.
PR
XX
XX 09-JAN-2001; 2001DE-01000586.
XX
XX (RIBO-) RIBOPHARMA AG.
PA
XX
XX Kreutzler R, Limmer S, Rost S, Hadwiger P;
PI
XX
XX WPI; 2002-270454/32.
DR
XX
XX Inhibiting gene expression in cells, useful for e.g. treating tumors, by
PT introducing double-stranded complementary oligonucleotide having unpaired
PT terminal bases.
XX
XX Claim 13; Page 27-28; 104pp; German.
XX
XX The invention relates to a method for inhibiting expression of a target
CC gene (ABL91685-ABL91797) in a cell by introducing at least one
CC oligoribonucleotide that has a double-stranded structure consisting of at
CC most 49 sequential nucleotide pairs, with at least part of one strand
CC complementary with the target gene and has at least one end a single-

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CC stranded segment of 1-4 nt. The method provides oligoribonucleotides for
CC anti-sense inhibition of gene expression useful e.g. for treating tumours
CC but the oligoribonucleotides may also be directed against genes present
CC in pathogens (e.g. plasmidium or viruses/viroids), pathogenic on humans,
CC animals or plants) or against cytokine, ID, developmental or prion genes.
CC The method provides more effective inhibition of gene expression than use
CC of known oligonucleotides, probably because the unpaired overhang
CC increases stability and thus intracellular concentration

XX Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3399
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-044-692-2 (1-1132) x ABL91685 (1-3399)

```
QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
DB 1 ATGCGCGCGCTCCCGCTGCGAGCGCTGCTCCCTGCTGCGAGCACTACCGCGAG 60
QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTyrPheArgLeuValGln 40
DB 61 GTGCTGCGCTGCGAGCTTCTGTCGCGGCGCTGCGGCGCCGAGGCTGCGCGCTGTCAG 120
QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
DB 121 CGGCGGAGACCGCGGCTTCCGCGCTGTCGAGCGCGCGCGAGAACGTCGCTGCGCTGG 180
QY 61 AspAlaArgProProAlaAlaProSerPheArgGlnValSerCysLeuArgGluLeu 80
DB 181 GAGCGACGCGCGCGCGCGCGCGCGCGCTTCCGAGGTCGCTGCTGAGAGAGCTG 240
QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyValAlaCysValLeuAlaPheGly 100
DB 241 GTGCGCGAGTGTCTGCGAGGCTGTGCGAGCGCGCGCGAGAACGTCGCTTTCGCGC 300
QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB 301 TTGCGCGCTGCGAGCGGCGCGCGCGCGCGCGCGCGCGCTTTCACACAGCGCTGCGC 360
QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
DB 361 AGCTACCTGCCAACACGTCGACCGACGCTGCGGAGGAGCGGCGGCTGAGCTG 420
QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
DB 421 CTGCGCGCGGTGGCGAGCGAGCTGTGTCACCTGTCGCGAGCGCTGCGGCTTTCG 480
QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB 481 CTGCTGCTCCCGCTGCGCTGACAGGTGCGCGCGCGCGCTGTCACAGCTGCGGCT 540
QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
DB 541 GCCACTAGGCGCGCGCGCGCGCGCACAGCTAGTGACCCGGAAGGCTCTGGAATGGAA 600
QY 201 ArgAlaTyrAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly 220
DB 601 CGGCGCTCGAAGCACTACGTCGAGGAGCGCGGCTGCTGCGGCTGCGAGCGCGGCT 660
QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB 661 GCGAGGAGGCGCGCGCGCGCGAGTCAGCGCAAGTCGCTGCGCAAGAGCGCGCGCT 720
QY 241 GlyAlaAlaProGlnProGlnArgGlyThrProValGlyGlnGlySerThrAlaHisProGly 260
DB 721 GCGGCTGCGCTGAGCGGAGCGGAGCGCGCTGAGGAGGAGGCTGCGGCGCGCGGCT 780
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QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu 280
DB 781 AGGACGCGGAGCGAGGAGCGAGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
QY 281 GlnAlaThrSerLeuGlnGlyValAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB 841 GAAGGACCTCTTTTGAAGGAGGCTCTGTGCGAGCGCGCTCCACCGCATCCCTGGAGC 900
QY 301 ArgGlnHisHisAlaGlyProProSerThrSerArgProArgProTyrAspThrPro 320
DB 901 CGCGAGCACACGCGGCGCGCGCGCGCATCCATGCGCGCACACAGCTCCCTGGAGACGCT 960
QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGlnGln 340
DB 961 TGTCCCGCGGTATAGCGGAGACCAAGCACTTCTCTACTCTCCTCAGCGAGCAAGAGGAG 1020
QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyValAlaArgArgLeu 360
DB 1021 CTGCGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 361 ValGlnThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
DB 1081 GTGAGACCATCTTCTGTGAGTTCAGGCGCTGATGCCAGGACTCCCGCAGGTTGCGC 1140
QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
DB 1141 CGCTGCGCGCACGCTACTGCGAATGCGCGCGCTGTTCTGTGAGCTGCTGTGGAACAC 1200
QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB 1201 GCGCAGTGCCTCTACGAGGAGTGTCTCTCAAGAGCACTGCGCTGCGAGCTGCGGTCACC 1260
QY 421 ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGlnGlu 440
DB 1261 CCAGCAGCGCGGTGTCTGTGCGCGGAGAGAGCCCGAGGCTCTGTGCGCGCGCGCGAGG 1320
QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB 1321 GAGGACACAGACCGCGCTGCTGCTGAGCTGCTCCGACAGACAGCAGCGCTGCGGCG 1380
QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuThrPheLys 480
DB 1381 GTGTAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 481 ArgHisAsnGluArgArgPheLeuArgAsnThrLysPheLeuSerLeuGlyLysHis 500
DB 1441 AGGCACACAGAACCGCGCTCTCTCAGAACACAGAGATTATCTCCCTGGAGAACAT 1500
QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
DB 1501 GCCAGCTCTCGCTGAGAGCTGACGTGGAAGATGACGCTCGGAGACTGCGCTTGGCTG 1560
QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlu 540
DB 1561 CGCAGAGGCGCGGAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
QY 541 LeuAlaLysPheLeuHisTyrPheLeuMetSerValTyrValAlaGlnLeuLeuArgSerPhe 560
DB 1621 CTGCGCAAGTCTCTGACTGCTGAGTGAATGATGATGATGATGATGATGATGATGAT 1680
QY 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPheTyrArgLysSerVal 580
DB 1681 TTTTATGTCAGGAGACCACTTTTCAAAGAACAGGCTCTTTTTCACCGGAAGAGTCT 1740
QY 581 TyrSerLysLeuGlnSerLysLysLysLysLysLysLysLysLysLysLysLysLys 600
DB 1741 TGGAGCAAGTTGCAAGGATTGGAATCAGACAGCACTTGAAAGGAGTGCAGCTCGGAGG 1800
QY 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
DB 1801 CTGTGGAAGCAGAGGTACAGGACATCGGAGAACAGGCGCGCTGCTGAGCTCACA 1860
QY 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
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1861 CTCCCTCATCCCAAGCCTGACGGGCTGCGGCAGATTGTGAACATGACATACGCGTG
QY 661 GYAAAGTGTPharArgArgLulysArgAlaGluArgLeuThrSerArgValLysAla 660
Db 1921 GAGGACAGAACTCTCCGAGAGAAAAGAGGCGCGAGCTCACCCTCGAGGGGTGAAGGCA 1980
QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal 680
Db 1961 CTGTTCAAGGTGCTCACTACAGAGCGGCGCGCGCCGCTCTTGAGGCCCTCTTG 2040
QY 661 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
Db 2041 CTGGGCTCGAGCATATCCACAGGGGCTGCGCACCTTGCTGCTGGGTGCGGGCCAG 2100
QY 701 AspProProGlnLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle 720
Db 2101 GACCCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGACGAGCGCGGTACACACCATC 2160
QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
Db 2161 CCCACGACAGGCTACAGAGGTCATCGCCAGCATCATAAACCCAGAAACATGACTCC 2220
QY 741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db 2221 GTGGCTCGGTATGCGGTGATCCAGAAAGCGCGCCCATGGGCACTCGCAAGGCTTCAAG 2280
QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db 2281 AGCCACGCTCTTCACTTGCACACACCTCCAGCGGTACATGACAGTTCGTGCTCACCG 2340
QY 781 GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGln 800
Db 2341 CAGAGAGACCAAGCCCGCTGAGGATGCCGTGCTCATGACAGACAGCTCTCTCTGAATGG 2400
QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2401 GCCACAGATGGGCTCTTGCACGCTTCTTCAAGCTTATGTCACACCGCGGCGCATC 2460
QY 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2461 AGGGGCAAGTCTTACGTCAGAGGCGAGGAGATCCCGCAGGGCTCCATCTCTCCACGCG 2520
QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860
Db 2521 CTCTGACGCTGTGCTACGCGCATGAGAAACAGCTTTTGGGAGATTGCGCGGAGC 2580
QY 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGGCTGCTCTGCTGTTGGTGAATTTCTTGTGGTGAACACTCACTCAACCCACGCG 2640
QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db 2641 AAAACCTTCTCAGGACCTGTGTCGAGGTGTCCCTGAGTATGCGCTGTGTGAACCTTG 2700
QY 901 ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2701 CGGAAGACAGTGTGAATCTTCTGTGAAGAGAGGCGCTGGGTGGCACGCGCTTTTGT 2760
QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAGATGCGCGGCCACAGGCTATTATCCCTGTGTGGGCTGTGCTGTGAATCCCGAGACCTG 2820
QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2821 GAGGTGACAGAGGACATCTCCAGCTATGCGCGACCTTCATAGAGCCAGTGTCACTTCC 2880
QY 961 AsnArgGlyPheLysValArgLysAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db 2881 AACCGCGGCTTCAAGGCTGGAGAGAACATGCTCGAAACTCTTGGGGTCTTGGCGGCTG 2940
QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000

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Db 2941 AAGTGTACAGCCTGTTCTTGATTTGCAAGGTGAACAGCTTCCAGACGCTGTGACCAAC 3000
QY 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATCTACAAAGATCTCTGCTGTCAGGCGGTACAGGTTTACAGCATGTGTGCTGCACTCCA 3060
QY 1021 PheHisGlnGlnValTyrLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3061 TTTCATCAGCAAGTTTGGAGAGAACCCCAATTTTTCCTGCGGCTCATCTGTACACGGCC 3120
QY 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly 1060
Db 3121 TCCCTCTGTACTTCATCTGTAAGCCCAAGAACGAGGATGTCCCTGGGGCCCAAGGGCC 3180
QY 1061 AlaIaGlyProLeuProSerGlnAlaValGlnTyrPheLysGlnAlaPheLeuLeu 1080
Db 3181 GCCGCGGCGCTCTGCTCCCTCCAGGCGGTGCGAGTGTGTGTCACCAAGCATTTCTGCTC 3240
QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3241 AAGCTGACTCGACACCGGTGACCTACAGTGCACCTCTGGGTCACTCAGAGACAGCCGAC 3300
QY 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db 3301 ACGCAGCTGAGTGGAGAGCTCCCGGGAGACAGCTGACTGCTCGAGGCGCCAGCCNAAC 3360
QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3361 CCGGCACTGCGCTCAAGACTTCAAGACATCTCGAGC 3396

RESULT 9
ADG90598
ID ADG90598 strand: DNA; 3399 BP.
XX
AC ADG90598;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human TERT gene SEQ ID NO:1.
XX
KW ds; gene; human; immune response; telomerase reverse transcriptase; TERT;
XX cytosolic; immunostimulant; cancer; cytotoxic T cell response.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 1..3399
FT FT /*tag= a
FT FT /product= "TERT"
XX
PN WO2004002408-A2.
XX
PD 08-JAN-2004.
XX
PF 24-JUN-2003; 2003WO-US019844.
XX
PR 27-JUN-2002; 2002US-0393295P.
XX
PA (GERO-) GERON CORP.
XX
PI Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX
DR MPI: 2004-071946/07.
XX
DR P-FSDB; ADG90599.
XX
PT Eliciting an immune response in a mammal specific for its own telomerase
PT reverse transcriptase (TERT), useful for treating or preventing cancer,
PT comprises administering a composition containing TERT of another
PT mammalian species.
XX
PS Disclosure; SEQ ID NO 1; 44pp; English.
XX
CC The invention relates to a novel method for eliciting an immune response

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in a mammalian subject that is specific for its own telomerase reverse transcriptase (TERT), comprising administering an immunogenic composition containing a protein with at least 20 consecutive amino acids of TERT of another mammalian species, or a nucleic acid encoding the protein. A composition of the invention has cytotoxic, and immunostimulant activity. The protein or the nucleic acid encoding the protein is useful in the manufacture of a medicament for the treatment of cancer in a human or for eliciting a cytotoxic T cell response in a human.

Sequence 3399 BP; 550 A; 1157 C; 1089 G; 603 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,38e-218	Length:	3399
Score:	5961.00	Matches:	1132
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12	Indels:	0
DB:		Gaps:	0

US-10-044-692-2 (1-1132) x ADG90598 (1-3399)

Qy	1	MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
Db	1	ATGCGCGCGCTCCCGCTCCGACCGCGTGGCTGCTGCGCAGCCACTACCGCGAG	60
Qy	21	ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln	40
Db	61	GTGCTGCGCGTGGCCAGCTTCGTGGCGCGCTGGGGGCCCGAGGGCTGGGGCTGGCAG	120
Qy	41	ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr	60
Db	121	CGCGGGAGCCCGGGCGCTTCGCGCGCTGGAGCCAGTGCCTGGTGGCGGCTCG	180
Qy	61	AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu	80
Db	181	GAGCGAGCG	240
Qy	81	ValAlaArgValLeuGlnArgLeuCysGlnArgGlyValAlaValAsnValLeuAlaPheGly	100
Db	241	GTGGCGCGAGTGCAGAGGCTGTGCGAGCGCGCGCGAGAAAGTGTGGCTTCGCG	300
Qy	101	PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg	120
Db	301	TTCGGCGCTGCGAGCGGGCGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCG	360
Qy	121	SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATPArgLeuLeu	140
Db	361	AGCTACCTGCCCAACACGGGTGACCGACCTGCGGGGAGCGGGGGGTGGCTG	420
Qy	141	LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
Db	421	CTGGCGCGCGTGGAGGAGCGAGCTGTGTTCACTGCTGGCACTCGCGCTTTGTG	480
Qy	161	LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
Db	481	CTGGCGCGCGTGGAGGAGCGAGCTGTGTTCACTGCTGGCACTCGCGCTTTGTG	540
Qy	181	AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln	200
Db	541	GCCACTCAGGCG	600
Qy	201	ArgAlaTTPAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly	220
Db	601	CGGGCGCTGGACCAATGCGTCAAGGAGCGCGGGCTCCCTGGGCTGCGAGCCCGGGT	660
Qy	221	AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProValArgProArgArg	240
Db	661	GGGAGAGGCGCGGGGCGAGTGCAGACCAAGTCTGCGTGGCCCAAGAGCGCGGGT	720
Qy	241	GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTTPAlaHisProGly	260
Db	721	GGCGCTGCGCTGAGCGGAGCGGAGCGCGGTTGGGCGAGGGGTCTGGGCCCAACCGGG	780

Qy	261	ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu	280
Db	781	AGAGCGGTGAGCGAGTACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	840
Qy	281	GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyTThrArgHisSerHisProSerValGly	300
Db	841	GAAGCCACTCTTGGAGGGGTGGCTCTGTGGACCGCGCACCCACCACTCGGGAGC	900
Qy	301	ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTTPAsnThrPro	320
Db	901	CGCAGACCAACCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	960
Qy	321	CysProProValTyrAlaGlnThrTyrHisPheLeuTyrSerSerGlyAspGlyGln	340
Db	961	TGTCCCGCGGTGATCGCGGAGACCAACCACTTCCTCACTCCAGCGCGCAAGAGCAG	1020
Qy	341	LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
Db	1021	CTGGCGCGCTCTCTCTCACTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1080
Qy	361	ValGlnThrThrPheLeuGlySerArgProTTPMetProGlyTTPArgArgLeuPro	380
Db	1081	GTGAGACCACTTCTTGTGGTTCAGAGCCCTGATGCGAGGACTCCCGCAGGTTGCC	1140
Qy	381	ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis	400
Db	1141	CG	1200
Qy	401	AlaGlnCysProTyrGlyValLeuLeuTyrThrHisCysProLeuArgAlaAlaValThr	420
Db	1201	GCGAGTCCCGCTTGGGGGTCTCTCAAGAGGACTGCGCGCGCGCGCGCGCGCGCG	1260
Qy	421	ProAlaAlaGlyValCysAlaArgGlnLysProGlnGlySerValAlaAlaProGlnGlu	440
Db	1261	CGAGAGCCGAGTGTGTGCGCGGAGAACCCCGAGGCTGTGGCGCGCGCGCGCGAG	1320
Qy	441	GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln	460
Db	1321	GAGGACAGACACCG	1380
Qy	461	ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTTPGlySer	480
Db	1381	GTGTACGGCTTGTGTGGGCTGTGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCG	1440
Qy	481	ArgHisAsnGlnArgArgPheLeuArgAsnThrTyrLysPheLeuLeuGlyLysHis	500
Db	1441	AGGCAACAAGACCGCGCTTCTCAGAGAACCAAGAAATTCTCTCTGGGAGAGCAT	1500
Qy	501	AlaLysLeuSerLeuGlnGlnLeuThrThrLysMetSerValArgAspCysAlaATPLeu	520
Db	1501	GCCAACTCTGCTGAGAGCTGACGTGGAAGATGACGTGCGGAGCTGGGCTTGGCTG	1560
Qy	521	ArgArgSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGluLeu	540
Db	1561	CGAGAGAGCGCGGGGTTGGTGTGTGCGCGCGAGAGCACCGTCTGTGAGAGAGATC	1620
Qy	541	LeuAlaLysPheLeuHisTTPLeuMetSerValTyrValAlaGlnLeuLeuArgSerPhe	560
Db	1621	CTGGCCAACTCTGCACTGCGTGAATGATGTGATGCTGTGAGCTGTGAGCTGCTTTC	1680
Qy	561	PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	580
Db	1681	TTTTATGTACGAGAGCACCGTTTCAAAAGAACAGGCTTTTCTACCGGAAGGTGTC	1740
Qy	581	TTPSerLysLeuGlnSerLysGlyLeuArgGlnHisLeuLysArgValGlnLeuArgGlu	600
Db	1741	TGGAGCAAGTTGCAAAAGCATTTGGAATCAGACACTTGAAAGGGGTGACGTGGGGAG	1800
Qy	601	LeuSerGlnAlaGluValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg	620
Db	1801	CTGTGGAAACCAAGGTGAGGAGCATCGGAGAGCCAGGCGCGCGCTGTGAGCTCCAGA	1860
Qy	621	LeuArgPheThrLeuProLysProAspGlyLeuArgProAlaAsnMetAspTyrValVal	640

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1861 CTCGCCCTCATCCCAAGCCTGACGGGCTGCGCGCATTTGTGAACATGTGACATCGCTG 1920
QY G1Y1AaAgThrPheArgArgGluValysArgAlaGluValLeuThrSerArgValysAla 660
Db 1921 GGAAGCAAGACCTTCGCGAGAAAAGAGGGCCGAGCCCTCACTCGAGGGGTGAAGGA 1980
QY LeuPheSerValLeuAsnTyrGluValArgAlaArgArgProGlyLeuLeuGluValAsnVal 680
Db 1981 CTGTTCAAGCTGCTCACTACAGAGGGGGCGGGCCCGGCTCTGAGGCGCTCTG 2040
QY LeuGlyLeuAspAspIleHisArgAlaTyrPheValPheValLeuArgValArgAlaGln 700
Db 2041 CTGGGCTCGAGATATCCAGAGGGCTGCGCACCTTGCTGCTGCTGCTGCGGGCCAG 2100
QY AspProProProGlnLeuTyrPheValValysValAspValThrGlyValArgPheThrIle 720
Db 2101 GACCCGCGCGCTGACCTGACTTTGTCAAGGTGATGTAGCGGGCGCTGACACACATC 2160
QY ProGlnAspArgLeuThrGluValIleAlaSerIleIleLeuProGlnAsnThrTyrCys 740
Db 2161 CCCCAAGACAGGCTACAGAGGTCATCCGACATCATTAACCCAGAAACAGTACTGC 2220
QY ValArgArgTyrAlaValAlaGlnValysAlaAlaHisGlyHisValArgValAspLeuys 760
Db 2221 GTGGCTCGGTATGCCGTGGTCCAGAAAGCGCCCATGGGACGTCGCGAAGGCTTCAAG 2280
QY SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
Db 2281 AGCCACGCTCTTCACTTTCAGACACCTCCAGCCGTACCTGACAGTTCCTGCTCACTCG 2340
QY GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerSerLeuAsnGln 800
Db 2341 CAGAGAGACAGCCCGCTGAGGAGATGCCGTGCTCATGAGACAGATCTCTCTGATAGG 2400
QY AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2401 GCCACAGTGGGCTCTTGCAGACGCTTCTCAAGCTTCATGTCACACAGCCGCGGCAATC 2460
QY ArgGlyValSerTyrValAlaGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2461 AGGGGCAAGTCTTACGTCCAGTGCAGAGGAGTCCGCGAGGGCTCCATCTCTCCACGCTG 2520
QY LeuCysSerLeuCysTyrGlyAspMetGluAsnValLeuPheAlaGlyIleArgArgAsp 860
Db 2521 CTCTGAGCTCTGCTACGCGCACATGAGAAACAGCTTTTGCGGGATTCGCGCGGAC 2580
QY GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db 2581 GGGCTGCTCTGCTGCTGCTGATGATTTCTTGTTGTGACACCTCACTCAACCGACGCG 2640
QY LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db 2641 AAAACCTTCTTCAGAGACCTCTGCTGAGGTGTCTCCGATATGCTGCTGCTGTAACCTTG 2700
QY ArgLeuThrValValAspPheProValGluAspGluAlaLeuGlyIleThrAlaPheVal 920
Db 2701 CGGAAGACAGTGTGAATCTTCCCTGTAGAGACAGAGCCCTGAGTGGCACGGGCTTTGTT 2760
QY GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2761 CAGATGCGGCGCCACAGGCTTATTCCTGCTGCTGCTGCTGCTGATACCGGAGCCCTG 2820
QY GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2821 GAGGTGACAGAGGACTACTCCAGCTATGCGGACCTTCATCAGAGCCGACTCTCACTTC 2880
QY AsnArgGlyPheValAlaGlyArgAsnMetArgArgValLeuPheGlyValIleuArgLeu 980
Db 2881 AACCGGCTTCAAGGCTGAGAGAAATGCGTCCGAACTCTTGAGGGCTTGCGGCTG 2940
QY LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
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2941 AAGTGTACAGCCTGTTCTTGATTTGCAAGGTGAACAGCTTCAGACGCTGTGACCAAC 3000
QY IleTyrValIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3001 ATCTCAAGATCTCTCTGTCAGGCGTACAGTTCACGATGTGTCTGCAAGCTCCCA 3060
QY PheHisGlnGlnValTyrPheAspProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3061 TTTCATCAGCAAGTTTGAAGAACCCCACTTTTCTCGCGGTATCTCTGACACGGCC 3120
QY SerLeuCysTyrSerIleLeuValAlaValAsnAlaGlyMetSerLeuGlyValAlaGly 1060
Db 3121 TCCCTCTGCTCTCATCTGCTGAAAGCAAGACGAGGATGTCCCTGCGGCGCAAGGCGC 3180
QY AlaAlaGlyProLeuProSerGlnAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
Db 3181 GCCGCGGCGCTCTGCTCCCTCCGAGGCGGTGAGTGTGTGACCAAGCATTCCTGCTC 3240
QY LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3241 AAGCTGACTCGACACCGTGTCACTACGTGCCACTCTGGGCTCACTCAGACAGCCAG 3300
QY ThrGlnLeuSerArgGlyLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db 3301 ACGCAGCTGAGTCCGAGAGCTCCCGGGAGCAGACGCTGACTGCCCTGAGAGCGCAGCAAC 3360
QY ProAlaLeuProSerAspPheLeuThrIleLeuAsp 1132
Db 3361 CCGGCACTGCTCTCAGACTTCAGAACCATCTGAGC 3396

RESULT 10
AAV27876
ID AAV27876 standard; cDNA; 3798 BP.
XX
AC AAV27876;
XX
AC 25-MAR-2003 (rev1sed)
DT 12-OCT-1998 (first entry)
XX
DE Human telomerase protein 2 (TP2) full-length cDNA.
XX
KW TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..3466
FT FT /*tag= a
XX
PN MO9821343-A1.
XX
PD 22-MAY-1998.
XX
PF 13-NOV-1997; 97WO-US021248.
XX
PR 15-NOV-1996; 96US-00751189.
PR 11-JUN-1997; 97US-00873039.
PR 16-OCT-1997; 97US-00951733.
XX
PA (AMGE-) AMGEN INC.
PA (AMGE-) AMGEN CANADA INC.
PI Harrington LA, Robinson MO.
XX
DR WPI; 1998-297946/26.
DR P-PSDB; AAV27876.
XX
PT New nucleic acid encoding human telomerase
PT regulating telomerase activity, e.g. f
PT immune deficiency syndrome.
XX
PS Claim 1c; Fig 8; 150bp; English.
XX
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CGCCAGCCCGGGT 727
ProArgArg 240
CGGT 787
260
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This full-length cDNA clone codes for a human telomerase protein 2 (TP2, see AAW61350), a novel protein of the telomerase complex. The sequence was deduced from overlapping partial clones #32 (see AAW27872) and TP2-15 (see AAW27875), which were obtained from a human colon tumour cell line LIM1863 cDNA. Expressing TP2 genes in a cell is used to increase telomerase activity and thus proliferation for treatment of e.g. HIV infection, AIDS and ageing disorders, while expressing an inactive mutant of TP2 (or molecule antisense to the gene) is used to decrease telomerase activity, e.g. for treatment of cancer. TP2 polypeptides can also be used to screen for agents that inhibit TP2 activity or its binding to TRP1 (see AAW61347) or telomerase RNA, potentially useful therapeutically, also to raise specific antibodies useful in immunoassays and as diagnostic probes for detecting/quantifying TP2 DNA. Also contemplated are transgenic animals in which the TP2 gene has been inactivated or is overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or they are delivered from engineered cells or gene therapy vectors.

CC (Updated on 25-MAR-2003 to correct PR field.)

CC

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Db 1496 AGGCACACGAAAGCGCTTCTCTCAGGAACACCAAGATTCTATCTCTCCGTGGGAAGCAT 1555
Qy 501 AAlaValSerLeuSerLeuGlnGluLeuThrTrpPlySerMetSerValArgAspCysAlaIlePhe 520
Db 1556 GCCAAGCTCTCCCTCAGAGAGCTGAGTGAAGATGAGCGTGGGACCTGGCTGGCTG 1615
Qy 521 ArgAspSerProGluValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle 540
Db 1616 CGCAGAGACCCAGGGGTTGGCTGTGTTCCGGCCGAGACCGCTCTGCTGAGAGATC 1675
Qy 541 LeuAlaValPheLeuHisIleTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
Db 1676 CTGGCCAAAGTTCTCTCAGCTGCTGATGAGTGTGATCCTGCTGAGCTGCTCAGGCTTTTC 1735
Qy 561 PheTyrValThrGlnThrThrPheGlnGlyAsnAlaGluPhePheTyrArgLysSerVal 580
Db 1736 TTTTATGTTCACGGAGACCAAGCTTTTCAMAAAGAACAGGCTCTTTTCTACCGGAAGAGTGT 1795
Qy 581 TrpSerLysLeuGlnSerIleGlyIleArgGlnHisIleuLysArgValGlnLeuArgGlu 600
Db 1796 TGGACCAAGTTTCAGAAAGCATTTGGATTCAGACAGCTTGAGAGGGTGCAGCTGGGGAG 1855
Qy 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaIleuLeuThrSerArg 620
Db 1856 CTGTGGAAGCAGAGAGTCAAGCAGCATCGGAGACCGAGCCGCTGCTGACGTCCAGA 1915
Qy 621 LeuArgPheIleProLysProArgGlyLeuArgProIleValAsnMetCaspTyrValVal 640
Db 1916 CTCCCTTCATCCCAAGCGCTGACGGGCTGCGCGCATTTGTGAACATGACATCAGTCTGTG 1975
Qy 641 GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla 660
Db 1976 GGAGCAGAGACCTTCGAGAGAAAGAGGGCCAGCGTCTCACTCGAGGGGTGAAGGCA 2035
Qy 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyLysIleSerVal 680
Db 2036 CTGTTCAAGGTCTCACTACAGAGCGGGCGCGCGCTCTCTGGGCCCTCTGTG 2095
Qy 681 LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln 700
Db 2096 CTGGGCTCGAGAGATTCACAGAGGGGCTGGCCACCTTGTGTGTGTGGGGCCAG 2155
Qy 701 AspProProGluLeuThrPheValLysValAspValThrGlyAlaThrAspThrIle 720
Db 2156 GACCCGCGCTGAGCTGACTTTGTCAAGGTGATGATGACGGGCGCGTGAACACACATC 2215
Qy 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
Db 2216 CCCAGGACAGGCTCACAGAGGTCATCGCCAGCATCATCAACCAGAACACGTRATGC 2275
Qy 741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys 760
Db 2276 GTGGCTCGGTATGCGGTGTCCAGAAAGCGCCCATGGGCAAGTCCGCAAGGCTTTCAAG 2335
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
Db 2336 AGCCACGTTCTTACCTTGACAAACCTCCAGCGGTAAATGACAGTTCGTGGCTCACTG 2395
Qy 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuLeuGln 800
Db 2396 CAGGAGACCAAGCCCGCTGAGGATGCGCTGTCATGACAGACAGCTCTCTCTGAATGAG 2455
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
Db 2456 GCCACACAGTGGCTCTTCAAGCTCTTCTTCAAGCTTATGTCACCAAGCCCGTGCATC 2515
Qy 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db 2516 AGGGGCAATCTTACCTCAGTGCAGGGGATGCCAGAGGCTCCATCTCTCCAGGCTG 2575
Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860

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Db 2576 CTCTCAGACCTGTGCTACGGGACATGAGAACAAAGCTGTTTCCGGGGATTCGCGGAGC 2635
Qy 861 GlyLeuLeuLeuArgLeuValAspAspPheLeuValThrProHisIleuThrHisAla 880
Db 2636 GGGCTGCTCTCGCGTTGGTGGATATTTCTGTGGAGACCTTCACTCAACCCAGCGG 2695
Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
Db 2696 AAAACCTTCTCAGGACCCCTGGTCCGAGGTGCCCTGAGTATGCTGGGTGGTGAACCTTG 2755
Qy 901 ArgLysThrValAlaAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
Db 2756 CGGAAGACAGTGTGAACCTTCCCTGTAGAAGCAGAGGCTGGGTGGACCGGCTTTTGT 2815
Qy 921 GlnMetProAlaHisGlyLeuPheProThrProCysGlyLeuLeuLeuAspThrArgThrLeu 940
Db 2816 CAGATGCGGCGCCACAGGCTTATTTCCCTGTGCGGCGCTGCTGCTGATACCCGAGACCTTG 2875
Qy 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db 2876 GAGGTGCAGAGGACTTACTCCAGCTATGCGCGACCTTCATCAGAGCCAGTCTCACTTC 2935
Qy 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db 2936 AACCGCGCTTCAAGGCTGGAGGAACATGCGTCCAAACTTTTGGGGTCTTGGCGGCTG 2995
Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValLysThrAsn 1000
Db 2996 AAGTGTCAAGCTTCTTCTGATTTGACAGTGAACAGCTTCAACAGGTGTGCACCAAC 3055
Qy 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
Db 3056 ATCTACAAAGATCTCTCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGTGTGACGCTCCA 3115
Qy 1021 PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
Db 3116 TTTTCATCAGCAAGTTTGGAGAACCCCAATTTTCTGCGGCTCATCTGTACACAGGCGC 3175
Qy 1041 SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyLysAlaGly 1060
Db 3176 TCCCTCTGTACTTCATCTCCTGAAGCCAAAGCAGAGATGCTCGGGGCGCAAGGGCG 3235
Qy 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
Db 3236 GCGCGCGGCTCTCTGCTCCGAGGCGTGCAGTGGTGTGCCACCAAGCATTCCTGCTC 3295
Qy 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
Db 3296 AAGCTGACTCGACACCGTGTCACTACGTGCCATCTCTGGGGTCACTCAGACAGCCGAG 3355
Qy 1101 ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
Db 3356 ACGCAGCTGAGTGCAGAACTCCGGGAGAGCAGAGCTGAGCTGCGCTGAGAGGCCAGCAAC 3415
Qy 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
Db 3416 CCGGACGTGCTCTCAGACTTCAAGACCATCTGGAC 3451

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RESULT 12
 AA200724
 ID AA200724 strand: DNA; 4015 BP.
 XX
 AC AA200724;
 XX
 DT 06-OCT-1999 (first entry)
 XX
 DE Human telomerase catalytic domain DNA.
 XX
 KW Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
 KW body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
 KW acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
 KW breast cancer; ss.
 XX

OS Homo sapiens.
 XX DE19804372-A1.
 XX
 XX
 XX
 PD 05-AUG-1999.
 XX
 XX 04-FEB-1998; 98DE-01004372.
 XX
 XX 04-FEB-1998; 98DE-01004372.
 XX
 XX (DAHM/) DAHM M W.
 XX
 XX DAHM MM;
 XX
 XX WPI; 1999-431408/37.
 XX
 XX
 PT Quantifying tumor cells by amplifying mRNA encoding the catalytic subunit
 of telomerase.
 XX
 XX
 PS Example; Fig 1A-B; 26pp; German.
 XX
 XX
 CC This invention describes a novel method for the quantitation of tumor
 CC cells in a body fluid which comprises (1) enrichment or isolation of
 CC tumor cells in the sample, (2) amplification of mRNA from these cells
 CC that encodes the catalytic subunit of telomerase and (3) quantifying the
 CC amount of amplified mRNA. The method is applied to tumor cells derived
 CC from (micro)metastases, e.g. associated with a wide range of tumors such
 CC as T-cell lymphoblastoma, chronic myeloid or acute lymphatic leukemia,
 CC melanoma, pulmonary carcinoma, cancer of colon or breast etc. This
 CC sequence encodes a human telomerase protein catalytic domain
 XX
 SO Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,76e-218 Length: 4015
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-10-044-692-2 (1-1132) x AA200724 (1-4015)

QY 1 MetProArgAlaProArgCysArgAlaValArgSerLeuArgSerHisTyrArgGlu 20
 DB 56 ATGGCGGCGCTCCCGCTGCGAGCGCTGCGCTCTGCGCGACCACTACCGGAG 115
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
 DB 116 GTGCTGCGGCTGGCGCACTTGTGCGGCGCTGGGCGCCCAAGGCTGGCGGTGCGAG 175
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValProTyr 60
 DB 176 CGCGGCGACCGGCGGCTTCCGCGCTGCTGGCGCCCAAGTGGTGGTGGCTGG 225
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80
 DB 236 GACCAAGCGCGCGCGCGCGCGCGCGCTCTTCCGCAAGTGTCTTCCGAGAGACTG 295
 QY 81 ValAlaArgValLeuGlnArgLeuCysGlnArgGlyValAlaLysAsnValLeuAlaPheGly 100
 DB 296 GTGGCCCGAGTGTGCAAGAGGCTGTGCGAGCGCGCGCGCAAGACGTGTGGCTTGGCG 355
 QY 101 PheAlaLeuLeuAspGlyValArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 DB 356 TTTCGCGCTGTGACGCGGCGCGCGCGCGCGCGCGCGCGCTTCCACCAAGCGTTCGCG 415
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATPGLYLeuLeu 140
 DB 416 AGCTAAGTCCCAACCGGTACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTCTG 475
 QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160

DB 476 CTGGCGCGCGTGGCGAGACGCTGCTGCTTCACTGCTGGACGCTGCGGCTCTTGTG 535
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyValAla 180
 DB 536 CTGGTGGCTCCACCTGCGCTTACAGGTGTGCGGCGCGCGCTGTACAGCTTGGCGCT 595
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
 DB 596 GCCACTAGGCG 655
 QY 201 ArgAlaTyrPheAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
 DB 656 CGGCGCTGAAACATAGCGTCAGGAGGCGCGGCGTCCCTGGGCGCTGGCGCGCGCGCG 715
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 DB 716 GCGAGAGAGCGCGGCGGAGTGTCCAGCGGAAGTCTGCGTGGCCAGAGGCCCGAGGCT 775
 QY 241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTyrPheAlaHisProGly 260
 DB 776 GCGCGTGGCGCGTGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 835
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 DB 836 AGGACGCGTGGACCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
 QY 281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 DB 896 GAAAGCACTCTTGTGAGAGGTGCGTCTTGTGACGCGCGCGCGCGCGCGCGCGCGCG 955
 QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTyrPheThrPro 320
 DB 956 GCGCAGACACAGCGGCG 1015
 QY 321 CysProProValTyrAlaGlnThrIleHisPheLeuTyrSerSerGlyAspLysGlnGln 340
 DB 1016 TGTCCCGCGGTGTACCGCAGACCAAGACATTCCTCTCACTTCCAGGCGCAAGAGCAG 1075
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 DB 1076 CTGGCGCGCTCTTCTCTACTACGTCTGTAGGCCCAAGCTGACGTGGCGTGGAGGCTC 1135
 QY 361 ValGlnThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
 DB 1136 GTGAGACCATCTTCTGGGTTCAGCGCGCTGAGTCCAGGAGACCTCCCGAGGTTGCC 1195
 QY 381 ArgLeuProGlnArgTyrTyrGlnMetArgProLeuPheLeuGlnLeuLeuGlyAsnHis 400
 DB 1196 CGCTGCGCCAGCGCTACTGGCAATGCGGCCCTGTCTTGTGAGCTGCTTGGAAACAC 1255
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLeuGlyThrHisCysProLeuArgAlaAlaValThr 420
 DB 1256 GCGCAGTGCCTTACGCGGTGTCTTCCCAAGACGCACTGCCGCTGAGACTCGGTCAC 1315
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGln 440
 DB 1316 CCAGACCGCGGT 1375
 QY 441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
 DB 1376 GAGGACACAGACCCCGT 1435
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgValProProGlyLeuTyrGlySer 480
 DB 1436 GTTTAGGCTGT 1495
 QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheHisSerLeuGlyLysHis 500
 DB 1496 AGGCACAAAGAACGCGCTTCTCAGAGAACACCAAGAGTTATCTCCCTGGGAGAGCAT 1555
 QY 501 AlaLysLeuSerLeuGlnGlnLeuThrTyrLysMetSerValArgAspCysAlaTyrLeu 520
 DB 1556 GCCAAGCTCTGCTGAGAGGCTGACGTGAGAGATGAGCGTGGGAGCTGCGGCTTGGCTG 1615

QY 521 ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGlu 540
 DB 1616 CGCAGAGACCCAGGGGTTGGCTGTTCGGCCGAGAGACCGTCTGGTGAAGAGATC 1675
 QY 541 LeuAlaIysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe 560
 DB 1676 CTGGCCAAAGTTCCTGACCTGAGTGAAGTGTAGTGTGCTGCTGAGCTGCTCAGGTCTTTC 1735
 QY 561 PheTyrValThrGluThrThrPheGlnIysAsnArgLeuPhePheTyrArgIysSerVal 580
 DB 1736 TTTTATGTCACGGAACACCGTTTCAAAAGAACAGGCTTTTTCATCCGGAAGAGTGTTC 1795
 QY 581 TrpSerIysLeuGlnSerIleGlyIleArgGlnHisLeuIysArgValGlnLeuArgGlu 600
 DB 1796 TGGACCAAGTTCACAAAGCATTTGGATCAGACAGCACTTGAAGGGGTGACGCTCGCGAG 1855
 QY 601 LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg 620
 DB 1856 CTGTGGAAGCAGAGGTGACGAGCATCGGAAGCCAGGCCCTGCTGACGTCACAG 1915
 QY 621 LeuArgPheIleProIysProArgSerGlyLeuArgProIleValAsnMetAspTyrValVal 640
 DB 1916 CTCCGCTTCATCCCAAGCCTGACGGGCTGCGCGCGATTGTGAACATGGAACCTACGTCGTG 1975
 QY 641 GlyAlaArgThrPheArgArgGluIysArgAlaGluArgLeuThrSerArgValIysAla 660
 DB 1976 GGAGCCAGAACCTTCGAGAGAAAGAGGCGGAGCGCTCTACCTCGAGGGGTGAAGGCA 2035
 QY 661 LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyValAsnVal 680
 DB 2036 CTGTTCAAGGTGCTCACTACAGAGCGGGCGCGCGCTGCTGGGCGCTCTGTGTG 2095
 QY 681 LeuGlyLeuAspAspIleHisArgAlaTyrArgThrPheValLeuArgValArgAlaGln 700
 DB 2096 CTGGGCTCGAGAGATATCCAGAGGCGGCTGCGCACCTTGTGTGTGTGGGCGCCAG 2155
 QY 701 AspProProGluLeuTyrPheValIysValAspValThrGlyValTyrAspThrIle 720
 DB 2156 GACCCGCGCGCTGAGTGTACTTGTTCAGAGTGTGATGTGACGGCGCGTGAACACCATTC 2215
 QY 721 ProGlnAspArgLeuThrGluValIleAlaSerIleIleIysProGlnAsnThrTyrCys 740
 DB 2216 CCCAGAGACAGGCTACCGAGGTCATCGCACATCATCAACCAGAACACGTATCTGC 2275
 QY 741 ValAlaArgTyrAlaValAlaValGlnIysAlaAlaHisGlyHisValArgIysAlaPheIys 760
 DB 2276 GTGCGTCCGTTATGCGGTGTCCAGAGGCGCGCCCATGGGCAAGCTCGGCAAGGCTTCAAG 2335
 QY 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisIleu 780
 DB 2336 AGCCACGTTCTTCACTTGAACAACCTCCAGCCGATCATCGAACAGTTCGTGGCTACCTCG 2395
 QY 781 GlnGluThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGln 800
 DB 2396 CAGAGAGACCAAGCCCGTGAGGATGCCGTGTCATGACACAGACCTCCCTGATATGAG 2455
 QY 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle 820
 DB 2456 GCCACAGAGTGGCTCTTCAACGCTCTTCCATACGCTTCATGTGCACACCCCGTGGCCATTC 2515
 QY 821 ArgGlyIysSerTyrValGlnCysGlnIyIleProGlnGlySerIleLeuSerThrIleu 840
 DB 2516 AGGGGCAAGTCTACGTCACAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTCG 2575
 QY 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnIysLeuPheAlaGlyIleArgArgAsp 860
 DB 2576 CTCTGACGCTGTGTGCTAGCGGACATGAGAACAGACTTTTGGGGGATTCGGCGGGAGC 2635
 QY 861 GlyLeuLeuLeuValAspAspPheLeuValThrProHisLeuThrHisAla 880
 DB 2636 GGGCTGCTCTCGCTGTGTGATGATTTCTTGTGTGTGACACTCACCTCACCCACGCG 2695

QY 881 LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu 900
 DB 2696 AAAACCTTCTCAGAGACCTGGTCCGAGGTGTCCCTGATATGCTGGGTGTGAACCTTG 2755
 QY 901 ArgIysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal 920
 DB 2756 CGGAAGACAGTGTGTAACTTCCCTGTAGAAAGCAGAGGCGCTGGGGTGACAGGCTTTTGT 2815
 QY 921 GlnMetProAlaHisGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu 940
 DB 2816 CAGATGCGGCCCCACGGCTATTCCTGTGTGTCGACCTGTGCTGTGATACCCGAGCCTTG 2875
 QY 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
 DB 2876 GAGGTGACAGAGGACCTATCTCCAGTATGCGCGGACCTTCATCAGAGCCAGTCTACCTTC 2935
 QY 961 AsnArgGlyPheLeuAlaGlyArgAsnMetArgGlyGluPheGlyValLeuArgLeu 980
 DB 2936 AACCCGCGCTTCMAAGCTGGGAGGAACATGCTCCCAAACTTTTGGGGTCTTGGCGCTG 2995
 QY 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
 DB 2996 AAGTGTACAGCTGTCTTGTGATTTGACAGTGAACAGCTTCACAGAGGTGTGCACCAAC 3055
 QY 1001 IleTyrIysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
 DB 3056 ATCTACAAAGATCTCTCTGTCGAGGCGTACAGGTTTCAACGATGTGTGTGACAGTCCCA 3115
 QY 1021 PheHisGlnGlnValTyrIysAsnProThrPhePheLeuArgValIleSerAspThrAla 1040
 DB 3116 TTTTCATCAGCAAGTTTGGAGAACCCCAATTTTCTGCGGTGTATCTTCACACAGGCGC 3175
 QY 1041 SerLeuCysTyrSerIleLeuIysAlaIysAsnAlaGlyMetSerLeuGlyAlaIysGly 1060
 DB 3176 TCCCTCTGTACTCATCTCTGAAGCCCAAGAACGAGGATTCCTGGGGGCGCAAGGCGC 3235
 QY 1061 AlaAlaGlyProLeuProSerGluAlaValGlnTyrPheCysHisGlnAlaPheLeuLeu 1080
 DB 3236 GCGCGCGGCTCTGCTCCCTCCAGGCGCGTGCAGTGTGTGTCACCAAGCATTCCTCGCTC 3295
 QY 1081 LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln 1100
 DB 3296 AAGCTGACTCGACACCGTGTCACTACGTCGACATCTGTGGGTCACTCAGGACAGCCAG 3355
 QY 1101 ThrGlnLeuSerArgIysLeuProGlyThrThrThrLeuThrAlaLeuGluAlaAlaAsn 1120
 DB 3356 ACGCAGCTGAGTCCGAAAGCTCCCGGGGACGAGCGTGAAGCTCTGGAGGCGCCAGCCAAAC 3415
 QY 1121 ProAlaLeuProSerAspPheLysThrIleLeuAsp 1132
 DB 3416 CCGGCACTGCCTCAGACTTCAAGACATCTCGAAC 3451

RESULT 13
 AA220279
 ID AA220279 standard; cDNA; 4015 BP.
 XX
 AC AA220279;
 XX
 XX 17-JAN-2000 (first entry)
 DT
 XX Human telomerase reverse transcriptase (hTERT) cDNA.
 DE
 XX Telomerase reverse transcriptase; human; hTERT; cell proliferation;
 KM cancer; ss.
 KM
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 56..3454
 FT CDS /*tag= a
 XX
 XX MO9950386-A2.

PD 07-OCT-1999.
 XX 31-MAR-1999; 99WO-US007097.
 PF 31-MAR-1998; 98US-00052864.
 PR 03-AUG-1998; 98US-00128354.
 XX (GERO-) GERON CORP.
 PA Morin GB;
 PI WPI: 1999-610842/52.
 DR P-PSDB; AA132050.
 XX
 PT New catalytic polypeptide and polynucleotide, useful for increasing
 catalytic activity in a cell.
 PS Disclosure; Fig 2; 24pp; English.
 XX
 CC This is the nucleotide sequence of cDNA encoding human telomerase reverse
 transcriptase (hTERT, see AA132050). Human telomerase is a target for
 CC diagnosing and treating diseases relating to cell proliferation and
 CC senescence, such as cancer, or for increasing the proliferative capacity
 CC of a cell. A claimed method for increasing the proliferative capacity of
 CC a vertebrate cell, especially a human or other mammalian cell, involves
 CC introducing into the cell a recombinant hTERT polynucleotide encoding an
 CC hTERT variant in which residues 192-323, 200-323, 192-271, 200-271, 222-
 CC 240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A
 CC claimed method for reducing telomerase activity in a cell involves
 CC introducing a recombinant polynucleotide encoding an hTERT variant having
 CC a deletion of amino acids 192-450, 560-565, 637-660, 748-764 or
 CC 1055-1071. The polynucleotides are obtained by mutagenesis of the hTERT
 CC coding sequence
 XX
 SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 2 76e-218 Length: 4015
 Score: 5961.00 Matches: 1132
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-10-044-692-2 (1-1132) x AA20279 (1-4015)
 QY 1 MetProAlaAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 20
 Db ATGCGCGCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCT 115
 QY 21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
 Db GTGCTGCGCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCT 175
 QY 41 ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTyr 60
 Db 176 CGCGGGGAGCCCGGGGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGGCTGG 235
 QY 61 AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuValGlnLeu 80
 Db 236 GACGACGCTG 295
 QY 81 ValAlaArgValLeuGlnArgLeuGlyArgGlyAlaValAsnValLeuAlaPheGly 100
 Db GTGGCCCGAGTGTCTGCAAGGCTGTGCGAGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAG 355
 QY 101 PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
 Db 356 TTCCGGCTGTGAGAGCGGGCCCGCGGGGGCCCGCGAGGCTTCCACACAGCGGTGCGC 415
 QY 121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyValATrGlyLeuLeu 140
 Db 416 AGCTACCTGCCCAACACGAGTGAACGACCTGCGGGGAGAGCGGGGCGGTGGGGCTGCTG 475

QY 141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 160
 Db CTGCGCGCGCTGGGCGAG 535
 QY 161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
 Db CTGGTGGCTCCACAGCTGGCTTACAGAGTGGCGGGCCGCGCTGTACAGCTGGCGCT 595
 QY 181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 200
 Db GCGACTCAGCG 655
 QY 201 ArgAlaTTPAsnHisSerValArgGlyAlaGlyValProLeuGlyLeuProAlaProGly 220
 Db 656 CGGCGCTGGAACATAGCTAGTGAAGAGCGCGGGTCCCGCTGGCGCTGCCAGCGCGGT 715
 QY 221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
 Db GCGAGAGAGCGCGGGGCGAGTGCAGCGCGAGAGTCTGCGCTGGCCAGAGAGCGCGCT 775
 QY 241 GlyAlaAlaProGlnProGlnArgThrProValGlyGlnGlySerTTPAlaHisProGly 260
 Db 776 GCGCTGCGCTGAGCGCGAGCGAGCGCGCGCTGGGCGAGGGGTCTGGGCGCGCGCGCG 835
 QY 261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
 Db 836 AGGAGCGCTGGAGCGAGGACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 895
 QY 281 GluAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
 Db 896 GAAGCCACTCTTTGGAGGGTGGCGCTCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCG 955
 QY 301 ArgGlnHisAlaGlyProProSerThrSerArgProProArgProTTPAspThrPro 320
 Db 956 CGCCAGACACAGCT 1015
 QY 321 CysProProValTyrAlaGlnThrLysHisPheLeuTyrSerSerGlyAspLysGln 340
 Db 1016 TGTCCCGCGGTATGACCGGAGACCAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1075
 QY 341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
 Db 1076 CTGCGCGCT 1135
 QY 361 ValGlnThrIlePheLeuGlySerArgProTTPMetProGlyThrProArgArgLeuPro 380
 Db 1136 GTGAGACCATCTTTCTGTGCTTCCAGGCGCTGGATGCCAGGAGCTCCCGCGAGTTGCC 1195
 QY 381 ArgLeuProGlnArgTyrTTPGlnMetArgProLeuPheLeuGlnLeuGlyLysHis 400
 Db 1196 CGCTGCG 1255
 QY 401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
 Db 1256 GCGCAATGCGCGCTACGAGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1315
 QY 421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGlnGlu 440
 Db 1316 CAGAGCGCGGT 1375
 QY 441 GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTTPGln 460
 Db 1376 GAGAGACAG 1435
 QY 461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTTPGlySer 480
 Db 1436 GTTATCGGCTGT 1495
 QY 481 ArgHisAsnGlnArgArgPheLeuArgAsnThrLysLysPheHisLeuSerLeuGlyLysHis 500
 Db 1496 AGGCAACAAGAGAGCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1555

QY	501	AlAlvYLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaThrLeu	520
Db	1556	GCGAGCTCTCGCTGCAGAGGTGACGGGAAAGATGAGCGGAGCTGGCGCTTGGCTG	1615
QY	521	ArgAspSerProGluYValGlyCysValProAlaAlaGluHisArgLeuArgGluGluLe	540
Db	1616	CGCAGAGACCCAGAGGGGTGGCTGGTCTTCGGGCGGAGAGCAACCGCTCCGTGAGGAGATC	1675
QY	541	LeuAlaLysPheLeuHisTrpLeuMetSerValTrpValGluLeuLeuArgSerPhe	560
Db	1676	CTGGCGCAAGTTCCTGCACCTGGCTGATGATGGTGTACGTCCGTCCAGAGCTCTCAGGCTTTC	1735
QY	561	PheTrpValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTrpArgLysSerVal	580
Db	1736	TTTATATGTCAGGAGAACCAACGTTTCAAAAGAACAGGCTCTTTTCTTCCAGGAAGAGTTC	1795
QY	581	TrpSerTrpLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGluLeuArgGlu	600
Db	1796	TGGAGCAAGTTCGAAAGCATTTGGATTCAGACAGCACTTGAAGAGGGGTCAAGCTCGGGAG	1855
QY	601	LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	620
Db	1856	CTGTGGAAGCAGAGAGTCAAGGACGATCGGGAAGCCAGGCGCCGCTCTGACGTCAGCA	1915
QY	621	LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTrpValVal	640
Db	1916	CTCCGCTTCATCTCCCAACCTGACGGGTGGCGCGCATTTGGACATGATGACTTACCTCTGTG	1975
QY	641	GlyAlaArgThrPheArgArgGluLysValArgAlaGluArgLeuThrSerArgValLysAla	660
Db	1976	GGAAGCCAAACGTTCCGAGAGAAAGAGGCGGAGCTTCACTCCAGGGGTGAAGGCA	2035
QY	661	LeuPheSerValLeuAsnTrpGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	680
Db	2036	CTGTTCAAGCGTCTCAACTACGAGCGGGCGCGGCGCCCGGCTCTGGCGGCTCTGTG	2095
QY	681	LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	700
Db	2096	CTGGGCGCTGGAGCGAATTCACAGGGGCTGGGCGCACCTTCGTCGCTCGGTCCGGGCGCAG	2155
QY	701	AspProProGlnLeuLeuTrpPheValLysValAspValThrGlyAlaTrpAspThrIle	720
Db	2156	GACCGCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTGACACCACTC	2215
QY	721	ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTrpCys	740
Db	2216	CCCCAGACAGGCTCAGCGAGGTATCCCGCAGCATCATCAAAACCCAGAACACGTACGTC	2275
QY	741	ValArgArgTrpAlaValAlaGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	760
Db	2276	GTCGCTCGGATGTGCGGTGGTCCAGAAAGGCGCGCCCATGGGACAGTCCGACAAAGGCTTCAAG	2335
QY	761	SerHisValSerThrLeuThrAspLeuGlnProTrpMetArgGlnPheValAlaHisLeu	780
Db	2336	AGCCACGCTCTCACTTACCAAGACTCTCAGCGGTACATGACGACACTTGGTGGCTCACTG	2395
QY	781	GlnGlnThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAsnGlu	800
Db	2396	CAGAGAGACAGCGCCGCTAGAGGATCCGCTCGTACATGACAGAGAGTCTCTCCTGATATAG	2455
QY	801	AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle	820
Db	2456	GCCAGCAGATGGGCTCTTGCAGCGTCTTCCACGCTTCATGTGCCACACAGCGGTGGGCATC	2515
QY	821	ArgGlyLysSerTrpValGlnCysGlnGlyIleProGlnGlySerTrpLeuSerThrLeu	840
Db	2516	AGGGGCAAGTCTTACGTCCAGGCGCAGGGGAGTCCCGCAGGGGTCCATCTCTCCACGCTG	2575
QY	841	LeuCysSerLeuCysTrpGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	860
Db	2576	CTCTGCACGCTGTGTGACGGCGACATGAGAAACAAGCTGTTTGGCGGGAATTCGGCGGAGC	2635
QY	861	GlyLeuLeuLeuArgLysValAlaAspAspPheLeuLeuValThrProHisLeuThrHisAla	880

Db	2636	GGGCTGCTCCCTGCTTTGGTGGATGATTTCTTGTGGTGAACCTCACTCAACCGC	2635
Qy	881	LysThrPheLeuArgThrLeuValArgGlyValProGlnTyrglyCyseValValAsnLeu	900
Db	2696	AAACCTTCCTCAGACACCTCGTCCGAGAGTGTCCCTGAGTATGCTGGTGTGAACCTTG	2755
Qy	901	ArgIyThrValValAsnPheProValGlnAspGlnAlaLeuGlyGlyThrAlaPheVal	920
Db	2756	CGAAGACAGTGGTGAACCTTCCTCGTGGAAACACAGAGCCCTGGGTGGCACGGCTTTGT	2815
Qy	921	GlnMetProAlaHsGlyLeuPheProTyrCysGlyLeuLeuLeuAspThrArgThrLeu	940
Db	2816	CAGATGCCGCGCCACCGGCTATTCCTCCGCGCGGCTGCTGCTGGATACCCGGAACCTG	2875
Qy	941	GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
Db	2876	GAGGTGCAGAGCCGACTACTCCAGCTATGCCCGGACCTCCATCAAGACGACTCACTCC	2935
Qy	961	AsnArgIyPheIyValArgValArgAsnMetArgArgIyLeuPheGlyValLeuArgLeu	980
Db	2936	AACCGCGGCTTCAAGGCTGGGAGGAAACATCGTGGCAAACTTTGGGGTCTTCCGGCTG	2995
Qy	981	LysCysHsSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
Db	2996	AAGTGTACACACCTGGTTCCTGGATTGGAGGTGAACAGCTTCCAGACGATGTGACCAAC	3055
Qy	1001	IleTyrIyIleLeuLeuLeuGlnAlaTyrArgPheHsIalCyseValLeuGlnLeuPro	1020
Db	3056	ATCTACAAAGATCCCTCTGCTGACAGCGTACAGGTTTACGCGATGTGTGCACTCCA	3115
Qy	1021	PheHsGlnGlnValTTPLyAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
Db	3116	TTTCATCAGCAAGTTTGGAGAACCCACATTTTCTGCGCGCTCATCTTGACACCGCC	3175
Qy	1041	SerLeuCystrYsrIleLeuValIlyAsnAlaIyMetSerLeuGlyAlaIyGly	1066
Db	3176	TCCCTCTGCTACTCATCTGTAAGCCAAAGAACGAGGAGTGTGCGGGGGCCAAAGGC	3235
Qy	1061	AlaAlaGlyProLeuProSerGlyAlaValGlnTyrPheuCyHsGlnAlaPheLeuLeu	1086
Db	3236	GCCCGCGGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTTCTGCTC	3295
Qy	1081	LysLeuThrArgHsArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
Db	3296	AAGCTGACTGCACACCGTGTCACTTACGTGCCATCTCCGGGGTCACTCAGGACGCCAG	3355
Qy	1101	ThrGlnLeuSerArgIyIyLeuProGlyThrThrLeuThrAlaLeuGlnAlaAlaAsn	1120
Db	3356	ACGCAAGCTGACTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCGCGACCAAC	3415
Qy	1121	ProAlaLeuProSerAspPheIyThrIleLeuAsp	1132
Db	3416	CCGGACTGCCCTCAGACTTCAGACATCTCTGGAC	3451
RESULT 14			
ID	AAZ30154	standard; cDNA; 4015 BP.	
AC	AAZ30154;		
DT	26-JAN-2000	(first entry)	
DE	cDNA encoding a human telomerase reverse transcriptase (TRT).		
KM	Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;		
KM	dendritic cell; telomerase activity; cancer cell; proliferating cell;		
KM	immunological destruction; telomerase; cancer; proliferation disease; ss.		
OS	Homo sapiens.		
FT	Key	Location/Qualifiers	
CDS	56..3454		

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FT      /tag= a
FT      /product= "telomerase reverse transcriptase"
XX
XX      MO950392-A1.
XX
XX      07-OCT-1999.
XX
XX      30-MAR-1999; 99WO-US006898.
XX
XX      31-MAR-1998; 98US-0112006P.
XX
XX      (GERO-) GERON CORP.
XX
XX      Gaeta FCA;
XX
XX      WPI; 1999-610845/52.
XX
XX      P-PSDB; AAY43621.
XX
XX      Eliciting an in vivo immune response for prevention and treatment of
XX      cancers.
XX
XX      Disclosure; Fig 2; 26pp; English.
XX
XX      The present sequence encodes a human telomerase reverse transcriptase
XX      (TRT) polypeptide. The protein is used in the method of the invention.
XX      The specification describes a method for activating a T lymphocyte,
XX      comprising contacting the T lymphocyte with a dendritic cell that
XX      expresses a TRT peptide in the context of a MHC class I or MHC class II
XX      molecule. The protein causes induction of an in vivo immunological
XX      response to telomerase activity. Cancer cells are characterized by
XX      expression of endogenous TRT gene and the presence of detectable
XX      telomerase activity. Therefore, by eliciting a specific immune response
XX      to TRT or to TRT-expressing cells, it is possible to selectively target
XX      proliferating cells for immunological destruction. The method is used for
XX      eliciting an in vivo immune response to telomerase by activating a T
XX      lymphocyte, and is useful for prevention and treatment of cancers and
XX      other proliferation diseases/conditions
XX
XX      Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 2.76e-218 Length: 4015
Score: 5961.00 Matches: 1132
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-044-692-2 (1-1132) x AA230154 (1-4015)
QY      1 MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTYrArgGlu 20
DB      |||||
DB      56 ATGGCGCGCGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCCAGCACTACCGGAG 115
QY      21 ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTTPArgLeuValGln 40
DB      |||||
DB      116 GTGCTGCGCGTGGCCAGCTTCGTGGCGGCTGGGGGCCCGCAGGGCTGGCGCTGTGAG 175
QY      41 ArgGlyAspProAlaAlaPheArgAlaValAlaGlnCysLeuValCysValProTyr 60
DB      |||||
DB      176 CCGGGGAGACCCGGCGGCTTTCGCGCGCTGTGGGCCAGTGTGCTGTGTGCTGCTG 235
QY      61 AspAlaArgProProProAlaAlaIlePheSerPheArgGlnValSerCysLeuGlyGln 80
DB      |||||
DB      236 GACGCAAGCGCGCCCGCCCGCGCTTCCTTCGCGCAAGTGTCTGCTGAGAGAGCTG 295
QY      81 ValAlaArgValLeuGlnArgLeuGlyGlnArgGlyAlaValAsnValHLeuAlaPheGly 100
DB      |||||
DB      296 GTGGCCCGAGTGTCTGAGAGGCTGTGCGAGCGCGCGGCAAGAAAGTGTGCTGCTG 355
QY      101 PheAlaLeuLeuAspGlyValAlaArgGlyGlyProProGlnAlaPheThrThrSerValArg 120
DB      |||||
DB      356 TTGCGCGTGTCTGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCA 415

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QY      121 SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTyrGlyLeuLeu 140
DB      |||||
DB      416 AGTACTCTGCCCAACAGCGTGAACGACGACCTCGGGGGAGCGGGCGTGGGGGCTGTG 475
QY      141 LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgGlyAlaLeuPheVal 160
DB      |||||
DB      476 CTGGCGCGCGTGGGCGAGCAGCTGTGTGTTCACCTGTGTGCAAGCTGTGGCGCTTTGTG 535
QY      161 LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 180
DB      |||||
DB      536 CTGTGTGTCTCCAGCTGTGCTTACAGGTGTGGGGCGCGCGCTGTACAGCTGTGGGCT 595
QY      181 AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGln 200
DB      |||||
DB      596 GCCACTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 655
QY      201 ArgAlaTyrPheAsnHisSerValArgGlnAlaGlyValProLeuGlyLeuProAlaProGly 220
DB      |||||
DB      656 CGGGCTGTGAACATAGCTGTCAGGAGCGCGGGTCTCCCTGGGCGCTGCGCGCGCGGCT 715
QY      221 AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg 240
DB      |||||
DB      716 GCGAGAGAGCGCGGGGCGAGTCCAGCGCAAGTCTGCCGTGGCCCAAGAGGCCAGCGCT 775
QY      241 GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTTPAlaHisProGly 260
DB      |||||
DB      776 GCGCGTCCCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 835
QY      261 ArgThrArgGlyProSerAspArgGlyPheCysValAlaSerProAlaArgProAlaGlu 280
DB      |||||
DB      836 AGGAGCGGTGACCGAGGACCGGTGTTCTGTGTGTGTGTCTGCAAGCCGCGCGGAA 895
QY      281 GlnAlaThrSerLeuGlnGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly 300
DB      |||||
DB      896 GAGCGACCTCTTGTGAGGGGTCTCTGTGACGCGCGCACTCCATCCATCCGTGTGGGC 955
QY      301 ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTyrAspThrPro 320
DB      |||||
DB      956 CCGCAGACACCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1015
QY      321 CysProProValTyrAlaGlyThrThrHisHisPheLeuTyrSerSerGlyAspGlyGln 340
DB      |||||
DB      1016 TGTCTCCCGGTATAGCGGAGCAAGCACTTCTCTGCTGAGCGAGCAAGAGGAG 1075
QY      341 LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu 360
DB      |||||
DB      1076 CTGGCGCGCTCTCTCTACTGACTCTGTGAGGCCAGCGCTGAGCGCTGAGAGGCTC 1135
QY      361 ValGlnThrIlePheLeuGlySerArgProTyrMetProGlyThrProArgArgLeuPro 380
DB      |||||
DB      1136 GTGGAGACCATCTTCTGTGGGTTCAGGCCCTGTGATGCCAGGAGCTCCCGCAGTGTGCCC 1195
QY      381 ArgLeuProGlnArgGlyTTPGlnMetArgProLeuPheLeuGlnLeuGlyAsnHis 400
DB      |||||
DB      1196 CGCTTCGCCAGGCGTACTGCGAAATGGCGCGCTTCTGTGAGACTGCTTGGAAACCC 1255
QY      401 AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr 420
DB      |||||
DB      1256 GCGCAGTGGCCCTTACCGGGGTGTCTCTCAAGAGCACTGCGCGCTGTGAGACTCGGTACC 1315
QY      421 ProAlaAlaGlyValCysAlaArgGlyLysProGlnGlySerValAlaAlaProGluGln 440
DB      |||||
DB      1316 CAGCAGCGCGGTGTCTGTGCGGGAGAGCCCGAGGCTGTGTGGCGCGCGCGCGGAG 1375
QY      441 GlnAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTyrGln 460
DB      |||||
DB      1376 GAGGAGACAGACCCCGTGTGCTGTGAGCTGTCTCCGACACAGCAGCGCGCTGGGCG 1435
QY      461 ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTyrGlySer 480
DB      |||||
DB      1436 GTGTACGGCTTGTGTGGGGCTGTGCGCGGCTGTGCGCGCGCGCGCGCGCGCGCGCTC 1495

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481 ArgHisaAngluAArgPheLeuAArgAnthrLyLysPheIleSerLeuGlyLysHis 500
Db AGGCAACAGAACGGCGCTTCTCCAGAACACAGAAAGTTATCTCCCTGGGAAAGCAT 1555
Qy 501 AAlaLysLeuSerLeuGlnGlnLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu 520
Db GCCAAGCTCTCGCTCAGAGAGCTGACGTGGAAGATGAGCGTGGGAGACTGCGCTGGCTG 1615
Qy 521 ArgAspSerProGlyValGlyCysValProAlaAlaGlnHisArgLeuArgGlnGlnIle 540
Db CGCAGAGACCCCGAGGAGTGGCTGTGTCCGGCCGAGACACCGTCTGCGTAGAGAGATC 1675
Qy 541 LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGlnLeuLeuArgSerPhe 560
Db CTGGCAAGTCTCTGCACTGGCTGATGAGTGTCTGCTGCTGCTGCTGCTGCTGCTTTC 1735
Qy 561 PheTyrValThrGlnThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal 580
Db TTTTATGTCACGGAGACCGCTTTCAAAGAACAGGCTTTTCTTCTTCTTCTTCTTCTTCT 1795
Qy 581 TrpSerLysLeuGlnSerIleGlyTleArgGlnHisLeuLysArgValGlnLeuArgGln 600
Db TGGACCAAGTTGCAAGCATTTGAAATCAGACAGCACTTGAAAGAGGTGCGCTGGGAG 1855
Qy 601 LeuSerGlnAlaGlnValArgGlnHisArgGlnAlaArgProAlaLeuLeuThrSerArg 620
Db CTGTGGAAAGCAGAGAGTCCAGGACATCGGGAAGCCAGGCCCGCTGCTGACGTCACGA 1915
Qy 621 LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal 640
Db CTCCCTTCATCCCAAGGCTGACGGGCTGCGGCGCATTTGTGAACATGTGACATACGCGTG 1975
Qy 641 GlnAlaArgThrPheArgArgGlnLysArgAlaGlnArgLeuThrSerArgValLysAla 660
Db GAGGCGAAGACCTTCGCGAGAAAGAGAGCGCGGCTCTCACTCGAGGGGTGAAGGCA 2035
Qy 661 LeuPheSerValLeuAsnTyrGlnArgAlaArgArgProGlyLeuLeuGlnValAspSerVal 680
Db CTGTTCAAGCTCTCACTACACAGCGGCGGCGCGCGCTCTCTGGGCGCTCTCTG 2095
Qy 681 LeuGlyLeuAspAspIleHisArgAlaTyrPargThrPheValLeuArgValArgAlaGln 700
Db CTGGGCTCTGAGCATATCCACAGGCGCTGGCCCACTTCTGCTGCTGCTGCGGCGCCAG 2155
Qy 701 AspProProProGlnLeuTyrPheValLysValAspValThrGlyValArgTrpSerThrIle 720
Db GACCCGCGCGCTGACCTGACTTGTTCAGAGTGTGATGTACGGGCGCGTACACACCATC 2215
Qy 721 ProGlnAspArgLeuThrGlnValIleAlaSerIleIleLysProGlnAsnThrTyrCys 740
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Qy 741 ValArgArgTyrAlaValAlaGlnLysAlaAlaHisArgLysValArgLysAlaPheLys 760
Db GTGGCTCGGTATGCGGTGTCCAGAAAGCGCCGCAATGGGCACTCGGCAAGGCTTCAAG 2335
Qy 761 SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu 780
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Qy 781 GlnGlnThrSerProLeuArgAspAlaValIleGlnGlnSerSerSerLeuAnglu 800
Db CAGGAGACACAGCCCGCTGAGGAGATGCGTCTCATTCGACAGAGCTCTCTCTGAAATGAG 2455
Qy 801 AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisAlaValArgIle 820
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Qy 821 ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu 840
Db AGGGGCAACTCTTACGTCAGTGCAGGGGATCCCGCAGAGGCTTCTTCTTCTTCAAGCTG 2575
Qy 841 LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp 860

2576 CTCTCAGACCTGTGTGATCGGAGCATGAGAAACAAGTGTGGCGGAGTTCGGCGGAGC 2635
Qy 861 GlnLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla 880
Db GGGCTGCTCTCGCGTTGTGTGATGATTTCTTTGTGGACACCTCACCTCAACCCAGCG 2695
Qy 881 LysThrPheLeuArgThrLeuValArgGlyValProGlnTyrGlyCysValValAsnLeu 900
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Qy 901 ArgLysThrValValAsnPheProValGlnAspGlnAlaLeuGlyGlyTThrAlaPheVal 920
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Qy 941 GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe 960
Db GAGGTGCAAGGAGCTTACTTCCAGCTATGCGCGAGCTTCCATAGAGCCAGTCTACCTTC 2935
Qy 961 AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu 980
Db AACCGGCGCTTCAAGGCTGGAGAGAAATGCGTCCCAAACTTTGGGGCTTTGGCGGCTG 2995
Qy 981 LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn 1000
Db AAGTGTCAAGCTCTTCTTCTGTGATTTGACAGGTGAACAGCTTCCACACCGTGTGCAC 3055
Qy 1001 IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro 1020
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Qy 1021 PheHisGlnGlnValTrpLysAspProThrPhePheLeuArgValIleSerAspThrAla 1040
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AAH45901
ID AAH45901 standard; DNA; 4015 BP.
XX AAH45901;
AC
XX
XX
DT 06-SEP-2001 (first entry)
XX
XX
DE Human hTERT gene.
XX Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;
KW detection; beta-region; diagnosis; cancer; ds.
XX
OS Homo sapiens.

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XX Key Location/Qualifiers
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FT /number= 16
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XX 20-JUN-2001.
PD 15-DEC-2000; 2000EP-00127228.
XX 16-DEC-1999; 99US-00465491.
XX (HOF ) HOFFMANN LA ROCHE & CO AG F.
XX Chang SP, Santini CD;
XX WPI; 2001-376930/40.
DR Quantitating expression of mRNA encoding hTERT, the catalytic subunit of
PT telomerase, as an indicator of cancer, by amplifying RNA using primers
PT complementary to hTERT gene sequence and quantitating amplified products.
XX Claim 1; Page 5-7; 29pp; English.
XX
XX The present sequence is that of the hTERT gene encoding the catalytic
CC subunit of the human telomerase, comprising 16 exons, which is useful in
CC a method for quantitating hTERT mRNA. The method is useful for detecting
CC the presence of beta-region (a 182 nucleotide region consisting of exons
CC 7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis
CC of cancer. The method provides an accurate measure of telomerase activity
CC by selectively measuring mRNA that encodes an active hTERT protein
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XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
SQ
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 81 ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaValAsnValLeuAlaPheGly 100
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QY 201 ArgAlaTyrPheAsnHisSerValArgGlyValArgGlyValProLeuGlyLeuProAlaProGly 220
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Search completed: October 28, 2004, 13:10:02

Job time : 1416 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2004, 10:29:52 : Search time 11545 Seconds

(without alignments)
12672.631 Million cell updates/sec

Title: US-10-044-692-1

Perfect score: 4015

Sequence: 1 GCACGCGCTCCCTCCCTGC.....TTTTTCACTTTGAAAAA 4015

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1308.6	32.6	1584	9	AY407350 Pan trogl
3	911.4	22.7	1835	9	AY407351 Mus muscu
4	806	20.1	925	4	BM453198 AGEMCOURT
5	500.2	12.5	851	5	BU702370 UI-M-FIO-
6	465.4	11.6	468	2	AM270031 x57603. x
7	445	11.1	492	4	BM824748 K-EST0036
8	419	10.4	851	4	BG917907 602820830
9	416	10.4	416	2	AA281296 x11012. x
10	385.8	9.6	389	1	AA281296 z10802. x
11	381.4	9.5	408	7	CN274427 170005313
12	346.2	8.6	689	7	CN274427 170005313
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18	284.4	7.1	315	1	AA748707 6012805.8
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20	252.2	6.3	715	2	BE36925 601250610
21	249.6	6.2	409	1	AA311750 EST182469
22	243.2	6.1	649	2	BE36606 601289077
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ALIGNMENTS

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DEFINITION	Homo sapiens TERT gene, VIRTUAL TRANSCRIPT, partial sequence,				
ACCESSION	AY407349				
VERSION	AY407349.1	GI:39763320			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1826)				
AUTHORS	Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1826)				
AUTHORS	Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.				
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ORIGIN					
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Best Local Similarity	86.7%	Pred. No. 0:			
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 Db 61 TGCAGTGGCTGATGATGATGTGTAGTGTGAGTGTGCTCAGTCTTTCTTTATGATGACGG 120
 QY 1749 AGACCAAGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAGCAAGTTGC 1808
 Db 121 AGACCAAGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAGCAAGTTGC 180
 QY 1809 AAGGATTTGGAATCAGACAGACATTTGAAGAAGGTGCACTGCGGAGAGCTGTGGAAAGCAG 1868
 Db 181 AAGGATTTGGAATCAGACAGACATTTGAAGAAGGTGCACTGCGGAGAGCTGTGGAAAGCAG 240
 QY 1869 AGGTGAGGAGCATGCGGGAAGCCAGGCGCGCCCTGCTGACAGTCCAGACTCCGTTATCC 1928
 Db 241 AGGTGAGGAGCATGCGGGAAGCCAGGCGCGCCCTGCTGACAGTCCAGACTCCGTTATCC 300
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 Db 301 CCAAGCTTGAACGGGCTGCGGCGCGATTTGTGAACATGGAATCAGTGTGGAGCCAGAACGT 360
 QY 1989 TCCGCAAGAAAAAGAGAGGCGGAGCGTCTCAGCTCGAGGTTGAAGGCACTGTTCAAGCTGC 2048
 Db 361 TCCGCAAGAAAAAGAGAGGCGGAGCGTCTCAGCTCGAGGTTGAAGGCACTGTTCAAGCTGC 420
 QY 2049 TCAACTACGAGCGGCGGCGCGCGCGCTCTGAGGCGCTGTGTGCTGGGCGTGGAGC 2108
 Db 421 TCAACTACGAGCGGCGGCGCGCGCGCTCTGAGGCGCTGTGTGCTGGGCGTGGAGC 480
 QY 2109 ATATCCACAGAGGCTTGGCGCACCTTCTGTGCTGCGGTCGCGGCCAGAGCCCGCGCTG 2168
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 Db 661 NNN 720
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 Db 721 CCTTGCACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCACTCGAGAGACAGAGCC 780
 QY 2409 CGCTGAGGATGCGCTGCTCATCGACAGAGTCTCTCCTGAATGAGGCGAGCATGAGCC 2468
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 QY 2469 TCTTCAAGCTCTTCAAGCTTCATGTGCCACAGCCGCTGGCATCAGGGGCAAGTCT 2528
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 Db 1021 GTTTGTGATGATTTTCTTGTGTGTGACACCTCACTCAACCAACCGGAAACCTTCTCA 1080
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 Db 1081 GGACCCCTGATCGAGAGGTCCCTGAGTATGAGTGTGCTGTGTGAACCTTGCAGAAAGCAGTGG 1140

QY 2769 TGAACCTCCCTGTGAGAGAGCAGAGCCCTGGGAGGCAAGGCTTTTGTGATGCGCGGCC 2828
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 AY407350 1584 bp DNA linear GSS 15-DEC-2003
 LOCUS Pan troglodytes TERT gene, VIRUTAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY407350
 VERSION AY407350.1 GI:39763321
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 REFERENCE
 AUTHORS Clark A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.V., Shtinsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1584)
 AUTHORS Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 source
 gene
 ORIGIN
 Query Match
 Best Local Similarity
 Matches 1188; Conservative 0; Mismatches 618; Indels 9; Gaps 3;

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.D.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302
 2 (bases 1 to 1835)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.D.,
 Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 Location/Qualifiers
 1. 1835
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 <1. >1835
 /gene="TERT"
 /locus_tag="HCM2861"

22.7%; Score 911.4; DB 9; Length 1835;
 64.7%; Pred. No. 1.8e-179;
 0; Mismatches 618; Indels 9; Gaps 3;

1629 GGGTGGCTGTGTCCGCGCGAGACCGCTGCGTGAAGAGATCTGGCCAAATTC 1688
 1 GGAAGACCGTGTCCCGCTGCGAGACCGCTGAGAGAGAGATCTGGCTTC 60
 1689 TGCACTGGCTGATGAGTGTACGTGCTGAGCTGCTCTTTTATGTCACGG 1748
 61 TGTTCTGGCTGATGAGACACATACGTGGTACAGCTGCTTAGCTATTCTTTAATCATCAG 120
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 481 GACATCTACAGAGCTGCGGCGGCTTGTGCTGCTGCTGCTGCTGAGCAACAGCC 540
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 541 AGGATGTACTTTGTAAAGNN 600
 2228 CTCAGAGGATCATCGCAGATCATCAACCCAGAAACAGTACTGTGCTGCTGCTAT 2287
 601 NNN 660

2288 GCCGTGTCAGAAAGCCGCCCATGGGACGTCGCAAGGCTTCAAGAGCCAGCTCT 2347
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 3240 CCGGCGCTGCTGAGGAGGAGAACTGCTGCAAACTTTTGGGCTTCTGCGGCTGAGTGT 3299
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 3300 TGAAGTGAAGGAGGAGAACTGCTGCAAACTTTTGGGCTTCTGCGGCTGAGTGT 3359
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DB 1741 TGCTGGCCGGAAGCTCCCGAGGGGAGCAATGACATCTTAAGCTGAGCGACCCAG 1800
QY 3420 CACTGCGCTCAAGCTTCAAGACCATCTCTGACTGA 3454
DB 1801 CCTAAGCAGACATTTTCAACCATTTTGGACTAA 1835

RESULT 4
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LOCUS BM453198 925 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6387556 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5529840
5', mRNA sequence.
ACCESSION BM453198
VERSION BM453198.1 GI:18502238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 925)
NIH-MGC http://mgi.mgi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaab-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM12208 row: P column: 01
High quality sequence step: 646.
Location/Qualifiers
1. 925
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/clone_id="NIH_MGC_71"
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Average insert size 2.1 kb."

ORIGIN
Query Match 20.1%; Score 806; DB 4; Length 925;
Best Local Similarity 99.2%; Pred. No. 1.7e-157;
Matches 821; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
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DB 2 GGGCCGAGACCGCCCTGAGCTGACTTGTTCAGAGTGTGATGACGGGCGGTACGA 61
QY 2209 CACCATCCCCCAGAGACGCTCAAGAGTGCATGCGCAGCATCATCAAAACCCAGAAC 2268
DB 62 CACCATTTCCCAAGACGAGCTCAAGAGTGCATGCGCAGCATCATCAAAACCCAGAAC 121
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DB 182 CTTCAAGAGCAGAGTCTTACCTTGAAGAGCTCCAGCCGTACATCGACAGTTCGTGGC 241
QY 2389 TCACCTGAGAGAGACGAGCCCGCTGAAGGATGCGGTGTCATGAGCAGAGCTCTCCCT 2448
DB 242 TCACCTGAGAGAGACGAGCCCGCTGAAGGATGCGGTGTCATGAGCAGAGCTCTCCCT 301

QY 2449 GAATGAGGCGAGCAGTGGGCTCTTGAAGCTCTTCTTACGCTTCATGTGACACCGCGT 2508
DB 302 GAATGAGGCGAGCAGTGGGCTCTTGAAGCTCTTCTTACGCTTCATGTGACACCGCGT 361
QY 2509 GGGCATGAGGGGCAAGTCTTACAGTGCAGGAGGAGATCCCGAGGCTCATCTCTTC 2568
DB 362 GGGCATGAGGGGCAAGTCTTACAGTGCAGGAGGAGATCCCGAGGCTCATCTCTTC 421
QY 2569 CAGCTGCTCTGACACCTGTGTAGCGGAGCATGAGAACAGCTGTTGGGGGATTCG 2628
DB 422 CAGCTGCTCTGACACCTGTGTAGCGGAGCATGAGAACAGCTGTTGGGGGATTCG 481
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DB 482 GCGGAGCGGAGCTCTCTGCTGTTGGTGTGATATTTCTTGTGTGACACCTACCTCAG 541
QY 2689 CCAGCGGAAACCTTCTCAGAGACCTGTGTCGAGGTGCTCTGATGATGCTGCTGT 2748
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DB 662 TTTTGTGATGATGCGGCGCCAGGCTATTCCTCTGTGTCGAGCTGCTGATACCGG 721
QY 2869 GACCTGTGAGTGCAGAGAGTACTTCCAGTATCCCGAGCTTCATGAGCCAGTCT 2928
DB 722 GACCTGTGAGTGCAGAGAGTACTTCCAGTATCCCGAGCTTCATGAGCCAGTCT 781
QY 2929 CACCTTCAACCGCGCTTCAA--GGCTGAGAGAACATGCTCGGAAA 2974
DB 782 CACCTTCAACCGCGCTTCAAAGGCTGAGAGAACATGCTCGGAAA 829

RESULT 5
BU702370
LOCUS BU702370 851 bp mRNA linear EST 15-JUL-2003
DEFINITION UI-M-F10-byx-f-12-0-ui.r1 NIH_BMAP_F10 Mus musculus cDNA clone
IMAGE:6400523 5', mRNA sequence.
ACCESSION BU702370
VERSION BU702370.1 GI:23627105
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 851)
NIH-MGC http://mgi.mgi.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaab-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lih, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyx-5.
Location/Qualifiers
1. 851
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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 QY 3843 GTGAGAACCCCTGAGAAAGAACCCCTGAGAGCTCTGAGAAATTTGAGTACCAAGAGTGTGCC 3902
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 QY 3903 CTGTACACAGCGGAGAGAACCCCTGAGAGCTCTGAGAGTGTGCCCTGTGAGTCAATTTGGGAGGA 3962
 Db 108 CTGTACACAGCGGAGAGAACCCCTGAGAGCTCTGAGAGTGTGCCCTGTGAGTCAATTTGGGAGGA 49
 QY 3963 GGTGCTGTGGAGTAAATACTGAAATATGATTTTTCAGTTTGA 4010
 Db 48 GGTGCTGTGGAGTAAATACTGAAATATGATTTTTCAGTTTGA 1

RESULT 7

LOCUS BM824748 492 bp mRNA linear EST 06-MAR-2002
 DEFINITION K-EST0096335 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-99-E07
 5', mRNA sequence.
 ACCESSION BM824748
 VERSION BM824748.1 GI:19181161
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 492)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, Y.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 COMMENT Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 99 row: E column: 07
 High quality sequence stop: 492.
 Location/Qualifiers
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 /sex="F"
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 /cell_type="Lymphoblast-like"
 /cell_line="SNU-16"
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 /clone_lib="S22SNUI6n1"
 /note="Organ: Stomach; Vector: pT713-Pac; Site 1: EcorI;
 Site 2: NotI; The S22SNUI6 library was constructed as described by
 Soares laboratory and it was constructed as described by
 Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
 Research 6(9): 791-806. RNA was prepared from harvested
 cells of SNU-16 culture. SNU-16 cell was obtained from
 Korean Cell Line Bank (KCLB). SNU-16 cell was established from
 ascitic fluids of Korean patients by Park J.G. et al.
 (1990), Cancer Res 50: 2773-2780."

FEATURES

source

1..181
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 /clone="IMAGE:4949887"
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 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI_COAP_Mam6"

ORIGIN

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 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 CACGGCTATATTCCTCTGTGGCGGCTGTCTGTATATCCCGAGACCTGGAGGTGACAGC 120
 QY 2888 GACTACTCCAGCTATAGCCCGGACCTTCATCAGAGCCAGTCTTCACTTCAACCGCGCTTC 2947
 Db 121 GACTACTCCAGCTATAGCCCGGACCTTCATCAGAGCCAGTCTTCACTTCAACCGCGCTTC 180
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 Db 361 GTTGGAAAGACCCCAATTTTCTGCGCGTCACTGTGACACGCGCTCCCTCTGTAC 420
 QY 3188 TCCATCTGAAAGCCAGAACGACGAG 3212
 Db 421 TCCATCTGAAAGCCAGAACGACGAG 445

RESULT 8

LOCUS BG917907 851 bp mRNA linear EST 05-JUN-2001
 DEFINITION 602820830F1 NCI_COAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
 mRNA sequence.

ACCESSION BG917907
 VERSION BG917907.1 GI:14298383
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 851)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10903 row: K column: 08
 High quality sequence stop: 753.
 Location/Qualifiers
 1..851

FEATURES

source

1..851
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4949887"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI_COAP_Mam6"

ORIGIN

/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

Query Match 10.4%; Score 419; DB 4; Length 851;
Best Local Similarity 71.9%; Pred. No. 1.1e-76;
Matches 579; Conservative 0; Mismatches 215; Indels 11; Gaps 2;

2651 TTGGTGAATGATTTCTTGTGTGACACCTCACCTGACCCGCAAACTTCTCTCAG 2710
38 TTGTGATGATCTTCTGTAGTGAAGCCCTCATCTTGACCAAGCAAACTCTCTCAG 97
2711 ACCCTGATCGAGAGTCTCTGTATGATGCTGCTGTGAACCTTGGGGAAGCAGTG 2770
98 ACCCTGATCGAGAGTCTCTGTATGATGCTGCTGTGAACCTTGGGGAAGCAGTG 157
2771 AACCTCCCTAGAGAGCAGGCGCTGGTGACAGCTTTTGTTCAGATGCGGCGCCAC 2830
158 AACCTCCCTAGAGAGCTGTACCTGGTGGTGACAGCTTCATACAGCTGCTGTAC 217
2831 GAGCTATTTCCCTGTGCGGCTGTGCTGATACCCGACCTGAGAGTGACAGCAG 2890
218 TGCTGTTTCCCTGTGCTGTGCTGTGACACCTGAGAGGTCTGTGAC 277
2891 TACTCCAGCTATGCGGAGCTCCATCAGAGCAGTCTCACTTCAACCGGCTTCAAG 2950
278 TACTCAGATGATGCGGAGCTCCATCAGAGCAGTCTCACTTCAACCGGCTTCAAG 337
2951 GCTGGAGAGAAATGCTGCGCAAACTTTTGGGCTTTTGGGCTGAAAGTGTACAGCT 3010
338 GCTGGAGAGAAATGCTGCGCAAACTTTTGGGCTTTTGGGCTGAAAGTGTACAGCT 397
3011 TTTCTGATTTGAGTGAAGAGCTTCCAGAGCTGTGACCAATCTTCAAGATCTTC 3070
398 TTTCTGATTTGAGTGAAGAGCTTCCAGAGCTGTGACCAATCTTCAAGATCTTC 457
3071 CTGCTGAGAGGCTACAGTGTGACAGTGTGCTGAGCTCCATTTCAAGCAAGTT 3130
458 CTGCTGAGAGGCTACAGTGTGACAGTGTGCTGAGCTCCATTTCAAGCAAGTT 517
3131 TGAAGAAGCCCAATTTTCTGCGGCTATCTTGAACAAGGCTTCTGTCTACTCC 3190
518 AGGAAGAAGCCCAATTTTCTGCGGCTATCTTGAACAAGGCTTCTGTCTACTCC 577
3191 ATCTGTAAGAGCAAGAGGATGCTGCTGGGAGGCAAGGAGCGCGGCTCTG 3250
578 ATCTGTAAGAGCAAGAGGATGCTGCTGGGAGGCAAGGAGCGCGGCTCTG 627
3251 CCCTCCGAGCGGCTGAGTGTGACCAAGCAATTTCTT-GCTCAAGCTGACTGACA 3309
628 TCCTCTGAGAGCGAGCTGTGCTGCTGACAGGCTTCTGAGCTCAAGCTGTGCTCA 687
3310 CCGTGTGACAGTGTGACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3369
688 TTCTGTATCTCAAAATGCTCTCTGAGAGCTCTGAGAGCAGCCCAAAACCGCTGTGCG 747
3370 GAAAGTCCCGGAGAGAGCTGAGTGTGCTGAGAGCGGAGAGAGAGAGAGAGAG 3429
748 GAAAGTCCCGGAGAGAGCTGAGTGTGCTGAGAGCGGAGAGAGAGAGAGAGAG 807
3430 AGACTTCAAGAGCAATCTGAGTGA 3454
808 AGACTTCAAGAGCAATCTGAGTGA 832

RESULT 9
AM276315 416 bp mRNA linear EST 03-JAN-2000
LOCUS x10b12.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3',
DEFINITION mRNA sequence.
ACCESSION AM276315

VERSION AM276315.1 GI:5663345
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 416)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -40up from Gibco
High quality sequence stop: 413.
Location/Qualifiers
1. 416
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2759711"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/clone_1b="NCI_CGAP_Lu28"
/note="Organ: lung; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."

FEATURES

source

ORIGIN

Query Match 10.4%; Score 416; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3594 AGGCTGCAATGTCGCGGAGAGCTGAGTGTGAGGCTGAGAGAGTGTCCAGC 3653
416 AGGCTGCAATGTCGCGGAGAGCTGAGTGTGAGGCTGAGAGAGTGTCCAGC 357
3654 AAGGCTGAGTGTCCAGACACCTGCGCTTCACTTCCCAAGAGCTGCGCTC 3713
356 AAGGCTGAGTGTCCAGACACCTGCGCTTCACTTCCCAAGAGCTGCGCTC 297
3714 CACCCAGAGGAGCTTTTCTGACAGAGAGCGGCTTCCACTCCCAATAGAGATG 3773
296 CACCCAGAGGAGCTTTTCTGACAGAGAGCGGCTTCCACTCCCAATAGAGATG 237
3774 TCCATCCCAAGATGTCGCAATGTTCAACCCCTGCGCTGCTTGTGCTTCAACCC 3833
236 TCCATCCCAAGATGTCGCAATGTTCAACCCCTGCGCTGCTTGTGCTTCAACCC 177
3834 ACCATCAGATGAGAGCCTTGAGAGAGCCTTGAGAGCTTGTGAGATTTGAGTCAA 3893
176 ACCATCAGATGAGAGCCTTGAGAGAGCCTTGAGAGCTTGTGAGATTTGAGTCAA 117
3894 AGGTGTCCTGTTGACAGAGAGAGCCTTGACCTGATGAGAGAGAGAGAGAGAG 3953
116 AGGTGTCCTGTTGACAGAGAGAGCCTTGACCTGATGAGAGAGAGAGAGAGAG 57
3954 TTGGGAGAGAGTGTGAGAGATTAATCTGAATATAGATTTTCAATTGTA 4009
56 TTGGGAGAGAGTGTGAGAGATTAATCTGAATATAGATTTTCAATTGTA 1

RESULT 10
AA281296 389 bp mRNA linear EST 14-AUG-1997
LOCUS AA281296

DEFINITION	zr08962.1 nci_cgap_gcbl Homo sapiens cDNA clone IMAGE:712562 5', mRNA sequence.
ACCESSION	AA281296
VERSION	AA281296.1
KEYWORDS	GI:1924194
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eumalotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 389)
JOURNAL	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
	Unpublished (1997)
	Contact: Robert Stransberg, Ph.D.
	Email: cgapbs-rc@mail.nih.gov
	This clone is available royalty-free through LML ; contact the
	IMAGE Consortium (info@image.llnl.gov) for further information.
	Insert Length: 2187 Std Error: 0.00
	Seq primer: -28m13 rev2 ET from Amersham
	High quality sequence stop: 385.
FEATURES	
source	1..389 Location/Qualifiers

ORIGIN

	Query Match Best Local Similarity	9.6%; 99.5%;	Score 385.8; Pred. No. 8.3e-70;	DB 1;	Length 389;	
	Matches 387;	Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1679	GCCAAAGTTCCTGCACACTGGCTGATGATGTGTGTAACGTGCTGAGACTGCTCAGGCTCTTTCTTT	1738			
Db	1	GCCAAAGTTCCTGCACACTGGCTGATGATGTGTGTAACGTGCTGAGACTGCTCAGGCTCTTTCTTT	60			
Qy	1739	TATGTACGAGAGACCAGCTTTCAAAAAGAACAGGCTCTTTTTCCTACGGAAGTGTCTGG	1798			
Db	61	TATGTACGAGAGACCAGCTTTCAAAAAGAACAGGCTCTTTTTCCTACGGAAGTGTCTGG	120			
Qy	1799	AGCAAGTTGGCAAAGCATTTGGAATCGACAGACATCTTGAAGAGGTGCACTCCGGACGTC	1858			
Db	121	AGCAAGTTGGCAAAGCATTTGGAATCGACAGACATCTTGAAGAGGTGCACTCCGGACGTC	180			
Qy	1859	TCGGAAGCAGAGAGTCAGGCAGCATCGGGAAGCCAGGCCCGCTGCTGACATCCAGATC	1918			
Db	181	TCGGAAGCAGAGAGTCAGGCAGCATCGGGAAGCCAGGCCCGCTGCTGACATCCAGATC	240			
Qy	1919	CGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTACGTGCTGGGA	1978			
Db	241	CGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTACGTGCTGGGA	300			
Qy	1979	GCCAAAGCGTTCGGAGAGAAAAGAGGGCCGAGCGCTCCACTCGAAGGTTAAAGCACTG	2038			
Db	301	GCCAAAGCGTTCGGAGAGAAAAGAGGGCCGAGCGCTCCACTCGAAGGTTAAAGCACTG	360			

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Oy      2039  TTCAGCGTGCTCACTACGAGCGGGCCGC 2067
Db      361  TTCAGCGTGCTCACTACGAGCGGGCCGC 389

RESULT 11
CN274427
LOCUS      170005311226763 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN274427
ACCESSION  CN274427.1 GI:47290841
VERSION    EST.
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 409)
AUTHORS   Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
            Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
            Lebkowski, J and Stanton, L.W.
TITLE      Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
JOURNAL    Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT    Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
FEATURES   Insert length: 409 Std Error: 0.00.
            Location/Qualifiers
SOURCE     1..409

```

ORIGIN

Query Match	Best Local Match	Similarity	9.5%: Score 381.4; DB 7; Length 409;
Matches	382; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
QY	1	GCAGCGCTCGCTCTTCGTCGCGACAGTGGAGAACCCCTGAGCCCCCGGCACACCCCGCGATGCC	60
Db	27	GCAGGCGTGGCTCTCGTCGCGCACGTGGAGAACCTTGAGCCCCCGGCACACCCCGCGATGCC	86
QY	61	GCGGGCTTCCCCGCTGCGCGCGAGGCGCTGCGCTCTCTCTCTGCGACAGCCACTTACCGCGAGTGCCT	120
Db	87	GCGGGCTTCCCCGCTGCGCGCGAGGCGCTGCGCTCTCTCTGCGACAGCCACTACCGCGAGTGCCT	146
QY	121	GCCGCTGGCGCACTTTCGTCGCGCGCGCCCGAGGCGTGGCGGCGCTGTCGTCGACAGCGCGG	180
Db	147	GCCGCTGGCGCACTTTCGTCGCGCGCGCCCGAGGCGTGGCGGCGCTGTCGTCGACAGCGCGG	206
QY	181	GGACCCCGCGGCTTTCGCGCGCGCTGTCGCGCCAGTGCCTGTCGTGCTGCTGCGCTTGGAGAGC	240
Db	207	GGACCCCGCGGCTTTCGCGCGCGCTGTCGCGCCAGTGCCTGTCGTGTCGTGCGCTTGGAGAGC	266
QY	241	ACGGTCGCGCCCCCGCGCGCGCTCTCTTTCGCGCAGATGTCTCTGACGAGAGGCTGTGTCGC	300
Db	267	ACGGTCGCGCCCCCGCGCGCGCTCTCTTTCGCGCAGATGTCTCTGACGAGAGGCTGTGTCGC	326
QY	301	CCGAGTGTGTCAGAGCTGTGTCGAGCGCGGCGCGCAAGAACGTGCTGCGCTTCGCGCTTCGC	360
Db	327	CCGAGTGTGTCAGAGCTGTGTCGAGCGCGGCGCGCAAGAACGTGCTGCGCTTCGCGCTTCGC	386
QY	361	GCTGCTGGACGGGCGCGCGCGGGG 383	

Db 387 GCTGCTGAGAGGGGCGCGGG 409

|||||

RESULT 12
CF531121 688 bp mRNA linear EST 12-SEP-2003
LOCUS UI-M-FYO-CGP-m-21-0-UI.r1 NIH_BMAP_FYO Mus musculus cDNA clone
DEFINITION IMAGE:30355988 5', mRNA sequence.

ACCESSION CF531121
VERSION CF531121.1 GI:34583085
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 688)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pyx-5.
Location/Qualifiers

1. 688
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355988"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5,dpcc"
/lab_host="DH10B (TI phage resistant)"
/clone_1lb="NIH_BMAP_FYO"
/note="Organ: Brain; Vector: pyx-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 8.6%; Score 346.2; DB 7; Length 688;
Best Local Similarity 73.9%; Pred. No. 1.7e-61;
Matches 438; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 40 CCGGCGACCCCGGAGTGGCGGCGTCCCGGTGGCGAGCGGTGGCTCCCTGTCGCG 99
Db 63 CCGGCGCTTGAGCAAAATGACCCCGGCTCTCTGTTGCCCGCGGTGGCTCTCTGCTGCG 122
QY 100 CAGCGACTACCGGAGGTGTCTGCGCTGGCCACGCTTGCTGCGGCGCTTGCGGCGCCCAAGG 159
Db 123 CAGCGACTACCGGAGGTGTCTGCGCTGGCAACCTTTGTGCGGCGCTTGCGGCGCCCAAGG 182
QY 160 CTGCGCGCTGTGAGCGCGGCGGACCCGCGGCTTTCCGCGCGCTGTGCGCCCAAGTGCCT 219

Db 183 CAGCGCGCTTGAGCAACCCGAGGACCCGAGATCTACCGCACTTTGTTGCCCAATGCTT 242
QY 220 GGTGTGCTGCGCTTGAGGAGACGACGCGCGCCCGCGCTCTCTTTCGCGCAGTGTCTC 279
Db 243 AGTGTGATGACACTGGGGCTCAAGGCTTCACCTGCGGACCTTTCACAGAGTGTCTC 302
QY 280 CTGCGTGAAGAGCTGTGGCGCCGAGTGTCTGACAGGCTGTGCGAGCGCGCGGAGAA 339
Db 303 ATCCCTGAAGAGCTGTGGCGCGAGGTTGTGAGAGTCTGCGAGCCCAAGAGAA 362
QY 340 CGTGTGCTGCTTGGGCTTTGAGCTGTGAGAGGCTTGAAGAGGAGGAGGAGGAGGCTT 399
Db 363 CGTGTGCTGCTTGGGCTTTGAGCTGTGAGAGGCTTGAAGAGGAGGAGGAGGAGGCTT 422
QY 400 CACCAACGAGCTGCGCAGCTACCTGCCCAACAGGTGAACGACGACTGCGGAGGAGCGG 459
Db 423 CACTAGTACCGTGGCGCTAGTACTTGCCCAACACTTTATTGAGACCTTGCGGTGATGG 482
QY 460 GCGGTGGGGGCTGTGCTGCGCGCGCGTGGGCGGACGACTGTGTTACCTGTGGCAGC 519
Db 483 TGCATGAGATGCTACTGTTGAGCGAGTGGCGACGACCTGTGCTGTACCTGTGGCACA 542
QY 520 CTGCGCGCTCTTGTGCTGTGGTGGCTCCGAGCTGGCCTACGAGTGTGGCGCGCGCT 579
Db 543 CTGTGCTCTTATCTTCTGTGTGCGCCCGAGCTGTGCTTACGAGGAGATGGCCANAGC 602
QY 580 GTACCAAGCTCGCGCTGCACTCAGAGCGCGCGCGCCGACACGCTAGTGAC 632
Db 603 GTCTAAACCCCTCATTTCTACTCAGANCTCAGCTTAATTGACTGGGCGC 655

RESULT 13
CF531069 649 bp mRNA linear EST 12-SEP-2003
LOCUS UI-M-FYO-CGP-c-19-0-UI.r1 NIH_BMAP_FYO Mus musculus cDNA clone
DEFINITION IMAGE:30355746 5', mRNA sequence.

ACCESSION CF531069
VERSION CF531069.1 GI:34583033
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 649)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pyx-5.
Location/Qualifiers

1. 649
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355746"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5,dpcc"
/lab_host="DH10B (TI phage resistant)"
/clone_1lb="NIH_BMAP_FYO"
/note="Organ: Brain; Vector: pyx-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose

QY 62 CGCGCTCCCGCTCCGAGCCGCTGCTCTCTGCTGCGAGCCACTACCGCGAGGCTGCT 121
 DB 121 CGCGCTCTCTGCTCCCGCGGCGCTCTCTGCTGCGAGCCGATACCGGAGGCTGCT 180
 QY 122 CGCGCTGCGAGCTGCTGCGGCGCTGCGGCGCCGAGGCTGCGGCTGCTGCGAGCG 181
 DB 181 CGCGCTGCGAGCTGCTGCGGCGCTGCGGCGCCGAGGCTGCGGCTGCTGCGAGCG 240
 QY 182 GACCGCGCGCTTCCGCGGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 241
 DB 241 GACCGCGAGATCTACCGCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 QY 242 CG 301
 DB 301 GACCGCTCCACTCTCCGCACTTCTCTTCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 302 CGAGTCTGCGAGGCTGCTGCGAGCGCGCGCGCGAGAGAGCTGCTGCTGCTGCTGCTGCT 361
 DB 361 AGGCTTGTGAGAGACTCTGCGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 362 CTGCTGAGCGGCG 421
 DB 421 CTGCTTAAACGAGGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
 QY 422 CTGCGCGCAACGCTGAGCCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
 DB 481 TTGCGCAACCTGTTATTTAGAGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 482 CGCGTGGCGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 539
 DB 541 CGAGTGGCGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 598

RESULT 15
 LOCUS BQ258274 664 bp mRNA linear EST 06-MAY-2002
 DEFINITION NISC Kp11904.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone
 IMAGE:5409222, mRNA sequence.
 ACCESSION BQ258274
 VERSION BQ258274.1 GI:20459030
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 664)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 cDNA Library Preparation: J. Baker (Stanford University)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: info@image.llnl.gov
 MGI:1845958
 Plate: L1AM12043 row: N column: 7
 Seg primer: SP6 primer.
 Location/Qualifiers
 1..664
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:5409222"
 /tissue_type="embryo, late gastrula"
 /dev_stage="embryo, 7.5 dpc"
 /lab_host="X11-Blue"

/clone_11b="Baker mouse embryo e7.5"
 /note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned into SalI/NotI sites using the following 5' adaptor: 5'-TGGACCCAGGCTCCG-3'. Size-selected for average insert size 1.8-1.9 Kb. Library constructed by J. Baker (Stanford University)."

Query Match 7.9%; Score 317.8; DB 5; Length 664;
 Best Local Similarity 68.3%; Pred. No. 1.4e-57; Indels 45; Gaps 1;
 Matches 479; Conservative 0; Mismatches 177;

QY 1108 GCCCGACCTGACTGCGCGCTGCGAGGCTGCTGAGAGACATCTTCTGAGTTCCAGGCTG 1167
 DB 9 GCTTAACCTGATGAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 68
 QY 1168 GATGCCAGGAGACTCCCGGAGGTTGCCCCGCTGCCCCAGGGCTATCTGGCAATGCGGCG 1227
 DB 69 GACATCAGAGACCACTTGCAGAGACACACCGCTTATCGGTGATATCTGGCAAGTGGCGC 128
 QY 1228 CCGTCTTTCGAGCTGCTTGGAGACACCGCGAGTCCCTTACGGGAGTCTCTCAAGAC 1287
 DB 129 CCGTCTTTCGAGCTGCTTGGAGACACCGCGAGTCCCTTACGGGAGTCTCTCAAGTTC 188
 QY 1288 GCACTGCGCGCTGCGAGCTGCGAGTCCAGCCAGACCGGCTGCTGCTGCTGCTGCTGCT 1347
 DB 189 ACATTGCAAGTTTCGAG 232
 QY 1348 CCAAGGCTCTGTTGGCGGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1407
 DB 233 -----TGAACACAGAGCCAGCCAGCCAGCTATGATGATTT 263
 QY 1408 GCTCCGCGAGACAGAGCGCCCTGCGAGAGTGTACAGGCTTCTGCGGAGCTGCTGCGCG 1467
 DB 264 GCTCCGCGCTGACAGAGAGTCCCTGCGAGTATATGTTTCTTCCGGGCTGTCTCGGAA 323
 QY 1468 GCTGTGCCCCAGAGGCTTGGGCGCTCCAGGACAAAGAGAGAGAGAGAGAGAGAGAG 1527
 DB 324 GGTGTGTGCTGCTGAGCTCTGGGAGTACAGGACAAATGAGCCGCTCTTTTAAAGACTT 383
 QY 1528 CAAGAAGTTCATCTCCCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1587
 DB 384 AAGAAGTTCATCTCTTGGGAG 443
 QY 1588 GATGAGCTGCGGAG 1647
 DB 444 GATGAG 503
 QY 1648 CGCAGAGACCGTCTGCGAGAGAGATCTTGGCCAAAGTTCTGCACTGGCTGATGAGT 1707
 DB 504 TGCAGAGACACCGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563
 QY 1708 GTACGCTGCGAG 1767
 DB 564 ATACGCTGAG 623
 QY 1768 CAGGCTCTTCTTCTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1808
 DB 624 CAGGCTCTTCTTCTACCGAG 664

FEATURES
 SOURCE
 RESULT 16
 LOCUS AA811084/c 340 bp mRNA linear EST 19-FEB-1998
 DEFINITION OAS5C05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1319048.3',
 mRNA sequence.
 ACCESSION AA811084
 VERSION AA811084.1 GI:2880695
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence 5' GAGAGAGATCTCGAGTTAAATTAAATATATCCCCCCCC 3'.

ORIGIN

Query Match 7.2%; Score 290.8; DB 2; Length 614;
Best Local Similarity 74.7%; Pred. No. 6,2e-50; Mismatches 127; Indels 1; Gaps 1;
Matches 378; Conservative 0;

2 CAGCGCTGCTCTCTGCGCAGTGGAGAGCCCTGCGCCGCGCCGCGATGCCG 61
61 CACCTTGCATCTTGTGTTCCCGCAGCGGAGGCCATCCCGGCTTGAAGCAATAGACC 120
62 CCGGCTCCCGCTGCGCGAGCGCTGCGCTCTCTGCGCAGCCATGACCGGAGTCTG 121
121 CCGGCTCTCTGTTGCCCGCGGCTGCGCTCTCTGCGCAGCCGATACCGGAGGTTGG 180
122 CCGGCTCCCGCTGCGCGAGCGCGCTGCGCGCCCGAGGCGTGGCGTGGAGCGGG 181
181 CCGCTGGCAACTTGTGCGCGCGCTGCGCGCCGAGGCGAGCGCTTGGCAACCGGG 240
182 GACCCGCGCGCTTCCGCGCGCTGCGCGAGTGCCTGCTGCGTGCCTGCGAGCGA 241
241 GACCCGAGATCTACCGCACTTGTGTTGCCAATGCTAGTGTGATGACCTGGGGCTCA 300
242 CCGCGCGCGCGCGCGCGCGCGCTCTCTGCGCGAGTGTCTCTGCGAAGAGCTGGTGGC 301
301 CACCTTCCACTCTGCGCGAGCTTCTTCCACAGGTGTCTCTGAAAGAGCTGGTGGC 360
302 CGAGTGTGAGAGGCGTGGCGAGCGCGCGCGAGAGAGTGTGCGCTTGGCTTGGCG 361
361 AGGATGTGAGAGACTCTGCGAGCGCAAGAGAGAACTGCTGCTTGGCTTGGAG 420
362 CTGCTGACCGGCGCGCGCGCGCGCGCGCGCGAGGCTTCAACAACCGTGGCGAGTAC 421
421 CTGCTTAAAGAGGCGAAGGCGGGGCTCCGATGGCTTCACTAGTAGCGTGGAGTAC 480
422 CTGCTGACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGGC 481
481 TTGCGCCAACTGTATTTAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
482 CCGGT-GGGGAGAGCGTGGTTC 506
541 CGAGTGGGCGAGCACTGCTGGTTC 566

RESULT 18
AA748707/c 315 bp mRNA linear EST 18-FEB-1998
LOCUS
DEFINITION
AA748707 315 bp mRNA linear EST 18-FEB-1998
VERSION
AA748707.1 GI:2788665
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lemmon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrr/image/image.html
Insert Length: 1226 Std Error: 0.00
Seq primer: -40m13 fwd. Et from Amersham
High quality sequence stop: 281.

FEATURES

source

1..315
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1270592"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pUT73D-Pac (pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTACCATCTGAAGTGGAGAGCGCGCGCTCTTTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pUT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 7.1%; Score 284.4; DB 1; Length 315;
Best Local Similarity 96.2%; Pred. No. 1.2e-48;
Matches 302; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

3703 GGGCTGGCTCCACCCCGAGCGAGCTTTCTCAACGAGAGCGGGCTTCACCTCCCA 3762
314 GGGCTGGCTCCACCCCGAGCGAGCTTTCTCAACGAGAGCGGGCTTCACCTCCCA 255
3763 CATAGGATATGTCATCTCCAGATTCGCAATTTTCACCTCTGCGCTGCTCTTGGC 3822
254 CATAGGATATGTCATCTCCAGATTCGCAATTTTCACCTCTGCGCTGCTCTTGGC 195
3823 CTTC-ACCCCAACCATTCAGGTGAGAGCTTGAAGAGACCTTGGAGCTTGGAAAT 3881
194 GGGCGGGGCGCACCATTCAGGTGAGAGCTTGAAGAGACCTTGGAGCTTGGAAAT 135
3882 TGAGATGACCAAGATGTCCTCTGACAGAGCGAGGACCTTGCACCTGGATGGGGTCC 3941
134 TGAGATGACCAAGATGTCCTCTGACAGAGCGAGGACCTTGCACCTGGATGGGGTCC 75
3942 CTGTGGGTCAAAATTGGGGGAGAGTGTCTGAGAGTAAATAGATATATGATTTTC 4001
74 CTGTGGGTCAAAATTGGGGGAGAGTGTCTGAGAGTAAATAGATATATGATTTTC 15
4002 AGTTTGAAGAAAAA 4015
14 AGTTTGAAGAAAAA 1

RESULT 19
BE371943 866 bp mRNA linear EST 21-JUL-2000
LOCUS
DEFINITION
BE371943 866 bp mRNA linear EST 21-JUL-2000
VERSION
BE371943.1 GI:9317215
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 866)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLM8748 row: h column: 07
 High quality sequence stop: 639.

FEATURES

Source

1. 866
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH 11"
 /db_xref="taxon:10090"
 /clone="IMAGE:3586614"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 /lab_host="DH10B"
 /note="Organ: lung; Vector: PCMV-SPORT6; Site: 1: SalI; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 6.7%; Score 267; DB 2; Length 866;
 Best Local Similarity 75.2%; Pred. No. 6.1e-45;

Matches 333; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

2466 GCCTCTGCAGCTCTTCTACGCTTCATGTGCACACCGCGTGCATCAGGGCACT 2525
 2 GCCTGTTGACTTCTTCTGCACTTCGTCGACAGTGTGAAAGATTGGTGAAGT 61
 2526 CCTAGTCCAGTCCAGGGGATCCGAGGCTCCATCTCTCCAGCTGCTTGAAGCC 2585
 62 GGTATACGACAGTCCAGGGCATCCCAAGGCTCCAGCTTATCCCTGCTTGAAGTC 121
 2586 TGTGTCAGGCGACATGAGAAACAAGCTGTTGGGGGATTGGGGGAGCGGCTGCTCC 2645
 122 TGTGTTTGGAGACATGAGAAACAAGCTGTTGGAGTGACAGAGATGGGTGCTTT 181
 2646 TCGCTTGGTGAATGATTTCTTGTGTGACACCTTCACTCCACCCAGCAAAACCTTCC 2705
 182 TACGTTTGTATGACTTCTGTTGTGTGACGCTCACTTGACCAAGCAAAAACCTTCC 241
 2706 TCAGAACCTTGGTCCGAGGTGTCCTGAGTATGCTGCTGTGAACCTTGGAGAACAG 2765
 242 TCAGAACCTTGGTCCGAGGTGTCCTGAGTATGCTGCTGTGAACCTTGGAGAACAG 301
 2766 TGTGTAACCTTCCCTGTAAGAACAGGCGCTGCTGTCGACCGCTTTTGTTCAGATCCCGG 2825
 302 TGTGTAACCTTCCCTGTAAGAACAGGCGCTGCTGTCGACCGCTTTTGTTCAGATCCCGG 361
 2826 CCCACGAGCTATTTCCCTGTCGAGCTGCTGTCGATACCGGACCTTGAAGTGCAGA 2885
 362 CTCACGCTCTGTTTCCCTGTCGAGCTGCTGTCGATACCGGACCTTGAAGTGTCTCT 421
 2886 GCGACTACTCCAGCTATGCGCGG 2908
 422 GTGACTACTCAGGTAAGCAG 444

RESULT 20
 BE396925 715 bp mRNA linear EST 21-JUL-2000
 LOCUS BE396925
 DEFINITION 601290610F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621050 5',
 mRNA sequence.

ACCESSION BE396925
 VERSION BE396925.1 GI:9342290
 KEYWORDS EST

SOURCE

ORGANISM Homo sapiens (human)

REFERENCE

1 (bases 1 to 715)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.
 Unpublished (1999)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLM294 row: c column: 03
 High quality sequence stop: 634.

FEATURES

Source

1. 715
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3621050"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 8"
 /note="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 6.3%; Score 252.2; DB 2; Length 715;
 Best Local Similarity 93.9%; Pred. No. 7.3e-42;

Matches 307; Conservative 0; Mismatches 13; Indels 7; Gaps 4;

1627 AGGGTGTGGCTGTGTTCCGGCCGAGACACCTGCTGCTGAGAGATTCCTGCAAGTT 1686
 372 AGGGTGTGGCTGTGTTCCGGCCGAGACACCTGCTGCTGAGAGATTCCTGCAAGTT 431
 1687 CCTGCACTGCTGATGAGTGTGATGCTGCTGAGCTGCTGAGTCTTCTT-TATGTCA 1745
 432 CCTGCACTGCTGATGAGTGTGATGCTGCTGAGCTGCTGAGTCTTCTT-TATGTCA 491
 1746 CCGAAGCAACGTTTCAAAAGAACAGGCTTTTCTACCCGAAAGTGTCTGAGCACT 1805
 492 CCGAAGCAACGTTTCAAAAGAACAGGCTTTTCTACCCGAAAGTGTCTGAGCACT 551
 1806 TCCTAAGCACTTGTGATTCAGACGCACTTGAAGAGGTGACGTGGGGAGCT-GTTCGAA 1864
 552 TCCTAAGCACTTGTGATTCAGACGCACTTGAAGAGGTGACGTGGGGAGCTGTTCGAA 611
 1865 GCAGAGGTGAGGACAGATCGGG--AAGCAGGCGCGCTGCTGAGAGTCCAGACTCGCT 1922
 612 GCAGAGGTGAGGACAGATCGGGAAAGCCAGGCTTCTGCTGAGTCA--ACTCG 668
 1923 TCATCCCAAGCTGACGGCTGCGG 1949
 669 TTCATCCCAAGCTGAGGGCTGCGG 695

RESULT 21
 AA311750 409 bp mRNA linear EST 19-APR-1997
 LOCUS AA311750
 DEFINITION EST182469 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA

sequence.
 accession AA311750
 version AA311750.1 GI:1964077
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 409)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gooyne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Claydon,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geochagen,N.S., Gluck,A., Gnehm,C.L., Hanna,W.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,D.C., Liu,L.-I., Marmaro,S.M., Merrick,M., Moreno-Balanchues,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uteback,T.R., Weidman,J.F., Li,Y., Bedaric,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.F., Fritze,A., Fischer,C., Haerings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,D., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseeltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl.), 3-174 (1995)
 JOURNAL Nature 377 (6547 Suppl.)
 MEDLINE 96026280
 PUBMED 7566098
 COMMENT Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
 Seq primer: M3 Reverse.
 Location/Qualifiers
 1..409
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):158964"
 /db_xref="taxon:9606"
 /cell_type="T-lymphocyte"
 /clone_lib="Turkat T-cells VI"
 /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"
 ORIGIN
 Query Match 6.2%; Score 249.6; DB 1; Length 409;
 Best Local Similarity 97.7%; Pred. No. 2.3e-41;
 Matches 252; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 2649 GTTTGGTGAATGATTTTGTGTGACACCTCACTCAACGAGGAAACCTTCTCA 2708
 DB 1 GTTTGGTGAATGATTTTGTGTGACACCTCACTCAACGAGGAAACCTTCTCA 60
 QY 2709 GAGACCTGATCCGAGATGTCCTGAGATGAGTGGTGAACCTTCTCA 2768
 DB 61 GAGACCTGATCCGAGATGTCCTGAGATGAGTGGTGAACCTTCTCA 120
 QY 2769 TGAATCTCTGTAAGAGAGAGGCTTGGTGGACGAGCTTTTGTTCAGATGCGGCCC 2828
 DB 121 TGAATCTCTGTAAGAGAGAGGCTTGGTGGACGAGCTTTTGTTCAGATGCGGCCC 180
 QY 2829 AGCGGCTATTCCTCTGATGAGTATACCGGAGCTTGGAGAGTGAAGCG 2888
 DB 181 AGCGGCTATTCCTCTGATGAGTATACCGGAGCTTGGAGAGTGAAGCG 240

QY 2889 ACTAGTCCAGTATGCC 2906
 DB 241 ACTAGTCCAGTATGCC 258
 RESULT 22
 BE396606
 LOCUS
 DEFINITION
 BE396606 679 bp mRNA linear EST 21-JUL-2000
 601289077F1 NIH_MGC_8 Homo sapiens cDNA IMAGE:3619674 5',
 mRNA sequence.
 BE396606
 BE396606.1 GI:9341882
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 679)
 NIH-MGC <http://mgi.mcg.mcg.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LNCM290 row: 1 column: 19
 High quality sequence start: 2
 High quality sequence stop: 656.
 Location/Qualifiers
 1..679
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3619674"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_8"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN
 Query Match 6.2%; Score 248.8; DB 2; Length 679;
 Best Local Similarity 96.8%; Pred. No. 3.7e-41;
 Matches 275; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
 QY 1627 AGGGTGTGCTGTTCCGGCC-GCAGACACCGTGTGCTGAGAGATCTGGCCAGT 1685
 DB 371 AGGGTGTGCTGTTCCGGCCGTGAGACACCGTGTGAGAGATCTGGCCAGT 430
 QY 1686 TCTGTGATG-ECTGATGATGTGATGCTGTGACCTGCTCAAGTCTTTTATGTC 1744
 DB 431 TCTGTGATGCTGTGATGATGTGATGCTGTGACCTGCTCAAGTCTTTTATGTC 490
 QY 1745 ACGGAGACAGCTTTAAAGAAAGAGAGGCTTTTCTACCGAAGAGTGTGAGACAG 1804
 DB 491 ACGGAGACAGCTTTAAAGAAAGAGAGGCTTTTCTACCGAAGAGTGTGAGACAG 550
 QY 1805 TTGCAAGATTTGATGATGACAGACACTTGAAGAGGTGAGTGGAGAGTGTGGA 1864
 DB 551 TTGCAAGATTTGATGATGACAGACACTTGAAGAGGTGAGTGGAGAGTGTGGA 610
 QY 1865 GAGAGGTGAGGAGATGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1908

Db 611 GCAGAGTCAGCAGCATCGGAAAGCCAGCCCGCTGTGACGTC 654

RESULT 23
LOCUS BE514070 649 bp mRNA linear EST 07-AUG-2000
DEFINITION 601316575F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634962 5',
mRNA sequence.
ACCESSION BE514070
VERSION BE514070.1 GI:9721282
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM330 row: f column: 19
High quality sequence stop: 628.
Location/Qualifiers

FEATURES

source
1. 649
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3634962"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 6.1%; Score 243.2; DB 2; Length 649;

Best Local Similarity 98.2%; Pred. No. 5.4e-40; Mismatches 3; Indels 2; Gaps 2;
Matches 267; Conservative 0;

1627 AGGGGTTGGCTGTGTTCCGGCCGAGAGCAGCAGCTGTGCTGAGAGATCTGGCAAGTT 1686
367 AGGGGTTGGCTGTGTTCCGGCCGAGAGCAGCAGCTGTGCTGAGAGATCTGGCAAGTT 426
1687 CCTGC-ACCTGCTGATGAGTGTGTAAGTGTGCTGAGCTGCTCAAGTCTTTTATATGTA 1745
427 CCGCACTGGCTGATGAGTGTGTAAGTGTGCTGAGCTGCTCAAGTCTTTTATATGTA 486
1746 CGGAGACACAGCTTTCAAAAGAACAGGCTCTTTT-CTACCGAAGAGTCTCGAGCAAG 1804
487 CGGAGACACAGCTTTCAAAAGAACAGGCTCTTTTACTACCGAAGAGTCTCGAGCAAG 546
1805 TTGCAAGCATTTGATGATCAGACAGCACTTGAAGAGGTGTCAGCTCGGAGCTGTGGA 1864
547 TTGCAAGCATTTGATGATCAGACAGCACTTGAAGAGGTGTCAGCTCGGAGCTGTGGA 606
1865 GCAAGGTCAGCAGCATCGGAGAGCCAGGCC 1896
607 GCAGAGTCAGCAGCATCGGAGAGCCAGGCC 638

RESULT 24
LOCUS BE514188 610 bp mRNA linear EST 07-AUG-2000
DEFINITION 601316376F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634987 5',
mRNA sequence.
ACCESSION BE514188
VERSION BE514188.1 GI:9721400
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM330 row: g column: 20
High quality sequence stop: 610.
Location/Qualifiers

FEATURES

source
1. 610
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3634987"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 6.1%; Score 243; DB 2; Length 610;

Best Local Similarity 100.0%; Pred. No. 5.9e-40; Mismatches 0; Indels 0; Gaps 0;
Matches 243; Conservative 0;

1627 AGGGGTTGGCTGTGTTCCGGCCGAGAGCAGCAGCTGTGCTGAGAGATCTGGCAAGTT 1686
368 AGGGGTTGGCTGTGTTCCGGCCGAGAGCAGCAGCTGTGCTGAGAGATCTGGCAAGTT 427
1687 CCTGC-ACCTGCTGATGAGTGTGTAAGTGTGCTGAGCTGCTCAAGTCTTTTATATGTA 1746
428 CCGCACTGGCTGATGAGTGTGTAAGTGTGCTGAGCTGCTCAAGTCTTTTATATGTA 487
1747 GGAGACACAGCTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTCTCGAGCAAGTT 1806
488 GGAGACACAGCTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTCTCGAGCAAGTT 547
1807 GCAAGCATTTGATGATCAGACAGCACTTGAAGAGGTGTCAGCTCGGAGCTGTGGA 1866
548 GCAAGCATTTGATGATCAGACAGCACTTGAAGAGGTGTCAGCTCGGAGCTGTGGA 607
1867 AGA 1869
608 AGA 610

RESULT 25
CF531258

LOCUS CF531258 344 bp mRNA linear EST 12-SEP-2003
 DEFINITION UI-M-FY0-cgp-b-01-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 IMAGE:30355848 5', mRNA sequence.
 ACCESSION CF531258
 VERSION CF531258.1 GI:34583222
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 344)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 Email: cgaabs-@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP).
 Seq primer: pyx-5.
 Location/Qualifiers
 1..344
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 /lab_host="DH10B (T1 phage resistant)"
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 /note="Organ: Brain; Vector: pyx-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGACAGC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

FEATURES
 source
 1..344
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30355848"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_1lb="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: pyx-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGACAGC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
 Query Match 5.3%; Score 214; DB 7; Length 344;
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 Matches 262; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
 2765 GTGGTGAATCTCCCTGTGAAGAGAGAGCCCTGGTGTGACGGTTTGTTCAGATGCGG 2824
 1 GTGTGTAACCTCCCTGTGAGAGCTGTACCTGGGTGTGAGTCAATACCAAGTCCCT 60
 2825 GCCACAGGCTAATCCCTGGTGGCGCTGCTGTGATACCGGAGCCTGAGGTGACG 2884
 61 GCTACAGCTGCTTTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
 2885 AGCGACTACTCCAGCTATGCCCGGAGCTTCATCAGAGCCAGTCTACCTTCAACCGCGC 2944
 121 TGTGACTACTCAGGTATGCGCAAGCTCAATTAAGACGAGCCCTCACCTTCCAGAGTGTG 180
 2945 TTGAAGCTGGAGAGACATCCCTCGCAAACTCTTTGGGGCTTGGCGGCTGAAGTGTAC 3004
 181 TTCAAAGCTGGAGAGACATCCCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240

ORIGIN
 Query Match 5.2%; Score 208.6; DB 2; Length 779;
 Best Local Similarity 86.8%; Pred. No. 9.4e-33;
 Matches 289; Conservative 0; Mismatches 34; Indels 10; Gaps 5;
 1627 AGGGCTTGGCTGTGTTCCGGCGGAGAGACCGCTGCTGAGAGATCCTGCGCAAGTT 1686
 365 AGGGCTTGGCTGTGTTCCGGCGGAGAGACCGCTGCTGAGAGATCCTGCGCAAGTT 424
 1687 CTTGCACTGGATGATGATGTGTGATGCTGTGAGTGTCTCAGGTCTTTTATGTGAC 1746
 425 CTTGCACTGGATGATGATGTGTGATGCTGTGAGTGTCTCAGGTCTTTTATGTGAC 484
 1747 GGAGACCACTTTCAAAAGAAAGAGAGCTCTTTTCTACCGGAAAGATGCTT-GAAGCAAGT 1805
 485 GGAGACCACTTTCAAAAGAAAGAGAGCTCTTTTCTACCGGAAAGATGCTTGGAGAGCAAGT 544
 1806 TGCAGACA-TTGGATTCAGACAGCACTT--GAAGAGGGTGC-----AGTCGGGAGAGCT 1857
 545 TGCAGACA-TTGGATTCAGACAGCACTTGGAGAGGGGTGCTCGCTTGGCGGAAACTTG 604

FEATURES
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 /mol_type="mRNA"
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 /clone_1lb="NIH_MGC_8"
 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 Email: cgaabs-@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LHCW132 row: 1 column: 16
 High quality sequence stop: 535.
 Location/Qualifiers
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 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
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 /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Accession	Version	Keywords	Source	Organism
QY1858	1			
D0605	1			
QY1917	1			
D0665	1			

RESULT 27

BY775178

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BY775178 336 bp mRNA linear EST 23-MAR-2004

'BY775178 RIKEN full-length enriched, 17.5 days embryo whole body

Mus musculus cDNA clone L930091N09 5', mRNA sequence.

BY775178

BY775178.1 GI:39701816

EST.

Mus musculus (house mouse)

Mus musculus

REFERENCE	AUTHORS
1 (bases 1 to 336)	Carninci, P., Waki, K., Shitara, T., Konno, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kuwabara, M., Gustinich, S., Beisel, K., Pavan, W., Aldinis, V., Nakagawara, A., Held, W. A., Tate, H., Konno, T., Nakachi, H., Lyons, P., Wells, C., Hume, D. A., Pasjolin, M., Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, Y., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.
TITLE	Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia
JOURNAL	Genome Res. 13 (6B), 1273-1289 (2003)
MEDLINE	22703353
PUBMED	12819125
COMMENT	Contact: Yoshihide Hayashizaki

```

FEATURES
SOURCE

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.jp/) for
further details.

location/Qualifiers
1..336
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Db	2	GCGGACCTTTCTTCCACCAGGTGTCATCCTCGAAAGAGCTGTGTGACCAAGGATTGTGCAG	61		

Accession	Sequence	Position
QY	AGCGCTGTGGAGACGCGGGGCGCGAAGACGTGCTGGCTCTTGCGCTTGCGCTGGACGG	373
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Db	GTTATTGAAACCTCTGCGGTCAAGTGTGTGCAATGATGCTACTGTTGAGGCCGAGTGGCGAC	241
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Db	GCTTACGAGGAGATGGCC	321

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DEFINITION	BY783093 RIKEN full-length enriched, 17.5 days embryo whole body
	Mus musculus cDNA clone U930172A03 5', mRNA sequence.
ACCESSION	BY783093
VERSION	BY783093.1 GI:39709732
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE	AUTHORS
(Pages 1 to 343)	
Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M., Alzawa, K., Aikawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Suganara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watabiki, A., Hirokawa-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Pavan, W., Aidinis, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T., Nakachi, H., Lyons, P., Wells, C., Hume, D. A., Fogliolin, M., Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P., Muramatsu, M., Okazaki, Y., Kawaji, J. and Hayashizaki, Y.	
Targeting a complex transcriptome: the construction of the mouse full-length cDNA encyclopedia	
Genome Res. 13 (6B), 1273-1289 (2003)	
JOURNAL MEDLINE	22703353
PUBMED	12819125
COMMENT	Contact: Yoshinhide Hayashizaki

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.jp/>) for
further details.

Location/Qualifiers
1.343

FEATURES	SOURCE
Location/Qualifiers	
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/mol_type="mRNA"	
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Sulana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wymshew-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komori, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shitagawa, A., Yasunishi, A., Yoshino, M., Waterson, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9232
Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Komori, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN Integrated sequence analysis (RISA) system--384 format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

1..326
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/mol_type="mRNA"
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/tissue_type="whole body"
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/clone_idb="RIKEN full-length enriched, 17.5 days embryo whole body"

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Query Match 4.8%; Score 192.2; DB 5; Length 326;
Best Local Similarity 76.9%; Pred. No. 2.2e-29;
Matches 247; Conservative 0; Mismatches 73; Indels 1; Gaps 1;

254 GCCGCCCTCTCTCGCAGGTGCTCTGCTGAAGAGCTGTGCGCCGAGTGTGAG 313
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Db 2 GCCGACCTTCTCCCTTCACACAGGTGTATCCCTGAAGAAGCTGTGCGAGGTTTGACG 61
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Qy 314 AGGCTGTGAGAGCGCGCGGAGAACTGTGCTGTGCTGTGCGCTGTGAGCGGG 373
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182 TGTATTGAGACCTCGCGTGTGTCAGTGTGTCATGATGTGAGTGTGAGCGGAGCGCA 241
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Db 302 TGCCTACGAGGAGATGCGC 322

RESULT 31
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LOCUS 603767927F1 CSEQRBN14 Gallus gallus cDNA clone Chest696f7 5', mRNA
DEFINITION
ACCESSION BU452535
VERSION BU452535.1 GI:25941846
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 753)

REFERENCE
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., But, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 2235534
PUBMED 12445392

COMMENT

Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers

1..753
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/clone="CHEST696f7"
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/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI. This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996) 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 4.7%; Score 189.2; DB 5; Length 753;
Best Local Similarity 61.2%; Pred. No. 1.1e-28;

Matches 305; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

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 QY 3020 TTGCAGTGAACAGCCTCCAGAGGTGTGCACCAATCTCAAGAATCCCTCTGTCAG 3079
 DB 68 TTAAATATCAACAGCCTTCAAGAGTTCTTAATTAACATCTACAAAGATATTTTACTCAG 127
 QY 3080 GCGTACAGTTTACCGCATGTGTGTGCAGCTCCCATTTTCATCAGCAAGTTTGAAGAAC 3139
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 DB 188 CCGATTTCTCTTGAAGATCATCTGTATACGTCTTCACTGCTATTTTATCTGAAA 247
 QY 3200 GCCAAGAACGACGAGATGTGCTGTGGGGCCAGAGGCGCCGCTCTGCTCCGAG 3259
 DB 248 GCTAAATATCAAGAGATTTCTTTAGTAGCAAAAGATGATCTGTATGTTCCCTTTGAG 307
 QY 3260 GCGGTGAGTGTGTGTGTGCACCAAGATCTTCTGCTCAAGTGAACAGCCTGTACC 3319
 DB 308 GCAGCAGAAATGGGT 367
 QY 3320 TAGTGTCATCTCTGGGGTCACTCAGAGACGCCAGCGAGTGTGGAAGTCCCG 3379
 DB 368 TACAAATGCTTACTTAAGCCCTTAAAGTCTATTAAGTGTATCTGTTGGAAAGATCCA 427
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 QY 3440 ACCATCTGAGCTGATGG 3457
 DB 488 ACTATACTGACTAAGGG 505

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 ACCESSION CR688161.1 GI:51186068
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 SOURCE Tetraodon
 ORGANISM Tetraodon
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae.
 1 (bases 1 to 1424)
 Genoscope.
 AUTHORS Direct Submission
 JOURNAL Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage -
 : 2 rue Gaston Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE.
 COMMENT The sequences are based on single pass reads.
 More information available at
 http://www.genoscope.cns.fr/tetraodon.
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 Matches 377; Conservative 0; Mismatches 272; Indels 7; Gaps 2;

QY 2522 AAGCTCAAGTCCAGTGCAGGGAGATCCGACAGGGCTCATCTCTCCAGCCTGCTG 2581
 DB 150 AAAACATTAAGACAGTGCAGAGAGGGTCTCAGGATGCTGTGTCCAGTGTCTTTC 209
 QY 2582 AGCTGTGCTACGGGACATGGAAGAACAGCTGTTTGGCGGAAATTCGCGGAGAC--GGG 2638
 DB 210 TCCCTCTGTATGCTTATGGAAGACGCTTATTCAGAGCATATTAACAAAGGC 269
 QY 2639 CAGCTCCGCTGGTGGATGATTTCTGTGTGACACCTCACCTGACCCAGGAAA 2698
 DB 270 TCTTTAATAGACTGGTGAATATCTTCTTCAATCACTTCACTGAGCGACAGCAG 329
 QY 2699 ACCCTTCTCAGAACCTGTGTGAGAGTGTCTCTGATATGCTGTGTGAATCTTGGCG 2758
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 QY 2939 CCGGCTTCAAGCTGTGGAAGAACATGCTGCCAACTTTTGGGGTCTTGGGGCTGAAG 2998
 DB 570 CCTGTCACTG 625
 QY 2999 TGTCAAGCTG 3058
 DB 626 TGCCATGCTG 685
 QY 3059 TACAAGATCTCTCTG 3118
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 DB 746 GGTCAAGCTG 801

RESULT 33
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 subunit mRNA, complete cds, mRNA sequence.
 ACCESSION AW244516
 VERSION AW244516.1 GI:8051265
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 347)
 AUTHORS Bain,G., Mansergh,F.C., Wride,M.A., Hance,J.E., Isogawa,A.,
 Rancourt,S.L., Ray,W.J., Yoshimura,Y., Tsuzuki,T., Gottlieb,D.I.
 and Rancourt,D.E.
 COMMENT ES cell neural differentiation reveals a substantial number of
 novel ESTs
 JOURNAL Func. Integr. Genomics 1 (2), 127-139 (2000)
 MEDLINE 21652683
 PUBMED 11793228
 CONTACT: Rancourt DE
 Department of Biochemistry and Molecular Biology
 University of Calgary
 3330 Hospital Drive N.W., Calgary, Alberta, T2N 4N1, Canada
 Tel: 403 220 2888

Fax: 403 283 8727
Email: rancourt@ucalgary.ca; URL: <http://www.acs.ucalgary.ca/>
rancourt

DNA sequencing by: University Core DNA Services, University of Calgary. Submitted sequence has been trimmed at both ends to remove the adaptor oligos containing the EcoRI sites, i.e. GAATTCGACGTA (beginning) and TAGCTCCATTC (end) removed. Therefore, reported insert length is longer than actual EST sequence length.
Insert length: 359 Std Error: 10.00
Seq primer: T3 Or T7.

EcORI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., EMAS (1994) 91: 9228-9232 and Bonaldi et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 4.5%; Score 180.2; DB 5; Length 880;
Best Local Similarity 61.8%; Pred. No. 8.2e-27;
Matches 337; Conservative 0; Mismatches 203; Indels 5; Gaps 3;

2898 GGTATGCGCGAGCTCATGAGCCAGCTCACTTCAACCGCGGCTTCAAGCTGGGA 2957
266 GTTATGCTTCTTCTTATCATGATCAAGTCTTCTTCAATTAAGTAAATAGCTGGGA 325
2958 GGAACATGCTCGCAAACTTTTGGGCTTTGGCGGTGAAGTCAACAGCTTCTTCTGG 3017
326 AAAACATGAATGCAATTAAGTCAAGTCTTCAAACTGAATGCAATCCCTTACTTCTTG 385
3018 ATTGCAAGTGAACAGCTTCAAGCTGTCACCAATCTAAGATCTTCTGCTGC 3077
386 ACTTAAAGATCAACAGCTTCAAGCTTCAATTAAGTCAAGATATTTTACTTTC 445
3078 AGGCGTACAGCTTCAAGCTGTCAGCTCCCATTCATCAAGCTTGAAGA 3137
446 AGGCTTACAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTGAAGA 505
3138 ACCCAATTTTCTGCGGCTATCTGACACAGGCTCTTCTGCTACTCCATCTGA 3197
506 ATCTGATTTCTTCTTCAAGATCATCTGATTAAGTCTGCTATTTATCTGA 565
3198 AAGCAAGAACGAGGATGTCGTCGGGGCCAGAGGCGCGGCTCTGCTCTCG 3257
566 AAGTAAATTAATCAAGGATTTCTTAAAGTAAAGTATGATCTGG-CAATGTTCCCTTTG 624
3258 AGGCGTACAGCTTCAAGCTGTCAGCTTCAAGCTTCAAGCTTGAAGA 3317
625 AGGCAAGAACGAGGATGTCGTCGGGGCCAGAGGCGCGGCTCTGCTCTCG 682
3318 CTAAGTGCACCTCTGCGGCTCACTGACAGAGCC--AGACGAGCTGAAGTGAAGCT 3375
683 GTTATTAATTAATTAAGCTTAAAGCTTAAAGTATGATGATCTGTTGGGAAGAT 742
3376 CCGCGGACGAGCTGATGCTGCGGCGGCGGCGGCGGCGGCTCTGCACTT 3435
743 CCGAGGATTAATTAAGCTTAAAGCTTAAAGTATGATGATCTGTTGGGAAGAT 802
3436 CAGA 3440
803 CAAA 807

RESULT 35
BI388013 775 bp mRNA linear EST 26-AUG-2003
LOCUS BFL26.002716 Amphioxus 26hr cDNA library (Name convention: BFL26 or
DEFINITION MPMG531) Branchiostoma floridae cDNA clone MPMG531A0937 5', mRNA
sequence.
ACCESSION BI388013
VERSION BI388013
KEYWORDS EST.
SOURCE Branchiostoma floridae (Florida lancelet)
ORGANISM Branchiostoma floridae
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
1 (bases 1 to 775)
Panopoulou, G., Hennig, S., Groth, D., Krause, A., Pousetka, A.J.,
Herwig, R., Vingron, M. and Lehrach, H.
New evidence for genome-wide duplications at the origin of
vertebrates using an amphioxus gene set and completed animal
genomes

JOURNAL Genome Res. 13 (6A), 1056-1066 (2003)
MEDLINE 22683279
PubMed 12799346

COMMENT

Contact: Panopoulou G
Laboratory 145, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Institstr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones giving the same hybridisation pattern with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above EST is generated is available at the
amphioxus project site at: <http://www.molgen.mpg.de/amphioxus/>
Clones and filters are distributed via the Resource Center/Primary
Database of the German Genome Project (<http://www.rzpd.de>)
PCR Primers
FORWARD: 5' CCCAGGCTTACACTTATGCTCGGCTCG 3' (M13RSP)
BACKWARD: 5' GCTATACGCGAGCTGCGAAGGAGATG 3' (M13FSP)
Insert length: 1 Std Error: 0.00
Seq primer: 5'-CCGCTCCGGAATCCCGGAT-3' pSPORT3/86
High quality sequence stop: 775.
Location/Qualifiers
1..775
/organism="Branchiostoma floridae"
/mol_type="mRNA"
/db_xref="taxon:7739"
/clone="MPMG531A0937"
/issue_type="whole embryo"
/dev_stage="26 hrs (neurala stage)"
/lab_host="E.coli, XL1 blue"
/clone_lib="Amphioxus 26hr cDNA library (Name convention:
BFL26 or MPMG531)"
/note="Vector: pSPORT1 (Gibco BRL); Site 1: SalI, KpnI,
EcoRI (5'); Site 2: NotI, BamHI, HindIII (3'); OligodT
primed and directionally cloned in pSPORT1 vector using a
NotI (5')-pGACTAGTCTAGATCGCGAGCGGCGGCT (7)15-3' and a
SalI 5'-TCGACCAACGCTGCGG-3' adaptors (Gibco BRL)."

FEATURES

source

ORIGIN

Query Match 4.2%; Score 167.6; DB 4; Length 775;
Best Local Similarity 54.3%; Pred. No. 3.4e-24;
Matches 366; Conservative 0; Mismatches 299; Indels 9; Gaps 1;

2497 CCACACGCGCGGATCAGGGGCAAGTCTACCTGACGAGGAGATCCCGAGGG 2556
17 CGATCAGTGATCCAGATCGGGGGAGCTACTACCGGAGATCAGGGAGATCAGTAGGG 76
2557 CTCATCTCTCCACGCTGCTGACGCTGCTGCTACGCGACATGAGAGAAAGCTGTT 2616
77 ATCTGCTGCTGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 136
2612 TCGGGGATTCGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2676
137 CTGTGGCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
2677 ACCTACCTCAACCCAGGCAAACTTCTCTCAAGACCTGATCCGAGAGTCCCTGAGTA 2736
197 CCACACCTGAGACAGGCTACAGCTTCTCTGATCAAGTGAATGATGATGATGATGATGATGAT 256
2737 TGGCT 2796
257 TGGGTGAGGATTCATCCGAGCAAAATCTGACCAATCTCCGTGTCACACAGAGAAATG 316
2797 GGGTGCACGAGCTTTTGTTCAGATGCGGCGCCAGGCTATTCCTGCTGCTGCTGCTGCT 2856
317 TGTGTGACATG-----CAGCCAGACAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367

QY 2857 GCTGATACCCGGACCGCTGAGTGCAGAGCTACTCCAGTATGCCCGGACCTCCAT 2916
 DB 368 GTTCCACACTCTTCCTGCTATGAGGAGCTATGAGACTACAAATATGACCAACTGCTGAT 427
 QY 2917 CAGAGCCAGCTCTCACCCTTCACACCGCGCTTCAAGGCTGGAGGAAACATGCTGCAAACT 2976
 DB 428 CAGGTACACTTGGACCTTGGACCTCCATGAGACTCCCGGTACAGGCATGAAACAGAGCT 487
 QY 2977 CTTGGGGCTTGGCGCTGAGTGCAGAGCTCTTTCGATTTGAGTTGACGTGAACAGCCT 3036
 DB 488 GATGAACACTGTCAAGGCGCAAGGTGATATCTCTTCTGAGGCCCAAGGTGATTTACAC 547
 QY 3037 CCAGACGGTGTGACCAACATCTCAAGATTCCTCCGCTGACAGGCGGTACAGGTTTACGC 3096
 DB 548 AGCTGTGATTCACAGACTCTCTCAAGAGCATTTCTGTTACAGAGCCACAGTTTCCACAG 607
 QY 3097 ATGTGTGCTGACAGCTCCATTTTCATCAGCAAGTTTGGAGAAACCCCAATTTTCTGCG 3156
 DB 608 CTACAAACGCTGTCTGCTCCATGTCATGTCAGAGGCTCAAGAACCCCTGATTTCTCTAC 667
 QY 3157 CGTCACTCTGACA 3170
 DB 668 AATGATCATGAGACA 681

RESULT 36
 EX886589 703 bp mRNA linear EST 27-JUL-2004
 LOCUS BX886589 tcdk Oncorhynchus mykiss cdna clone tcdk0036c.p.02 5prim,
 DEFINITION mRNA sequence.
 ACCESSION BX886589
 VERSION BX886589.2 GI:42819050
 KEYWORDS
 SOURCE
 ORGANISM
 Oncorhynchus mykiss (rainbow trout)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 703)
 REFERENCE
 Govoroun,M., Guiguen,Y. and Le Gac,F.
 Construction and primary characterization of normalized cDNA
 libraries in rainbow trout, Oncorhynchus mykiss
 Unpublished (2003)
 JOURNAL
 COMMENT
 On Dec 18, 2003 this sequence version replaced gi:40135983.
 Contact: Guiguen Y
 INRA - SCRIBE
 Campus de Beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at sigmasupport@jouy.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0036 row: p column: 2
 Seg primer: M13R

FEATURES
 source
 Location/Qualifiers
 1..703
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="tcdk0036c.p.02"
 /issue_type="multi-issues"
 /dev_stage="from embryos to adults"
 /lab_host="DH10B"
 /lab_lib="tcdk"
 /note="Vector: pTT73D-pac; AGENAE Rainbow trout
 multi-issues - normalized + 2 subtractions; Clone
 distribution: AGENAE Resource centre. Francois PIUMI,
 Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
 Etude du genome (LREO), Domaine de Vilvert, 78352,
 Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
 (0) 1.34.65.22.73"

ORIGIN

Query Match 4.0%; Score 162.4; DB 5; Length 703;
 Best Local Similarity 55.5%; Pred. No. 4,1e-23;
 Matches 333; Conservative 0; Mismatches 266; Indels 1; Gaps 1;

QY 2858 CTGATACCCGGACCGCTGAGTGCAGAGCTACTCCAGTATGCCCGGACCTCCATC 2917
 DB 1 CTGATACACACACCTTGAAGCTTACA-CAACTAGCCAGTACGCTGCTATCCCTG 59
 QY 2918 AGAGCCAGTCTCACTTCAACCGCGCTTCAAGGCTGGAGGAAACATGCTGCAAACTC 2977
 DB 60 CCTACAGCTGACCGCTAGGCTCCGCCCACTGCGCGGGCAGCAATGAGAGAGAGCTC 119
 QY 2978 TTTGGGGCTTGGCGCTGAGTGCAGAGCTCTTTCGATTTGAGTTGACGTGAACAGCCTC 3037
 DB 120 ATGTCCATCTTAAGTTCAAGTGCACAGCGCTCTTCTGAGACTCAAAACCAACTCCCTG 179
 QY 3038 CAGAGGTTGACCAACATCTCAAGATTCCTCTGCTGACAGGCGGTACAGTTCACGCA 3097
 DB 180 GAGGCTGTATAGCAAGCTCTATAAGTTAGTTGCTGCAAGCGTTACAGTTCCATGCC 239
 QY 3098 TGTGTGCTGACAGCTCCCATTTTCATCAGCAAGTTTGGAGAAACCCCAATTTTCTGCGC 3157
 DB 240 TGTGACAGAGTTTGCCTTGTGTCAGAAAGTGGCGGAAACCACTGTAATCTTCCCAAT 299
 QY 3158 GTCACTCTGACACGCGCTCCCTGTGCTACTCATCTGAAAGCCAAAGCGAGGATG 3217
 DB 300 CTGATCTGGAGTCTGCGGAGTACACCAACATCTAGTCACTGCAACAAAGGTGTG 359
 QY 3218 TCGCTGGGGGCAAGGAGGCGCGCCGCTCTGCGCTCCGAGGCGGTGACGTGCTGTC 3277
 DB 360 TCTCTAGGCTGTAAGGCTTAAACAGGTAGCTTCAAGTAAAGGACGTAAACGTGATAC 419
 QY 3278 CACCAAGCATTTCTGCTCAAGCTGACCTGCAACCGTTCACCTGCTGCGG 3337
 DB 420 TGTCTGGCGCTTCTGTTGTTGTTCTGTCCTGCTGATCGCCCTCTACTACATCTCTCGCT 479
 QY 3338 TCACTCAGACAGCCCAAGCGACGCTGAGTCCGAAAGCTCCCGGACAGACGCTGATGCC 3397
 DB 480 CCGCTACGACACGTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 539
 QY 3398 CTGAGAGCGCGACCAACCCGCGACCTCCCTGAGACTTCAAGACCTCTGAGCTGATGG 3457
 DB 540 ATCAGACAGGCTGCCACACCCAAATGCTTGAAGACTTCAAGGCCATCCAGGCTTGAAG 599

RESULT 37
 CK392784 619 bp mRNA linear EST 29-DEC-2003
 LOCUS CK392784
 DEFINITION K0850A03-5 NIA Mouse 8.5-dpc whole Embryo cDNA library (long) Mus
 musculus cdna clone NIA:K0850A03 IMAGE:30083138 5', mRNA sequence.
 ACCESSION CK392784
 VERSION CK392784.1 GI:40383303
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 619)
 REFERENCE
 Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
 Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 Genome Res. 11 (9), 1553-1558 (2001)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: K0850 row: A column: 03

Seq primer: M13 Reverse
High quality sequence stop: 619
POLYA=No.

FEATURES

source

Location/Qualifiers

1. 619

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="NIA:K0850A03 IMAGE:30083138"

/issue_type="whole embryo including extraembryonic

tissues at 8.5-days postcoitum"

/dev_stage="8.5-days postcoitum"

/lab_host="DH10B"

/clone_lib="NIA Mouse 8.5-dpc Whole Embryo cDNA Library

(Long)"

/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:

NotI; Mouse cDNA project by the Laboratory of Genetics,

National Institute on Aging (NIA), Intramural Research

Program, NIH (http://igsn.grc.nia.nih.gov/cDNA). This is

a long-transcript enriched cDNA library (Ref. Genome Res.

11: 1553-1558 (2001). (PMD: 1154191). Total RNAs were

extracted from a pool of 13 embryos at 8.5-days

postcoitum. Double-stranded cDNAs were synthesized with an

Oligo(dT) primer [Invitrogen:

5'-pGACTGCTTACATCGCAGCGCGCCCTTTT-TTTT-3'] from

9.1 ug of total RNA, treated with T4 DNA polymerase, and

purified by ethanol-precipitation. The cDNAs were ligated

to lone-linker L1-SalI, purified by phenol/chloroform, and

separated from free linkers by Centricon 100. Then, the

cDNAs were amplified by long-range high fidelity PCR using

Ex Taq polymerase (Takara) with a primer SalI-S. The

products were purified by phenol/chloroform and Centricon

100. The cDNAs were digested with SalI and NotI enzymes

and cloned into SalI/NotI site of pSPORT1 plasmid vector.

The DH10B E. coli host was transformed with the ligation

mixture by the standard chemical method. The average

insert size is about 2.5 kb. The library was constructed

by Yulan Piao (NIA)."

ORIGIN

Query Match 3.9%; Score 155.4; DB 7; Length 619;
Best Local Similarity 57.5%; Pred. No. 1.2e-21;
Matches 364; Conservative 0; Mismatches 251; Indels 18; Gaps 4;

679 GGAAGCCGGGCTCCCTGGGCTCCAGCCCGGGTCCAGAGAGGGCGGGGCACTGC 738
Db 2 GGAAGCACCCGAAACCCCTGGCTCGCATCTCGAGTCAAAAGGCGATCTGACTCAC 61
739 CAGCCGAAGTCTGCGCTTGCCTCAAGAGAGCCAGGCTGGCGCCCTGAGCCGAGCG 798
Db 62 CAGTACAAGTGTGCTTCAAGTAAAGAGCCAGATGCTATCTCTCCGAGAGTGAAGA 121
799 GACGCCCTGGGAGGAGGGTCTGGGCCCACCCGGGAGAGAGCGGTGACCGAGTACCG 858
Db 122 GGAAGCCCGACGAGGTGCTAACCAACCCCATCAGGCAATCATGGTGCAGTCTGCG 181
859 TGGTCTTGTGTGTGTCTGCTGCAAGCCCGGAAAGAGCCACTTTTGGAGGGTGC 918
Db 182 TCGGTCTCCCGCAGGTGTCTACTGCA-----GAGAAAGATTGTCTTAAAGAAA 232
919 GCTCTCTGGCAGCGCACTCCACCCATCCGTGGGCGCGCAGACAGCGGGCCCCC 978
Db 233 GGTGTCTGACTGAGTCTCTCTGGG---TCGGTGTGCTGTAAACAGCCAGCTCTCAC 289
979 ATCCACATCGGAGCACCAGCTCCCTGGAGACGCTTGTCCCGGTGACGCCGAGAC 1038
Db 290 ATCTCT---GCTGTACACACCCCGCAAAATGCTTTCAGTCAAGCCATTTATTGAGAC 346
1039 CAAAGCACTTCTCTACTCTCAGGCGA---CAAGAGAGAGTGGGGCCCTCTCTCACT 1095
Db 347 CAGACATTTCTTACTTCAAGGGAGATGGCCAAAGGCTTAAACCCCTCATCTCTACT 406

QY 1096 CAGTCTCTGAGAGCCCGACGCTGACTGGCGCTCGAGGCTCGTGAGACCATCTTCTGGG 1155
Db 407 CAGCAACTCTCAGGCTTACTGACTGGGGCCAGAGAGATGGTGAAGATCTTCTCTGGG 466
QY 1156 TTCCAGGCCCTGATGATGCAAGGACTCCCGCAGGTTGCCCGCTCCCGCAGCGTACTG 1215
Db 467 CTCAAGGCTTGAAGATCATGAGACCACTCTGAGGACACACCGTCTATGCGCTGACTACTG 526
QY 1216 GGAATAGGCGCCCGCTTGTGAGAGCTGTGGGAACACCGGAGAGTGGCCCTTACGGGGT 1275
Db 527 GGAAGTGGGCGCCCTGTTCACACAGCTGTGTGAACCATGACAGTGCATATGTCAG 586
QY 1276 GCTCTCAAGACGACATGCGCCGCTCGAGCTGC 1308
Db 587 ACTCTCAGGTCAATGAGTTTGAACAGC 619

RESULT 38
BUI39751 696 bp mRNA linear EST 25-NOV-2002
LOCUS 603134527F1 GSEQCHL24 Gallus gallus cDNA clone CHEST116f8 5', mRNA
DEFINITION
sequence.
ACCESSION
BUI39751
VERSION
BUI39751.1 GI:25354188
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 696)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
2235534
12445392
PUBMED
MEDLINE

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers

1. 696

/organism="Gallus gallus"

/mol_type="mRNA"

/strain="White Leghorn, HiseX"

/db_xref="taxon:9031"

/clone="CHEST116f8"

/dev_stage="16 day embryo"

/lab_host="DH10B"

/clone_lib="GSEQCHL24"

/note="Organ: Brain; Vector: pBluescript II KS(+); Site 1:

EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)

[Stratagene] vector to accommodate cDNA produced with the

T-trimmed protocol (Construction of uni-directionally

cloned cDNA libraries from messenger RNA for improved 3'

end DNA sequencing by Glenn Fu, et al. U.S. Patent #

6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.

Ligate in double stranded adaptor containing BspI and

BamHI sites [5'ggcgcgtgcagcccgatccgaaagaaag]

[5'aattcttttttcgataccggcgctgcagc]

ORIGIN

Query Match 3.9%; Score 154.8; DB 5; Length 696;
Best Local Similarity 56.0%; Pred. No. 1.6e-21;
Matches 319; Conservative 0; Mismatches 242; Indels 9; Gaps 1;

QY 28 GGAAGCCCTTGGCCCGGACACCCCGCGATGCGCGCGCTCTCCCGTGCAGACCGTGGC 87

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Db      20 GGAAGTCGGCGCTGCGGCGGCTCCGCAATGAGGCGGAGAGCCCTTCGCGCGGCTTCCT
Qy      88 CTCCTCTGCTGCGGCGGCTACCGGAGAGTGTCTGCGCTGCGGCGGCTTCGTGTGGGCGCT
Db      80 GGGCGCGCTGCGGCGGCTGTACGCGGAGGCGCAAGCGCTGAGGCGCTTCGTGTGGGCGGCT
Qy      148 G-----GGGCGCGGCTGCGGCGGCTGTGAGGCGGAGGAGCCCGGCGGCTTCGCT
Db      140 GAGAGAGGCTGCGGCGGAGAGTGTGAGGCTGTGCGGAGGCGGAGCGCTCAGTGTACCG
Qy      199 CGCGCTGTGCGGCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      200 GACCTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      259 CCCCTTCCTTCGCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      260 CATCTGTCTTCGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      319 GTGCGAGCGGCGGCGGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      320 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      379 CGGGGCGGCGGCGGAGGCTTTCAGCAAGCGGCTGCGGAGCTACCTGCGGCGGCGGAGT
Db      380 TTGTACCTTCAGAGTTTTCAGTCTTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      439 CGACGCACTGCGGCGGAGCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      440 AGAAAGCATTTCCATCAGTGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      499 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      500 GATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      559 CCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      560 CCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT

RESULT 39
CA380121      668 bp      mRNA      linear      EST 06-NOV-2002
LOCUS      659344 NCCOMA 1RT Oncorhynchus mykiss cDNA clone 1RT49P11_B_H06 5',
DEFINITION      mRNA sequence.
ACCESSION      CA380121
VERSION      CA380121.1 GI:24701509
KEYWORDS      EST.
SOURCE      Oncorhynchus mykiss (rainbow trout)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
      Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
      1 (bases 1 to 668)
      Rexroad,C.B. 3rd, Lee,Y., Keele,J.W., Karamycheva,S., Brown,G.,
      Koop,B., Gahr,S.A., Palti,Y. and Quackenbush,J.
      Sequence analysis of a rainbow trout cDNA library and creation of a
      gene index
      Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)
      Contact: Rexroad CE
      USDA, ARS, National Center for Cool and Cold Water Aquaculture
      11876 Leetown Road, Kearneysville, WV 25430, USA
      Tel: 304 724 8340 x2129
      Fax: 304 725 0351
      Email: crexroad@nccwa.ars.usda.gov
      Single pass sequencing. Bases called with phred v0.020425.c and
      trimmed with the aid of the trim_alt option. Vector identified by
      cross match v0.990329.
      Seg primer: ACCGATTAACAATTTACACAGA.
      Location/Qualifiers
      1..668
      /organism="Oncorhynchus mykiss"
      /mol_type="mRNA"

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/db xref="taxon:8022"
/clone="1RT49P11_B_H06"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1ib="NCCOMA 1RT"
/note="Vector: PCMV SPORT6; Site 1: NciI; Site 2: SalI;
library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

ORIGIN

Query Match      3.7%; Score 150.4; DB 6; Length 668;
Best Local Similarity 57.5%; Pred. No. 1.3e-20;
Matches 315; Conservative 0; Mismatches 221; Indels 12; Gaps 2;

Qy      1406 CTGCTCCCGCAGACAGAGCCCTGCGAGGTGTACGGTTGTGTGGGCGGCTGCGGCG
Db      7 CTCTGCGCCGACAGAGTGTACCTTCAACGGGAGTACTTTGTGTGTGTGTGTGTGTGTGT
Qy      1466 CGGCTGTGTGCGGCGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      67 GGGGTGTGTGCTCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      1526 ACCAAGAGTGTATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      127 GTGAGGAACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      1586 AAGATGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      187 AAGATGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      1646 GCCGAGAGCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      244 CCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      1706 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      304 GGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      1766 AACAGGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      364 AACGACGTGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      1826 CAGCACTTGAAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      424 GGTACCTTCTTAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      1886 GAAGCGAGGCGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Db      484 AAACCACTGTGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
Qy      1946 CGGCGCAT 1953
Db      535 AGACCCAT 542

RESULT 40
A1824948/c      148 bp      mRNA      linear      EST 16-DEC-1999
LOCUS      WB04C01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304672 3',
DEFINITION      mRNA sequence.
ACCESSION      A1824948
VERSION      A1824948.1 GI:5445619
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 148)
      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
      Tumor Gene Index
      Unpublished (1997)
      Contact: Robert Strausberg, Ph.D.

```


Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
 cDNA library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at: www.bio.1lnl.gov/bbrp/image/image.html
 Insert Length: 423 Std Error: 0.00
 Seg primer: -40UP from Gibco
 High quality sequence stop: 137.
 Location/Qualifiers

FEATURES

source

1. 148
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2304672"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_1b="NCI-CGAP GC6"
 /note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; plasmid DNA from the normalized library NCI CGAP GC4 was prepared, and as circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 3.5%; Score 140; DB 1; Length 148;
 Best Local Similarity 100.0%; Pred. No. 1.5e-18;
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3876 GGAATTGGAGTACCAAGGTGTCCTGTACACAGGAGACCTCGACCTGTGATGG 3335
 DB 148 GGAATTGGAGTACCAAGGTGTCCTGTACACAGGAGACCTCGACCTGTGATGG 89
 QY 3336 GGGTCCTGTGGTCAAAATTGGGGGAGTGTCTGTGGAGTAAATATCTGAATATATGAG 3395
 DB 88 GGGTCCTGTGGTCAAAATTGGGGGAGTGTCTGTGGAGTAAATATCTGAATATATGAG 29
 QY 3396 TTTTTCAGTTTGAATAAAA 4015
 DB 28 TTTTTCAGTTTGAATAAAA 9

RESULT 41
 AZ972318 641 bp DNA linear GSS 27-APR-2001
 LOCUS
 DEFINITION 2M0246F07F Mouse 10kb plasmid U06C2M library Mus musculus genomic
 accession AZ972318
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 641)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center

JOURNAL
 COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0246 row: F column: 07
 Seg primer: CATTGTAAACAGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 641.
 Location/Qualifiers

FEATURES

source

1. 641
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U06C2M0246F07"
 /sex="female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_1b="Mouse 10kb plasmid U06C2M library"
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.3%; Score 132; DB 8; Length 641;
 Best Local Similarity 61.6%; Pred. No. 9.1e-17;
 Matches 229; Conservative 0; Mismatches 140; Indels 3; Gaps 1;

QY 963 ACCACCGCGGCGCCCATCCATCGCGGCGACCAAGTCCCTGGAGACGCTGTGCC 1022
 DB 216 AACACAGGCCAGCTCCATCATCTCTGTACACCCCGCAAAATGCTTCAAGCTCA 275
 QY 1023 CGGTGACGCCGAGACCAAGCACTTCTCTACTCTCCAGGCGA---CAAGGAGCGTGC 1079
 DB 276 GGGCATTTATGTAGACCAAGCACTTCTTACTCCAGGAGATGGCCAAAGAGCTCTAA 335
 QY 1080 GGGCTCTCTTCTACTCAGCTCTGTGAGGCCAGCTGAGCTGGAGGCTGTGG 1139
 DB 336 ACCCTCATCTCTACTCAGCAAGCACTTCACTGAAGCTGGGCGCAGAGACTGTGG 395
 QY 1140 AGACCACTTTTGTGGTTCAGGCTCGATGACGAGGACTCCCGCAGTGGTCCCGCC 1199
 DB 396 AGATCATCTTTCTGGGCTCAAGGCTTGAAGCATCAGAGCACTCTCAGAGCACACCTGC 455
 QY 1200 TGGCCAGCGCTTCTGGAATGCGGCGCCCTGTTTCTGGAGCTGCTTGGAAACACGCG 1259
 DB 456 TATGCGCTCATCTGCGAGATCGGCGCTGTTCACAGCTGTGTGAACCAAGCGAG 515
 QY 1260 AGTGGCCCTTACGGGGTGTCTCTCAAGACGACATGCGCGCTGCGAGTGGCGGTACCC 1319
 DB 516 AGTGGCAATATGTCAAGCTCTTCAAGGTCATGTGAGGTTTGAACAGCAACCAAGAG 575
 QY 1320 CAGCGGTGTCT 1331
 DB 576 TGACAGATGCTT 587

RESULT 42
 BUI22597 875 bp mRNA linear EST 25-NOV-2002
 LOCUS 603148441F1 CSEBCHL18 Gallus gallus cDNA clone CHEST151a2 5', mRNA
 DEFINITION
 ACCESSION BUI22597.1 GI:25332991
 VERSION BUI22597.1
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 875)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.,
 A Comprehensive Collection of Chicken CDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 2235534
 MEDLINE 12445392
 PUBMED
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers

FEATURES

source

1..875
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton line 15T"
 /db_xref="taxon:9031"
 /clone="CHEST151a2"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEBCHL18"
 /note="Organ: small intestine; Vector: pBluescript II
 KS(+); Site 1: EcoRI; Site 2: NotI; Modification of
 pBluescript II KS(+) (Stratagene) vector to accommodate
 cDNA produced with the T-timed protocol (Construction of
 uni-directionally cloned cDNA libraries from messenger RNA
 for improved 3' end DNA sequencing by Glenn Fu, et al.
 U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
 NotI and EcoRI. Ligate in double stranded adaptor
 containing BglI and BamHI sites
 [5'ggcgctgcagcccgatccggaataaag]
 [5'aatcttttctcgatccgggctcagcgc]"

ORIGIN

Query Match 3.2%; Score 128.8; DB 5; Length 875;
 Best Local Similarity 58.0%; Pred. No. 4.4e-16;
 Matches 246; Conservative 0; Mismatches 177; Indels 1; Gaps 1;
 166 GGTGTGTCAGCGCGGAGCCCGGCGCTTCCGCGCTGTGTGGCCAGTGTGTGTG 225
 165 GGTGTGTCAGCGGAGGAGCGATGATGTAACCGACCTTCGTGTGCGAGTGTGTGTG 224
 226 CGTGGCCCTGGAGCGACGCGCGCGCGCGCGCGCGCTTCCGCGAGTGTGTGTG 285
 225 CGTGGCCCGCGGTG 284
 286 GAGAGAGCTG 345
 285 GAGCGAAGTCATACAAAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 344
 346 GGGCTTGGCTTG 405
 345 TGGTATGATATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 404

QY 406 CAGCTGCGCAGCTACTGTCGCCAACAAGGTCAGCCAGTGTGGGGGAGCGGGCGCTG 465
 DB 405 GTGTATATACACTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 464
 QY 466 GGGGCTG 524
 DB 465 GAGATATCTG 524
 QY 525 CGCTTTTG 584
 DB 525 CACTCTTATG 584
 QY 585 AACT 588
 DB 585 AACT 588

RESULT 43
 CN505902 846 bp mRNA linear EST 28-APR-2004
 LOCUS AGENCOURT 22432746 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7267941
 DEFINITION
 ACCESSION CN505902
 VERSION CN505902.1 GI:46818526
 KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 846)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Len Zon, Harvard
 cDNA Library Preparation: Open Biosystems
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.llnl.gov
 Plate: LLAM15246 row: h column: 19
 High quality sequence start: 21
 High quality sequence stop: 756.
 Location/Qualifiers

FEATURES

source

1..846
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:7267941"
 /tissue_type="whole body"
 /lab_host="DH10B"
 /clone_lib="NIH_ZGC_7"
 /note="Vector: pXpress1; Site 1: NotI; Site 2: EcoRV;
 Bulk tissue was collected from a whole adult individual
 from the Tuebingen strain. 1st strand cDNA was primed with
 a Not I - oligo(dT) primer, double-stranded cDNA was
 cloned into the Not I and EcoRV sites of pXpress-1.
 Library was size-selected for >1 kb fragments and
 normalized. A non-normalized version of this library is
 also available (NIH ZGC 10). Library was constructed by
 Open Biosystems (Huntsville, AL)"

ORIGIN

Query Match 3.2%; Score 128; DB 7; Length 846;
 Best Local Similarity 57.3%; Pred. No. 6.5e-16;
 Matches 252; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

QY 2463 GTGGCCCTTTCAGACGCTTCTTCAAGCTTCAATGTCACACACCGCCGTGGCATCAGGAGCA 2522
 DB 97 GAGACGCTTTCAGACGCTTCTTCAAGACGCTTCAATGTCAGACGCTTCAATGTCAGACGAG 156
 QY 2523 AGTCTTACGCTTTCAGACGCTTCTTCAAGACGCTTCAATGTCAGACGCTTCAATGTCAG 2582
 DB 157 AGTCTTACGCTTTCAGACGCTTCTTCAAGACGCTTCAATGTCAGACGCTTCAATGTCAG 216
 QY 2583 GCTTGTCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 2642
 DB 217 ATCTGTCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 216
 QY 2643 TCTGTCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 2702
 DB 277 TGTGTCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 336
 QY 2703 TCTGTCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 2762
 DB 337 TCTGTCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 396
 QY 2763 CAGTGTCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 2822
 DB 397 TGTGTCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 453
 QY 2823 CGGCCCCAGGCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACG 2882
 DB 454 CGTGTCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 513
 QY 2883 AGAGCGCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTT 2902
 DB 514 ATTAAGCTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 533

RESULT 44
 LOCUS BGI98331/c 813 bp mRNA linear EST 21-APR-2001
 DEFINITION RST11589 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
 ACCESSION BGI98331
 VERSION BGI98331.1 GI:13720018
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 813)
 Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,
 Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,
 Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Bozzer, S.,
 Mays, R., Smith, E., Veloso, N., Kliska, A., Hess, J., Cochran, K., Lo, K.,
 Offenbacher, J., Danzig, J. and Ducar, M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL 21227151
 MEDLINE 11329013
 PUBMED
 COMMENT Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave., Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scain@athersys.com
 High quality sequence stop: 533.
 Location/Qualifiers
 1..813
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="HT1080"
 /clone_lib="Athersys RAGE Library"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation

ORIGIN
 Query Match 3.1%; Score 123.8; DB 4; Length 813;
 Best Local Similarity 94.1%; Pred. No. 4,9e-15;
 Matches 128; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 3083 TACAGTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 3142
 DB 749 TTCAGTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 690
 QY 3143 ACATTTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 3202
 DB 689 ACATTTTTCAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCTTCAAGACGCTTCT 630
 QY 3203 AAGAACGCGGATCT 3218
 DB 629 AAGAACGCGGATCTT 614

RESULT 45
 LOCUS CA353864 632 bp mRNA linear EST 05-NOV-2002
 DEFINITION 625469 NCCCMW 1RT Oncorhynchus mykiss cDNA clone 1RT74012_C_H06 5',
 mRNA sequence.
 ACCESSION CA353864
 VERSION CA353864.1 GI:24599035
 KEYWORDS EST.
 SOURCE Oncorhynchus mykiss (rainbow trout)
 ORGANISM Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 632)
 Rexroad, C.E. 3rd, Lee, Y., Keeler, J.W., Karamcheva, S., Brown, G.,
 Koop, B., Gahr, S.A., Palci, Y. and Quackenbush, J.
 Sequence analysis of a rainbow trout cDNA library and creation of a
 gene index
 Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)

JOURNAL Contact: Rexroad CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@ncccmw.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alc option. Vector identified by
 cross_match v0.990329.
 Seg primer: AGCGATTAACAATTTTCACACAGGA.
 Location/Qualifiers
 1..632
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="1RT74012_C_H06"
 /issue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="NCCCMW 1RT"
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from brain, gill, liver,
 spleen, muscle, and kidney."

ORIGIN
 Query Match 2.9%; Score 116.8; DB 6; Length 632;
 Best Local Similarity 59.2%; Pred. No. 1.4e-13;
 Matches 218; Conservative 0; Mismatches 147; Indels 3; Gaps 1;
 QY 2417 GATGCGGTGTATCAGACGAGGCTCTCCGTAATGAGCGCAGCGTGGCTCTTCAG 2476
 DB 62 GATGCGGTGTATCAGACGAGGCTCTTCACAGATTCATGCGCAAGACGCTTCGAG 121
 QY 2477 GTCTTCTTACGCTTCAATGTCACACACGCGCGCATCAGGCGCAAGTCTTCAATGTCAG 2536

Db 122 GTCTGACCCAGATGCTCTAGCTGAGTTGACCAAGCTTGGGAAGAAATGTTCCGTACG 181
Qy 2537 TGCCAGGGGATCCCGCAGGGGCTCCATCTCTCAGGCTGCTGACGCTGTGCTACGCG 2596
Db 182 GGTCAAGGGATTCCTCAGGGGCTCCGAGAGCTGTCTGCTGGGCTCTGTGTAACGGG 241
Qy 2597 GACATGAGAAACAGCTGTTTGC---GGGATTTCGGCGGAGCGGGCTGCTCCGCTTTG 2653
Db 242 CACATGAGAACTTCTGTTTCTTAACGTCAAGCGGCGAGGGGTGTGATGAGACTG 301
Qy 2654 GTGATGATTTCTTGTGTGTCACCTCACTCAACCCAGCGGAAAACTTCTCTCAGAGC 2713
Db 302 GATGACGATTTCTCTCTCACTCTGACCTGACGACGACAGACCTTCTCTCAAGACC 361
Qy 2714 CTGTGTCAGAGTGTCTCTGATGAGCTGCTGCTGTCGTAATTTGCGAAGACAGTGTGAC 2773
Db 362 CTGATGCGGGGGTTCACAGGTACGGGTGTGTGAGAACCCCAAGAGGTGCTGTTAAC 421
Qy 2774 TTCCCTGT 2781
Db 422 TTCCCTTT 429

RESULT 46
BX889962 724 bp mRNA linear EST 27-JUL-2004
LOCUS BX889962 cdbk Oncorhynchus mykiss cdna clone tcdk0041c.i.20 5prim,
DEFINITION mRNA sequence.
ACCESSION BX889962
VERSION BX889962.2 GI:43411444
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)

REFERENCE
AUTHORS Oncorhynchus mykiss
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 724)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cdna
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Dec 18, 2003 this sequence version replaced gi:40140362.
CONTACT: Guiguen Y

JOURNAL
COMMENT INRA - SCRIB
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signeaasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0041 row: 1 column: 20
Seq primer: M13R.

FEATURES
source Location/Qualifiers

1..724
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcdk0041c.i.20"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_idb="tcdk"
/note="Vector: pT73D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution: AGENAE Resource centre, François PIUMI,
François Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Query Match 2.9%; Score 115.8; DB 5; Length 724;
Best Local Similarity 52.9%; Pred. No. 2.2e-13;
Matches 370; Conservative 0; Mismatches 287; Indels 42; Gaps 4;

Qy 1528 CAAAGATTATCTCTCTGCGGAGACATGACCAGCTCTGCTGACAGACTGACGTGAA 1587
Db 19 CAGGAATCTTCTGCTCATGAGGCAAGTTGAGAGGATGTCATTATGAGCTGACCTATGAGAA 78
Qy 1588 GATGACCGGCGGAGCTGCGCTGCTGCGGACGAGGCCAGGGGTGCTGTGTTCCGCG 1647
Db 79 GATGAAGGTAATGACTGATGATGCTGATGATGACGATGCAAGACAGAGCCGCTG---CCGCGC 135
Qy 1648 CCGAAGACACCGCTGCGTGAAGAGATCCGTGCAAGTTCTGCACTGCTGATGATGT 1707
Db 136 CAGTAGAGCTGTGATTCGAGCGGGGTGTAGCCAGGCTCTGAGCTGTGCTGTGATGG 195
Qy 1708 GTAGCTGCTGAGCTGCTGAGCTCTTTCTTTATGTACGAGAGACCACTTTCAAAAGAA 1767
Db 196 CTATGTGTAGGCTCGGTGAGAGCTATGTCTACGTCACAGAGAGCATGGAAGAA 255
Qy 1768 CAGGCTCTTTTCTACCGGAAAGTGTCTGAGCAAGTTGCAAGGATTGATGATGACA 1827
Db 256 CGCACTGGGCTTCTACAGATACAGAGTCTGGGCCAAGCTGCAAGAGCTGCTTTACGTGG 315
Qy 1828 GCACTTGAAGAGGTGACGCTGCGGAGCTGTGGAAGCAGAGTCAAGCAGCATCGGA 1887
Db 316 TCACCTCTTAAGGTCAAGTCAAGATGTCAAGATGTCACCTGGCCAGAGTGAAGTCCGCCAA 375
Qy 1888 AGCCAGAGCCCGCTGCTGACGTCACACTCCGCTTATCCCAAGCTGACGGCTGGG 1947
Db 376 AACCACTGTCCCC-----TCCGCTCTCGCTTCATCCCAAGACCGAAGGGATGAG 426
Qy 1948 GCGGATGTGACATGACATGACTAGTGTGGGACCCGAAGCGTCCGAGAGAAAGAGGCG 2007
Db 427 ACCCATACACAGGGTATAGGGGCTGAGCCCAAAACAAAGTT----- 468
Qy 2008 CAGAGCTCTACCTGAGGAGTGAAGGCACTGTTCAAGCTGCTCAACTACAGAGCGGCGG 2067
Db 469 -----GTTCCAGAACCCGTGTGAAGAGCTGTTAATGTGATGAGTGTGTGACGGT 522
Qy 2068 GCGCCCGGCGCTCTGCGGCGCTCTGTGTGCGGCTGACGATTCACAGAGGCGCTGGG 2127
Db 523 CTCTCCCTCTCTCTGCGGCTTACAGTGTGGGGTTGACCGCAATCCACAGAGTCTCTTC 582
Qy 2128 CACCTTGTGTCGCTGTGCGGCGCCCAAGCCCGCGCTGAGCTGACTTTGTCAAGGT 2187
Db 583 TTCCATACACCCCTGCTCAG-----AAAGACAAACCAAGCGCTCTACTTGTCAAGGT 636
Qy 2188 GGATGTGACGGCGGCTACGACACCATCCCGCAGGACAG 2226
Db 637 GGATGTGAGTGGGGCTATGACAGTCTACCACTCAG 675

RESULT 47
BX882610 646 bp mRNA linear EST 20-JUL-2004
LOCUS BX882610 cdbk Oncorhynchus mykiss cdna clone tcdk0060c.h.01 5prim,
DEFINITION mRNA sequence.
ACCESSION BX882610
VERSION BX882610.2 GI:42815406
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 646)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cdna
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
JOURNAL On Dec 18, 2003 this sequence version replaced gi:40127495.
COMMENT Contact: Guiguen Y

INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20

Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenassupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0060 row: h column: 1
Seq primer: M13R.

FEATURES

Source

Location/Qualifiers

1. 646

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

/db_xref="taxon:8022"

/clone="tcbk0060c.h.01"

/tissue_type="multi-tissues"

/dev_stage="from embryos to adults"

/lab_host="DH10B"

/clone_lib="tcbk"

/note="Vector: pT73D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution : AGENAE Resource centre. Francois PIUMI,
Francois.Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREB), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Query Match 2.9%; Score 114.8; DB 5; Length 646;
Best Local Similarity 55.2%; Pred. No. 3.6e-13;

Matches 224; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

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QY 3052 CAACATCTCAAGATCTCTGCTGAGGCGGTACAGATTTCAGCATGTCGTGACGCT 3111
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DB 2 CAACATCTTAAGTAACTGCTGTCGACGCGTTCAAGTTCATGCTGTCACAGAGTTT 61
    |||||
QY 3112 CCCATTTCATGACGAAGTTTGAAGAACCCCAATTTTCTGCGGTCATCTTGACAC 3171
    |||||
DB 62 GCGGTTGGTCAAGAAAGTGGCGGAACCACTGTAATCTTCATCTGAGGACTT 121
    |||||
QY 3172 GGGCTCCCTGCTACTCATCTCTGAAAGCAAGACGAGGATTCGCTGGGGCCCA 3231
    |||||
DB 122 GCGGAGTACACCAACATCTAGTCACTGCAACAAAGGTGTCCTCTAGGCTGTAA 181
    |||||
QY 3232 GGGCGCCGCGGCTCTGCTCCGAGGCGGTGAGTGGCTGTGACCAAGCATTTCT 3291
    |||||
DB 182 GGGTTTAACAGGAGGCTTCAAGTAAAGGAGTAACTGATTAATCTGTCGCTTCT 241
    |||||
QY 3292 GCTCAAGCTGACTGACACCGGTGTCACCTAAGTGCATCTGAGGTCACCTAGACAGC 3351
    |||||
DB 242 GTTGGTTCTGTCCCGTCATCGCCCTCTAATCAATCTCTGCTCCGCTAGGACAGC 301
    |||||
QY 3352 CCAGACGAGCTGAGTCGGAAGCTCCCGGGAGCAAGCTGACGCTCCGAGAGCCGACG 3411
    |||||
DB 302 TAAAGAGAAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 361
    |||||
QY 3412 CAACCGGCACTGCGCTCAGACTTCAAGACCAATCTCTGAGAGTATGG 3457
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DB 362 CACACCCAAATGCTGGAAGACTTCAAGGCAATCCAGGCTTAGAGG 407
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RESULT 48

EX315053

LOCUS BX315053 731 bp mRNA linear EST 14-MAY-2004
DEFINITION BX315053 tcaty Oncorhynchus mykiss cdna clone tcaty0029b.n.21 5prim,
mRNA sequence.

ACCESSION BX315053

VERSION BX315053.2 GI:42620226

KEYWORDS EST.

SOURCE Oncorhynchus mykiss (rainbow trout)

ORGANISM Oncorhynchus mykiss

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 731)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Construction and primary characterization of normalized cDNA
libraries in rainbow trout, *Oncorhynchus mykiss*
Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29595698.
Contact: Guiguen Y

INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20

Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenassupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

Plate: 0029 row: n column: 21
Seq primer: M13R.

FEATURES

Source

Location/Qualifiers

1. 731

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

/db_xref="taxon:8022"

/clone="tcaty0029b.n.21"

/tissue_type="adipose tissue, blood, brain,
differentiating gonade, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"

/dev_stage="from embryos to adults"

/lab_host="DH10B"

/clone_lib="tcaty"

/note="Vector: pT73D-pac; Rainbow trout multi-tissues -
normalized + 1 subtraction (tcaty) : Clone distribution :
AGENAE Resource centre. Francois PIUMI,
Francois.Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREB), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Query Match 2.9%; Score 114.8; DB 5; Length 731;
Best Local Similarity 55.2%; Pred. No. 3.6e-13;

Matches 224; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

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QY 3052 CAACATCTCAAGATCTCTGCTGAGGCGGTACAGATTTCAGCATGTCGTGACGCT 3111
    |||||
DB 2 CAACATCTTAAGTAACTGCTGTCGACGCGTTCAAGTTCATGCTGTCACAGAGTTT 61
    |||||
QY 3112 CCCATTTCATGACGAAGTTTGAAGAACCCCAATTTTCTGCGGTCATCTTGACAC 3171
    |||||
DB 62 GCGGTTGGTCAAGAAAGTGGCGGAACCACTGTAATCTTCATCTGAGGACTT 121
    |||||
QY 3172 GGGCTCCCTGCTACTCATCTCTGAAAGCAAGACGAGGATTCGCTGGGGCCCA 3231
    |||||
DB 122 GCGGAGTACACCAACATCTAGTCACTGCAACAAAGGTGTCCTCTAGGCTGTAA 181
    |||||
QY 3232 GGGCGCCGCGGCTCTGCTCCGAGGCGGTGAGTGGCTGTGACCAAGCATTTCT 3291
    |||||
DB 182 GGGTTTAACAGGAGGCTTCAAGTAAAGGAGTAACTGATTAATCTGTCGCTTCT 241
    |||||
QY 3292 GCTCAAGCTGACTGACACCGGTGTCACCTAAGTGCATCTGAGGTCACCTAGACAGC 3351
    |||||
DB 242 GTTGGTTCTGTCCCGTCATCGCCCTCTAATCAATCTCTGCTCCGCTAGGACAGC 301
    |||||
QY 3352 CCAGACGAGCTGAGTCGGAAGCTCCCGGGAGCAAGCTGACGCTCCGAGAGCCGACG 3411
    |||||
DB 302 TAAAGAGAAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 361
    |||||
QY 3412 CAACCGGCACTGCGCTCAGACTTCAAGACCAATCTCTGAGAGTATGG 3457
    |||||
DB 362 CACACCCAAATGCTGGAAGACTTCAAGGCAATCCAGGCTTAGAGG 407
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RESULT	49
LOCUS	BX521269
DEFINITION	BX521269 Sugano mouse kidney mKia Mus musculus cDNA clone
ACCESSION	IMAGP98M035892 ; IMAGE:2373290, mRNA sequence.
VERSION	BX521269
KEYWORDS	BX521269.1 GI:32295739
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 568) Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D. and Korn,B.
AUTHORS	Mouse Unigeneset - RZPD2 Unpublished (2003)
TITLE	Contact: Ina Rolfs
JOURNAL	RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
COMMENT	RZPD; IMAGP98M035892. RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Mouse Unigeneset - RZPD2 (RZPDL No.981) http://www.rzpd.de/Catalog/cgl- bin/showlib.pl.cgi?response?libNo=981 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel.: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD. Contact RZPD (clone@rzpd.de) for further information. Seq primer: BUGF, Primer sequence: CTCTGCTCTAAAGAAGTCGG.
FEATURES	Location/Qualifiers
source	1..568
	/organism="Mus musculus"
	/mol_type="mRNA"
	/strain="C57BL"
	/db_xref="taxon:10090"
	/clone="IMAGP98M035892 ; IMAGE:2373290"
	/sex="female"
	/dev_stage="adult"
	/lab_host="DH10B"
	/clone_lib="Sugano mouse kidney mKia"
	/note="Orgn: kidney; Vector: pME185-FL3; Site 1: DraIII (CACATGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [AATGGCCCTTTTCTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCCTACTGG], digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAGAAGTCGG and 3' end primer CGACCTGCAGCTCGAGACA."
ORIGIN	
	Query Match 2.8%; Score 113.4; DB 5; Length 568;
	Best Local Similarity 69.9%; Pred. No. 6,8e-13;
	Matches 153; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
OY	3236 GCCGCCGCCCTCGCCCTCGAGGCGGTGCAGTGCTGCACACCAAGCAATTCTGTCTC 3299
DB	143 GCCTTGCTCTTTCTTCCTGTAAGCCGCACTTGCTCTGTGTACAGACCTTCTGTCTC 202
OY	3296 AAGTGAATCGACACCCTGTACACTTAGCTGCACCTCTGGGGTCACTAGACAGCCCG 3355
DB	203 AAGCTGGCTGCTCATTTGTATCAAAAATGTCTCTGGGACCTCTAGGACAGCCCAA 262
OY	3356 AGCAGCTGAATGCGAAGCTCCCGGGGACGACGCTGAATGCCCTTGGAGCCGCGACCCAAC 3415

D6		263	AACCTGCTGTGGCCGAAGACTGCCAAGAAGCACAATGCATTCCTTAAGTGCAGCTGAC	322
OY		3416	CCGGCACTGCCCTTGACATTCAAGACCATTCTTGACTGA	3454
D6		323	CCAGCCTTAGCACACAGACTTTGACCATTTTGACTAA	361
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DEFINITION	Mus musculus molossinus DNA, clone:Msmg01-165A22.TU, genomic survey sequence.			
ACCESSION	AF363333	2332 bp	DNA	GSS 03-JUN-2004
VERSION	AF363333			
KEYWORDS	GI:47974538			
SOURCE	GSS.			
ORGANISM	Mus musculus molossinus Mus musculus molossinus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y. BAC end Sequences of Library Msmg01			
JOURNAL TITLE	Unpublished			
AUTHORS	2 (bases 1 to 2332) Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y. Direct Submission			
REERENCE JOURNAL	Submitted (17-Nov-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Shohri-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:h.tatori@gsc.riken.jp, URL:http://ngp.gsc.riken.go.jp/, Tel.:81-45-503-9111, Fax:81-45-503-9170)			
COMMENT	C clones are derived from the mouse BAC library Msmg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Teuhda Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Teuhda, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp PRIMERS Sequencing : TU LIBRARY Vector : pBRc3.6 R.Site 1 : EcoRI R.Site 2 : EcoRI Location/Qualifiers 1..2332 /organism="Mus musculus molossinus" /mol_type="genomic DNA" /sub_species="molossinus" /db_xref="taxon:57486" /clone="MSMG01-165A22.TU" /genex="male" /tissue type="mixture of kidney and spleen" /_clone_id="MSMG01 Mouse Male BAC Library"			
FEATURES				
source				
ORIGIN				
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Best Local Similarity		43.7%;	Pred. No. 1,4e-12;	
Matches 679;	Conservative 0;	Mismatches 864;	Indels 10;	Gaps 4;
OY		7	CTGGGTCTCGTGGCGACGTGGGAAGCTTGGCCCAGCACCCCCGCGATCGCGCGC	66
D6		695	CCGGCGATCG	754
OY		67	TCCCCGCTGGCGAACCTGTGGCTTCCCTGTGCGAGCAGCACTACCGCSAGTGTCTCGCT	126
D6		755	CGTCCGCGGCGT	814
OY		127	GGACCACTTGTGTGGGCGCGCTGGGAGCCCAAAGGTGTGCGCTGTGTGACGCGCGGAGACC	186
D6		815	CGCGCGGCG	874
OY		187	GAGCGCTTTCGCGCGCTGTGAGCCCAAGTGTGTGTGCGTGTGCTTGGAGACGACGACC	246

1529 AGCTTACCTGTTACCGCCAGAGCACCGTCTGCGTGGCCAGTTCC 1688

Db	GGGGTGGCGTGTGTCCGGCCGGAGAGCACCGTCTGCTGTGAGAGATCTCGGCAAGTTC	60
QY	1689 TGCATCGCGCTGATGAGTGTGTGACGTGCTGAGCTGTCAAGTCTTTTATATGTCA	1746
Db	61 TGCATCGCGCTGATGAGTGTGTGACGTGCTGAGCTGTCAAGTCTTTTATATGTCA	120
QY	1749 AGACCACGTTTCAAAAAGACAGAGCTCTTTTCTACCGGAAGTGTCTGGACAGTTC	1806
Db	121 AGACCACGTTTCAAAAAGACAGAGCTCTTTTCTACCGGAAGTGTCTGGACAGTTC	180
QY	1809 AAAGCATTTGGATTCAGACAGCATTTGAAGAGGTGCAGCTGCGGAGCTTTCGAAGCAG	1866
Db	181 AAAGCATTTGGATTCAGACAGCATTTGAAGAGGTGCAGCTGCGGAGCTTTCGAAGCAG	240
QY	1869 AGGTGAGGAGCATGCGGAGAGCCAGAGCCGCGCTGTCTGACGTCCAGACTCCGCTTATCC	1922
Db	241 AGGTGAGGAGCATGCGGAGAGCCAGAGCCGCGCTGTCTGACGTCCAGACTCCGCTTATCC	300
QY	1929 CCAAGCTTGAAGCGGCTGCGGCCGATTTGTGAACATGAATTAAGTGTGAGAGCCAGAAAGT	1988
Db	301 CCAAGCTTGAAGCGGCTGCGGCCGATTTGTGAACATGAATTAAGTGTGAGAGCCAGAAAGT	360
QY	1989 TCCGAGAGAAAAGAGGGCCGAGCGCTTCACTTCAAGAGGTGAAGGACATGTTCAAGCTGC	2048
Db	361 TCCGAGAGAAAAGAGGGCCGAGCGCTTCACTTCAAGAGGTGAAGGACATGTTCAAGCTGC	420
QY	2049 TCAACTAGAGCGGCGCGCGCCGCTCTTGAGGCGCTTGTGTGAGGCTGTGAGCG	2108
Db	421 TCAACTAGAGCGGCGCGCGCCGCTCTTGAGGCGCTTGTGTGAGGCTGTGAGCG	480
QY	2109 ATATTCACAGAGGCTCTGCGGCACATTTGCTGTGCTGTGTGCGGAGCCAGAGCCGCGCTGTG	2168
Db	481 ATATTCACAGAGGCTCTGCGGCACATTTGCTGTGCTGTGTGCGGAGCCAGAGCCGCGCTGTG	540
QY	2169 AGCTGTACTTTGTCAAGGTGTGATGTGACGGGCGGCTGACAGACCATCCCCAGGACAGGC	2228
Db	541 AGCTGTACTTTGTCAAGGTGTGATGTGACGGGCGGCTGACAGACCATCCCCAGGACAGGC	600
QY	2229 TCACGAGAGTCATGCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGTGCTGATG	2288
Db	601 NNN	660
QY	2289 CCGTGTGTCAAGAGGCGCGCCATGAGGACGTCGCGAAGGCTTCAAGAGCCAGCTCTTA	2348
Db	661 NNN	720
QY	2349 CCTTGAACAGACTCTCCAGCGCTTACATGACAGATTGCTGTGCTCACCTGACAGAGACCAAGC	2408
Db	721 CCTTGAACAGACTCTCCAGCGCTTACATGACAGATTGCTGTGCTCACCTGACAGAGACCAAGC	780
QY	2409 CGCTGAGGAGTACCGGTGTGATTCAGACGAGACTCTCCCTGAATGAGGCGCAGAGTGGCC	2468
Db	781 CGCTGAGGAGTACCGGTGTGATTCAGACGAGACTCTCCCTGAATGAGGCGCAGAGTGGCC	840
QY	2469 TCTTGCAGCTTCTCTAAGCTTCAATGTGCAACAGCGCGCTGTGCTATCAGAGGAGCAAGTCT	2528
Db	841 NNN	900
QY	2529 ACGTCCAGTGCAGAGGATTCGCCAGAGGCTTCATCTCTCTCAAGCTGTCTGTGACGCTGT	2588
Db	901 ACGTCCAGTGCAGAGGATTCGCCAGAGGCTTCATCTCTCTCAAGCTGTCTGTGACGCTGT	960
QY	2589 GCTACGGCGCATGAGAGCAAGCTGTTTGGCGGAGATTCCGCGGGAAGGAGTGTCTCTGC	2648
Db	961 GCTACGGCGCATGAGAGCAAGCTGTTTGGCGGAGATTCCGCGGGAAGGAGTGTCTCTGC	1020
QY	2649 GTTTGTGTGATGATTTCTTGTGTGTGACCTCACTTCAACCCAGCGCAAAACCTTCTCA	2708
Db	1021 GTTTGTGTGATGATTTCTTGTGTGTGACCTCACTTCAACCCAGCGCAAAACCTTCTCA	1080
QY	2709 GGAACCTTGTGTCGAGAGTGTCCCTGAGATGTGCTGTGAGAGCTTCCGGAAGACAGTGG	2768
Db	1081 GGAACCTTGTGTCGAGAGTGTCCCTGAGATGTGCTGTGAGAGCTTCCGGAAGACAGTGG	1140

QY	2769	TGAATTCCTCCGTAAABAACAGAGGCCCGCGGGTGCACAGCTTTTGTTCATATGCGGCC	2828
Db	1141	TGAATTCCTCCGTAAABAACAGAGGCCCGCGGGTGCACAGCTTTTGTTCATATGCGGCC	1200
QY	2829	ACGAGCTATTCCTCCGTAGTGCGGCGCTGCTGTGAATACCCGAACCTCGAGGTGCAGAGCG	2888
Db	1201	ACGAGCTATTCCTCCGTAGTGCGGCGCTGCTGTGAATACCCGAACCTCGAGGTGCAGAGCG	1266
QY	2889	ACTATCTCAGGTATATGCCCGGACCTCCATCABAAGCAGGTCAACCTTAAACCGCGGCTTCA	2948
Db	1261	ACTATCTCAGGTATATGCCCGGACCTCCATCABAAGCAGGTCAACCTTAAACCGCGGCTTCA	1320
QY	2949	AGGCTGGAGGAAACATGCGTCGCAACTCTTTGGGAGTCTTTCGCGCTGAAGTGCACAGCC	3008
Db	1321	AGGCTGGAGGAAACATGCGTCGCAACTCTTTGGGAGTCTTTCGCGCTGAAGTGCACAGCC	1380
QY	3009	TGTTTTCGGATTTTGCAGGTGAACAGGCTCCAGACGGTGTGCACCAATCTTACAAGATCC	3068
Db	1381	TGTTTTCGGATTTTGCAGGTGAACAGGCTCCAGACGGTGTGCACCAATCTTACAAGATCC	1440
QY	3069	TCTCTGTCAGAGGCTACAGTTCACGCATATGTGTGTGCAGAGCTCCCATTTTCATCAGAAAG	3128
Db	1441	TCTCTGTCAGAGGCTACAGTTCACGCATATGTGTGTGCAGAGCTCCCATTTTCATCAGAAAG	1500
QY	3129	TTTGGAGAATCCCAACATTTTCTCTGCGCGTCACTCTGACACAGGCTCCCTCTGTACT	3188
Db	1501	TTTGGAGAATCCCAACATTTTCTCTGCGCGTCACTCTGACACAGGCTCCCTCTGTACT	1560
QY	3189	CCATCTCGAAGAACCAAGAACGACAGGATATGTGCTGGGGGGCCAAAGGGCGCGCGCCCTC	3248
Db	1561	CCATCTCGAAGAACCAAGAACGACAGGATATGTGCTGGGGGGCCAAAGGGCGCGCGCCCTC	1620
QY	3249	TGCGCTCCGAGGGCGGTGCAGTGGTGTATGCCAACAGCATTTCTGTCTCAAGCTGACTGCAG	3308
Db	1621	TGCGCTCCGAGGGCGGTGCAGTGGTGTATGCCAACAGCATTTCTGTCTCAAGCTGACTGCAG	1680
QY	3309	ACCGTGTCACTAGTATGTCACCTCTGGGGGTCACTCAAGAACAGCCCAAGCCAGCTGATGC	3368
Db	1681	ACCGTGTCACTAGTATGTCACCTCTGGGGGTCACTCAAGAACAGCCCAAGCCAGCTGATGC	1740
QY	3369	GGAAGCTCCGGGGGACGACGCTGACTGCGCTCTGGAGGCGCGAGGCAACCCGGCACTGCGCT	3428
Db	1741	GGAAGCTCCGGGGGACGACGCTGACTGCGCTCTGGAGGCGCGAGGCAACCCGGCACTGCGCT	1800
QY	3429	CAGACTTCAAGACCATCTCTGACTGCA 3454	
Db	1801	CAGACTTCAAGACCATCTCTGACTGCA 1826	

[illegible]

Oy	3360	AGCTGAGTGGGAACACTCCCGGGGACGACGCTGATCTGCCCTGGAGCGCAGCAACC	CGG	3413
Dd	1741	TGCTGTGCGGGAAGCTCCCAAGAGCGACAAGAAGCAATCTTTAAAGCTGCAGCTGAC	CCAG	1800
Oy	3420	CACGTGCGCTCAGACTTCACAGACCATCTCCGAGCTGA	3454	
Dd	1801	CCCTAAGCACAGACTTTCAGAACCATTTTGGA	CTAA	1835
RESULT 4				
LOCUS	BM453198	925 bp	mRNA	linear EST 05-FEB-2002
DEFINITION	AGENCOURT_6387556 NIH_MGC_71 Homo sapiens CDNA clone IMAGE:5529840			
ACCESSION	BM453198			
VERSION	BM453198.1 GI:18502238			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
TITLE	NIH-MGC http://mgc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished (1999) Contact: Robert Stransberg, Ph.D. Email: cga@bs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LHAM1208 row: p column: 01 High quality sequence stop: 646.			
FEATURES				
source	Location/Qualifiers			
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	/clone="IMAGE:5529840"			
	/tissue_type="leiomyosarcoma"			
	/lab_host="DH10B (phage-resistant)"			
	/clone_lib="NIH MGC 71"			
	/note="Organ: uterus; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."			
ORIGIN				
Query Match	20.1%; Score 806; DB 4; Length 925;			
Best Local Similarity	99.2%; Pred. No. 1.7e-157;			
Matches	821; Conservative 0; Mismatches 5; Indels 2; Gaps 1;			
Dd	2149	GGCCGAGACCCGCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGCGGCTACGA	2208	
Oy	2	GGCCAGAGACCCGCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGCGGCTACGA	61	
Dd	2209	CACCATCCCCCAGACGAGCTCACGAGGTCAATGCCGACATCATCAAACCCAGACAC	2268	
Oy	62	CACCATCCCCCAGACGAGCTCACGAGGTCAATGCCGACATCAAACCCAGACAC	121	
Dd	2269	GTACTGCGTGGTGGTATGCGCGTAGTGCAGAAAGCGCGCATGGGACGTCGGAAGG	2328	
Oy	122	GTACTGCGTGGTGGTATGCGCGTAGTGCAGAAAGCGCGCATGGGACGTCGGAAGG	181	
Dd	2329	CTTCAAGACGACGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGATTCTGGC	2388	
Oy	182	CTTCAAGACGACGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGATTCTGGC	241	
Dd	2389	TCACTGCGAGAGACCAACCCGCTGAGGATGCGGTCTCATCGACAGAGCTCTCTCT	2448	
Oy	242	TCACTGCGAGAGACCAACCCGCTGAGGATGCGGTCTCATCGACAGAGCTCTCTCTCT	301	

	2449	GAATGAGGCCAGCAGTGTGGCTCTTTCCACGCTCTTCCTAAGCTTCATGTGGCAACCAGCGCGT	2508		
Dn	302	GAAATGAGGCCAGCAGTGTGGCTCTTTCCACGCTCTTCCTAAGCTTCATGTGGCAACCAGCGCGT	361		
Qy	2509	GGCGATCAGGGGGAAGAATGCTCACGAGCCAGTGCCCAAGGGGATCCCCGAGGGGCTTCATCTCTC	2568		
Dn	362	GGCGATCAGGGGGAAGAATGCTCACGAGCCAGTGCCCAAGGGGATCCCCGAGGGGCTTCATCTCTC	421		
Qy	2569	CACGCTGCTCTGCAGCCTGTGCTACGCGCGCATGTAGAGAACAAAGCTGTTTTGCGGGGATTGC	2628		
Dn	422	CACGCTGCTCTGCAGCCTGTGCTACGCGCGCATGTAGAGAACAAAGCTGTTTTGCGGGGATTGC	481		
Qy	2629	GGCGGAGCGGGCTGTCTCTGGGTTTGTGTGATGATTTCTTGTGGTAGACCTCACCTCCAC	2688		
Dn	482	GGCGGAGCGGGCTGTCTCTGGGTTTGTGTGATGATTTCTTGTGGTAGACCTCACCTCCAC	541		
Qy	2689	CCAAGCGCAAAAACCTTCTCTCAGAGACCTCTGTGCCAGTGTCCTCTGATGATGAGCTGCGTGT	2748		
Dn	542	CCAAGCGCAAAAACCTTCTCTCAGAGACCTCTGTGCCAGTGTCCTCTGATGATGAGCTGCGTGT	601		
Qy	2749	GAACCTTCGCGAAGACAGATGCTGAACTTCCCTGTGTAAGACAGAGGCTCTGGGTGGCACGCG	2808		
Dn	602	GAACCTTCGCGAAGACAGATGCTGAACTTCCCTGTGTAAGACAGAGGCTCTGGGTGGCACGCG	661		
Qy	2809	TTTTGTTCAGATGCGGGGCCCACAGCGCCATTTCCCTGGTGGGGGCGCTGTGCTGATACCG	2868		
Dn	662	TTTTGTTCAGATGCGGGGCCCACAGCGCCATTTCCCTGGTGGGGGCGCTGTGCTGATACCG	721		
Qy	2869	GACCTTCGAGGTGCAGAGCACACTACTCCAGCTATGCCCGAGACCTTCATCAGAGCCAGTCT	2928		
Dn	722	GACCTTCGAGGTGCAGAGCACACTACTCCAGCTATGCCCGAGACCTTCATCAGAGCCAGTCT	781		
Qy	2929	CACCTTCACCGCGGCTTCAA--GGCTGGAGAGAACTGGCTCGCAAA	2974		
Dn	782	CACCTTCACCGCGGCTTCAAAGGCTGGAGAGAACTGGCTCGCAAA	829		
RESULT_5	BUT02370	851 bp	mRNA	linear	EST 15-JUL-2003
LOCUS	UI-M-FI0-byx-f-12-0-UI.r1 NIH BMAP_FI0	Mus musculus	CDNA clone		
DEFINITION	IMAGE:6400523 5', mRNA sequence.				
ACCESSION	BUT02370				
VERSION	BUT02370.1	GI:23627105			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	1 (bases 1 to 851)				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
COMMENT	Contact: Robert Straube, Ph.D. Email: rgs@remail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLT at: http://image.llnl.gov This clone was contributed by the Brain Molecular Anatomy Project (BMAP) Seq primer: pyX-5. Location/Qualifiers 1..851 /organism="Mus musculus" /mo_type="mRNA" /scrain="CS7BL/6" /db_xref="taxon:10090" /clone="IMAGE:6400523"				
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Db 288 GCCACCTTTTCTCAGCAGAGAGCCGCGCTTCACCTCCACATAGGAATATGCATCCCC 229
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Db 228 AGATTGCGCATTTGTCACACCCCTGCGCCCTCCCTTCCTTCACCCCAACATCCAG 169
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Db 168 GTGAGAGACCCCTGAGAGAGACCCCTGAGAGCTCTGGGAATTTGAGTGAACCAAGTGTGCC 109
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Db 108 CTGTACACAGGAGAGACCCCTGAGAGCTCTGGGAATTTGAGTGAACCAAGTGTGCC 49
Qy 3963 GGTGCTGTGGAGTAAATATCTGAATATTTGAGTTTTCAGTTTGA 4010
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RESULT 7

LOCUS BM824748 492 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0096335 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-99-E07
5', mRNA sequence.

ACCESSION BM824748
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 492)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 99 row: E column: 07
High quality sequence stop: 492.
Location/Qualifiers

FEATURES

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/clone="S22SNUI6n1-99-E07"
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/cell_line="SNV-16"
/lab_host="DH10B"
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Site 2: NotI; The S22SNUI6 library was contributed by the
Soares laboratory and it was constructed as described by
Bonardo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNV-16 culture. SNV-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNV-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 11.1%; Score 445; DB 4; Length 492;
Best Local Similarity 100.0%; Pred. No. 3.7e-82;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2768 GTGAATTCCTCTGAGAGAGAGAGCCCTGGGTGAGCAGGCTTTTGTTCAGATGCCGCC 2827
Db 1 GTGAATTCCTCTGAGAGAGAGAGCCCTGGGTGAGCAGGCTTTTGTTCAGATGCCGCC 60
Qy 2828 CAGGACCTATTTCCCTGTGTGGGCTGTGTGTGTATACCCGAGCCCTGAGAGTGAAGC 2887
Db 61 CAGGACCTATTTCCCTGTGTGGGCTGTGTGTGTATACCCGAGCCCTGAGAGTGAAGC 120
Qy 2888 GACTACTCAGATAGCCCGAGCCCTCCATCAGAGCAGTCTACCTTCAACCGGGCTTC 2947
Db 121 GACTACTCAGATAGCCCGAGCCCTCCATCAGAGCAGTCTACCTTCAACCGGGCTTC 180
Qy 2948 AAGCTGGAGAGAGATGATGCTGCAAACTTTTGGGCTTTGCGGCTGAAGTGCAGAC 3007
Db 181 AAGCTGGAGAGAGATGATGCTGCAAACTTTTGGGCTTTGCGGCTGAAGTGCAGAC 240
Qy 3008 CTGTTTCTGATTTTTCAGGTGAACAGCTTCAGAGCGGTGTGACCAACTTCAAGATC 3067
Db 241 CTGTTTCTGATTTTTCAGGTGAACAGCTTCAGAGCGGTGTGACCAACTTCAAGATC 300
Qy 3068 CTCTCTGCTGAGGCTGACAGTTTTCAGCGATGTGTGTGACAGTCCCATTTTCAGCA 3127
Db 301 CTCTCTGCTGAGGCTGACAGTTTTCAGCGATGTGTGTGACAGTCCCATTTTCAGCA 360
Qy 3128 GTTGGAG 3187
Db 361 GTTGGAG 420
Qy 3188 TCCATCTCTGAAG 3212
Db 421 TCCATCTCTGAAG 445

RESULT 8
LOCUS BG917907 851 bp mRNA linear EST 05-JUN-2001
DEFINITION 602820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
mRNA sequence.

ACCESSION BG917907
VERSION BG917907.1 GI:14298383
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
TITLE NIH-MGC
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10903 row: K column: 08
High quality sequence stop: 753.
Location/Qualifiers

FEATURES

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/clone="IMAGE:4949887"
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/clone_1ib="NCI_CGAP_Mam6"

ORIGIN

/note="Organ: mammary; Vector: pCMV-Sport6; Site: 1: SalI; Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dt. library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

Query Match 10.4%; Score 419; DB 4; Length 851;
Best Local Similarity 71.9%; Pred. No. 1.1e-76;
Matches 579; Conservative 0; Mismatches 215; Indels 11; Gaps 2;

QY 2651 TTGGTGTGATGATTTCTTGTGTGACACCTCACTCCACCCAGGAAACCTTCCAGG 2710
DB 38 TTGTGTGATGATCTTCTGTAGAGAGCTCACTTGACACCAAAACCTTCTCCAGC 97
QY 2711 ACCCTGGTCCGAGGTGTCCTGTAGTATGAGTGGTGTGAACTTCCGAAAGACAGTGTG 2770
DB 98 ACCCTGGTCCAGCTTCTGTAGTATGAGTGGTGTGAACTTCCGAAAGACAGTGTG 157
QY 2771 AACTTCCCTGTAGAAAGACGAGCCCTGGTGGACGCTTTTGTTCAGATGCCGGCCAC 2830
DB 158 AACTTCCCTGTAGAGCTGGTACCTGGTGGTGGACGCTTCATACAGCTGGCTGTAC 217
QY 2831 GGCTATATCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2890
DB 218 TGCTGT 277
QY 2891 TACTCCAGTATGCTCCGAGCTTCATGAGACCACTTCATCTCAACCGGCTTCAAG 2950
DB 278 TACTCCAGTATGCTCCGAGCTTCATGAGACCACTTCATCTCAACCGGCTTCAAA 317
QY 2951 GCTGGGAGAAACATGCTCCGAACTCTTGGGGTCTTGGGGTGAAGTGTACAGCTG 3010
DB 338 GCTGGGAGAAACATGCTCCGAACTCTTGGGGTCTTGGGGTGAAGTGTACAGCTG 397
QY 3011 TTTCTGATTTGAGGTGAACAGCTTCAGAGCTGTGCAACCAATCTCAAGATCTTC 3070
DB 398 TTTCTGATTTGAGGTGAACAGCTTCAGAGCTGTGCAACCAATCTCAAGATCTTC 457
QY 3071 CTGCTGAGGCGTACAGCTTCAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3130
DB 458 CTGCTGAGGCGTACAGCTTCAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 517
QY 3131 TGGAAAGACCCCACTTTCTGAGGCTCATCTCTGACAGGCTCCCTCTGTCTCTCC 3190
DB 518 AGGAAGACCTTCACTTTCTGTGGGATCATCTCTGACAGGATCTGTGTGTGTGTGT 577
QY 3191 ATCTGAAAGCCCAAGACGAGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3250
DB 578 ATCTGAAAGCCCAAGATCTCAAGATGTACACTTAAAGGCTCTGTGTGTGTGTGT 627
QY 3251 CCTTCCGAGGCGT 3309
DB 628 TCTCTCCGAGGCGT 687
QY 3310 CCGTGTGACCTTGT 3359
DB 688 TTCTGTGATCTCAAAATGTCTCTGTGGACCTGTGAGACAGCCAAAACCGCTGTG 747
QY 3370 GAAGCTCCCGGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3429
DB 748 GAAGCTCCCGGAGAGAGCAATGATGATGATGATGATGATGATGATGATGATGAT 807
QY 3430 AGACTTCAGAGCACTTGGAGCTGA 3454
DB 808 AGACTTCAGAGCACTTGGAGCTGA 832

RESULT 9
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LOCUS AM276315/c
DEFINITION x10b12.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3',
RNA sequence.
ACCESSION AM276315

VERSION AM276315.1 GI:6663345
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 416)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Chris Mosekaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christina Pirange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/brd/image/image.html
Seq primer: -40bp from Gibco
High quality sequence stop: 413.
Location/Qualifiers
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/clone_11b="NCI_CGAP_Lu28"
/note="Organ: Lung; Vector: pCMV-Sport6; Site: 1: SalI;
Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies."

REFERENCE

AUTHORS

COMMENT

FEATURES

source

ORIGIN

Query Match 10.4%; Score 416; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 4.1e-76;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3594 AGGCTGCAATGTCGGGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGAGTGTCCAGC 3653
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QY 3654 AAGGCTGAGTGTCCAGCACACCTGCTTCACTTCCCAACAGCTGTGGCTGCTC 3713
DB 356 AAGGCTGAGTGTCCAGCACACCTGCTTCACTTCCCAACAGCTGTGGCTGCTC 297
QY 3714 CACCCAGGCGCAAGCTTTCTTCCACCAAGAGGCGGCTTCCACTGCCCATAGGAATAG 3773
DB 296 CACCCAGGCGCAAGCTTTCTTCCACCAAGAGGCGGCTTCCACTGCCCATAGGAATAG 237
QY 3774 TCCATCCCAAGATTTGCCATTTGTTCAACCCCTGCGCTGCTTGTGCTTCAACCCC 3833
DB 236 TCCATCCCAAGATTTGCCATTTGTTCAACCCCTGCGCTGCTTGTGCTTCAACCCC 177
QY 3834 ACCATCCAGTGAAGACCTCTGAGAAGACCTCTGAGAAGCTCTTGGAAATTTGGAGTGA 3893
DB 176 ACCATCCAGTGAAGACCTCTGAGAAGACCTCTGAGAAGCTCTTGGAAATTTGGAGTGA 117
QY 3894 AGGTGTGCTCTGTACACAGGCGAGACCTGTGACCTGTGATGGGGGTCTCTGTGGTCAAA 3953
DB 116 AGGTGTGCTCTGTACACAGGCGAGACCTGTGACCTGTGATGGGGGTCTCTGTGGTCAAA 57
QY 3954 TTGGGGGAGAGT 4009
DB 56 TTGGGGGAGAGT 1

RESULT 10
AA281296 389 bp mRNA linear EST 14-AUG-1997
LOCUS AA281296

DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
RNA sequence.	z08902.t1	NCI_GCAP_GCB1	Homo sapiens	CDNA clone IMAGE:712562 5',						
AA281296										
AA281296.1	GI:1924194									
EST.										
Homo sapiens (human)										
Homo sapiens										
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.										
1 (bases 1 to 389)										
NCI-CDAP http://www.ncbi.nlm.nih.gov/ncicgap .										
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index										
Unpublished (1997)										
Contact: Robert Strausberg, Ph.D.										
Email: cgapbs-remail.nih.gov										
This clone is available royalty-free through LINT ; contact the IMAGE Consortium (infoimage.lln.gov) for further information.										
Insert Length: 2187 Std Error: 0.00										
Seq primer: -28m13 rev2 ET from Amersham										
High quality sequence stop: 385.										
Location/Qualifiers										
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/lab_host="DH10B"										
/clone_id="NCI_GCAP_GCB1"										
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Straud (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). CDNA synthesis was primed with a Not I - oligo(dT) primer										
[5'-TGTTACCAATCTGAGTGGAGCGCGCCCTCATTTTCTTTTCTTTT-3']										
}. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."										
ORIGIN										
Query Match	9.6%	Score 385.8	DB 1;	Length 389;						
Best Local Similarity	99.5%	Pred. No. 8.3e-70;								
Matches 387;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;						
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QY	1739	TATGTCACGAGACCAAGCTTTCAAAAGAAACAGGCTCTTTTCTTACCGAAGAGTGTCTGG	1798							
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Db	121	AGCAAGTTGCAAGAGCATTTGAAATCAGACAGCACTTGAAGAGGATGACCTCGGGAGCTG	180							
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Db	181	TCGGAAGCAGAGGTTCAGGCTGAGCATTCGGGAAGCCAGGCCGCTGCTGCTGACGTCCAGATC	240							
QY	1919	CGCTTCATCCCAAGCTGAGCGGCTGGGCGCGATTTGAAATGAGATCTAGCTGTGGGA	1978							
Db	241	CGCTTCATCCCAAGCTGAGCGGCTGGGCGCGATTTGAAATGAGATCTAGCTGTGGGA	300							
QY	1979	GCCAGAAAGCTTCCGACAGAAAAGAGGCGCAGAGCTCTCAGCTCGAGGGTGAAGGCACTG	2038							
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RESULT 11
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 ACCESSION CN274427
 VERSION CN274427.1 GI:47290841
 KEYWORDS EST.
 ORGANISM Homo sapiens (human)
 SOURCE Homo sapiens
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo
 1 (bases 1 to 409)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
 Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,
 Lebkowski, J. and Stanton, L. W.
 Transcriptionome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
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 from und
 and H9

ORIGIN
 Query Match
 Best Local Similarity 9
 Matches 382; Conservat

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 Db | | | | | | | | | |
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 Db | | | | | | | | | |
 QY 61 GCGGCTGCTCC 302
 Db | | | | | | | | | |
 QY 87 GCGGCTGCTCC 339
 Db | | | | | | | | | |
 QY 121 GCCGCTGAGC 362
 Db | | | | | | | | | |
 QY 147 GCGCTGG 399
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 QY 181 GGACCCG 422
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 QY 207 GGACCCG 459
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 QY 241 ACGGCG 482
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 QY 301 CCGAG 542
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 QY 327 CCGAG 579
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 QY 361 GCTT 619

Page 10
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 GAGGCTGTGCGAGCGCGCGCGAAGAA 339
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 CCTCCCATGGCCTT 422
 GGGGGAGCGG 459
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Page 10

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and H9

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RESULT 12

CF531121

688 bp mRNA linear EST 12-SEP-2003
UI-M-FY0-cgp-m-21-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone

IMAGE:30355988 5', mRNA sequence.

ACCESSION

CF531121

CF531121.1 GI:34583085

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5.

FEATURES

Source

Location/Qualifiers
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/clone="IMAGE:30355988"
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ORIGIN

Query Match 8.6%; Score 346.2; DB 7; Length 688;
Best Local Similarity 73.9%; Pred. No. 1.7e-61;
Matches 438; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

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Db 183 CAGCGGCTGTCGACACCCG

Qy 220 GGTGTGCGTGCCTTGGAGCGCAGG

Db 243 AGTGTGATGACATCGGGGCTCACAGCCTC

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Qy 340 CGTGTGCGCTTGGCTTCCGCTGTCGACGCGGCGCGG

Db 363 CGTGTGCGCTTGGCTTCCGCTGTCGACGCGGCGCGG

Qy 400 CACCAACAGCTGCGACGACTACTCTGCCAACAGGTGACCGACGACTG

Db 423 CACTAGTAGCTGCGTGTGACTTGTCCCAACAGTGTATTAAGACCTGCTG

Qy 460 GCGGTGGGGGTGCTGCTGCGCGCGCGTGGGAGACAGTGTGCTGCTGCTG

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RESULT 13

CF531069

LOCUS

649 bp mRNA linear EST 12-SEP-2003
UI-M-FY0-cgp-c-19-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone

IMAGE:30355746 5', mRNA sequence.

ACCESSION

CF531069

CF531069.1 GI:34583033

KEYWORDS

EST.

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 649)
NIH-MGC <http://mhc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5.

FEATURES

Source

Location/Qualifiers
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RESULT 2
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AC
AC 17-JAN-2000 (first entry)
XX
XX
XX
XX Human telomerase reverse transcriptase (hTERT) cDNA.
DE
DE Telomerase reverse transcriptase; human; hTERT; cell proliferation;
KW
KW cancer; ss.
XX
XX
XX Homo sapiens.
OS
OS
XX

FH Key Location/Qualifiers
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 XX
 XX New catalytic polypeptide and polynucleotide, useful for increasing
 PT catalytic activity in a cell.
 XX
 PS Disclosure; Fig 2; 24pp; English.
 XX
 XX This is the nucleotide sequence of cDNA encoding human telomerase reverse
 CC transcriptase (hTERT, see AAY32090). Human telomerase is a target for
 CC diagnosing and treating diseases relating to cell proliferation and
 CC senescence, such as cancer, or for increasing the proliferative capacity
 CC of a cell. A claimed method for increasing the proliferative capacity
 CC of a vertebrate cell, especially a human or other mammalian cell, involves
 CC introducing into the cell a recombinant hTERT polynucleotide encoding an
 CC hTERT variant in which residues 192-323, 200-323, 192-271, 200-271, 222-
 CC 240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A
 CC claimed method for reducing telomerase activity in a cell involves
 CC introducing a recombinant polynucleotide encoding an hTERT variant having
 CC a deletion of amino acids 192-450, 560-565, 637-660, 748-764 or
 CC 1055-1071. The polynucleotides are obtained by mutagenesis of the hTERT
 CC coding sequence
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Db 2461 CAGTGGCTCTTTCAGAGCTTCTCTAGCTTCACTGTGTGCAACAGCGGTGCGCATCGAGG 2520
Qy 2521 CAACTTCTACGTCAGTGCAGGAGATCCCGAGGCTTCATCTCTCTCAACCTGTCTG 2580
Db 2521 CAACTTCTACGTCAGTGCAGGAGATCCCGAGGCTTCATCTCTCTCAACCTGTCTG 2580
Qy 2581 CAGCTGTGCTACGCGCGACATGGAAGAACAGCTGTTTGGGGGATTCGCGGGGAGCGGGCT 2640
Db 2581 CAGCTGTGCTACGCGCGACATGGAAGAACAGCTGTTTGGGGGATTCGCGGGGAGCGGGCT 2640
Qy 2641 GCTCTGCGTGTGAGATGATTTCTGTGTGTGACACTCACTCAACCCAGCGGAAAC 2700
Db 2641 GCTCTGCGTGTGAGATGATTTCTGTGTGTGACACTCACTCAACCCAGCGGAAAC 2700
Qy 2701 CTTCTCAGAGACCTGTGTCGAGGTGTCCCTGAGTATGAGCTGCTGAGTGAACCTTGGGAA 2760
Db 2701 CTTCTCAGAGACCTGTGTCGAGGTGTCCCTGAGTATGAGCTGCTGAGTGAACCTTGGGAA 2760
Qy 2761 GACATGTGTGAACCTTCCCTGTATGAAGACAGAGCCCTGGGTGGCAAGGCTTGTTCAGAT 2820
Db 2761 GACATGTGTGAACCTTCCCTGTATGAAGACAGAGCCCTGGGTGGCAAGGCTTGTTCAGAT 2820
Qy 2821 GCCGGCCCAAGCCTATTCCCTGGTGGCGGCTGCTGCTGATGATCCCGGACCTGGAGGT 2880
Db 2821 GCCGGCCCAAGCCTATTCCCTGGTGGCGGCTGCTGCTGATGATCCCGGACCTGGAGGT 2880
Qy 2881 GCAGAGCGACTTACTCAGCTATGCCGAGACCTTCATCAGAGCCAGTCTTCAACCG 2940
Db 2881 GCAGAGCGACTTACTCAGCTATGCCGAGACCTTCATCAGAGCCAGTCTTCAACCG 2940
Qy 2941 CGGCTTCAAGGCTGGAGAGAACATGCTGCAAACTCTTGTGGGTCTTGGGCTGAAGTG 3000
Db 2941 CGGCTTCAAGGCTGGAGAGAACATGCTGCAAACTCTTGTGGGTCTTGGGCTGAAGTG 3000
Qy 3001 TCACAGCCTGTTTCTGATTTGACATTTGACAGCTTCAGAGCGGTGCAACAATCTTA 3060
Db 3001 TCACAGCCTGTTTCTGATTTGACATTTGACAGCTTCAGAGCGGTGCAACAATCTTA 3060
Qy 3061 CAAAGTCTCTCTGTGCAAGGCGTACAGGTTTCAAGCATGTGTGTGCAAGCTTCAATTCA 3120
Db 3061 CAAAGTCTCTCTGTGCAAGGCGTACAGGTTTCAAGCATGTGTGTGCAAGCTTCAATTCA 3120
```


QY 1621 GAGCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCAACGTCGTGAGAGAGATCTGAGC 1680
DB 1621 GAGCCAGGGGTTGGCTGTGTTCCGGCCGAGAGCAACGTCGTGAGAGAGATCTGAGC 1680
QY 1681 CAAGTTCCTGACATGCTGATGATGTGATAGCTGTGAGCTGTGCTGCTCTTTTAA 1740
DB 1681 CAAGTTCCTGACATGCTGATGATGTGATAGCTGTGAGCTGTGCTCTTTTAA 1740
QY 1741 TGTACGGAAGACCAAGCTTTTAAAGAAAGAGCTTTTCTACCGAAGAGTGTGAGAG 1800
DB 1741 TGTACGGAAGACCAAGCTTTTAAAGAAAGAGCTTTTCTACCGAAGAGTGTGAGAG 1800
QY 1801 CAAGTTCGAAGATTTGGAATCAGACAGCACTTGAAGAGGTGAGTGGAGAGCTGTC 1860
DB 1801 CAAGTTCGAAGATTTGGAATCAGACAGCACTTGAAGAGGTGAGTGGAGAGCTGTC 1860
QY 1861 GGAAGCAGAGGTGAGAGCATGAGAGAGCCAGAGCCGCTGTGAGCTGCAAGACTCCG 1920
DB 1861 GGAAGCAGAGGTGAGAGCATGAGAGAGCCAGAGCCGCTGTGAGCTGCAAGACTCCG 1920
QY 1921 CTTTCATCCCAAGCCTGACGAGGCTGCGGCGGATTTGGAATGAGATGAGTGTGAGAGC 1980
DB 1921 CTTTCATCCCAAGCCTGACGAGGCTGCGGCGGATTTGGAATGAGATGAGTGTGAGAGC 1980
QY 1981 CAGAACCTTCCGAGAGAGAGAGAGGCGGAGCGTCTCACTCGAGGAGTGAAGCACTGTT 2040
DB 1981 CAGAACCTTCCGAGAGAGAGAGAGGCGGAGCGTCTCACTCGAGGAGTGAAGCACTGTT 2040
QY 2041 CAGGCTGCTCACTGAGAGGAGGCGGCGGCGGCGGCGGCTCTGAGGCGCTGTGCTGAG 2100
DB 2041 CAGGCTGCTCACTGAGAGGAGGCGGCGGCGGCGGCGGCTCTGAGGCGCTGTGCTGAG 2100
QY 2101 CTTGGAAGATATCCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2160
DB 2101 CTTGGAAGATATCCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2160
QY 2161 GCGGCTGAGCTGATCTTGTTCAGAGTGTGATGAGAGGCGGCGGCGGCGGCGGCGGCGG 2220
DB 2161 GCGGCTGAGCTGATCTTGTTCAGAGTGTGATGAGAGGCGGCGGCGGCGGCGGCGGCGG 2220
QY 2221 GGAAGGCTGACGAGAGGTGATGCGCAGCATGATCAAAACCCAGAAACGATGCGTGGC 2280
DB 2221 GGAAGGCTGACGAGAGGTGATGCGCAGCATGATCAAAACCCAGAAACGATGCGTGGC 2280
QY 2281 TCGGTATGCGGTGTCAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2340
DB 2281 TCGGTATGCGGTGTCAGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2340
QY 2341 CGTCTTACCTTGAAGAGCTGCGCAGCATGATGAGAGAGTGTGCTGAGAGAGAGAGAG 2400
DB 2341 CGTCTTACCTTGAAGAGCTGCGCAGCATGATGAGAGAGTGTGCTGAGAGAGAGAGAG 2400
QY 2401 GACCAAGGCTGAGAGAGTGTGATGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAG 2460
DB 2401 GACCAAGGCTGAGAGAGTGTGATGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAG 2460
QY 2461 CAGGAGCTGCTGAGAGAGTGTGATGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAG 2520
DB 2461 CAGGAGCTGCTGAGAGAGTGTGATGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAG 2520
QY 2521 CAAGTCTTACCTGAGAGAGTGTGATGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAG 2580
DB 2521 CAAGTCTTACCTGAGAGAGTGTGATGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAG 2580
QY 2581 CAGGCTTGTGCTGAGAGAGTGTGATGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAG 2640
DB 2581 CAGGCTTGTGCTGAGAGAGTGTGATGAGAGAGAGTGTGCTGAGAGAGAGAGAGAGAG 2640
QY 2641 GCTTCGAGGTTGTGATGATTTCTTGTGTGAGAGAGTGTGCTGAGAGAGAGAGAGAG 2700
DB 2641 GCTTCGAGGTTGTGATGATTTCTTGTGTGAGAGAGTGTGCTGAGAGAGAGAGAGAG 2700

QY 2701 CTTCTCAGAGACCTTGTGTCAGAGTGTGCTGAGATGAGCTGAGTGAACCTTGGGAA 2760
DB 2701 CTTCTCAGAGACCTTGTGTCAGAGTGTGCTGAGATGAGCTGAGTGAACCTTGGGAA 2760
QY 2761 GACAGTGTGAACTTCCCTGTGTAAGAGAGAGGCTGTGAGTGTGAGAGAGAGAGAGAG 2820
DB 2761 GACAGTGTGAACTTCCCTGTGTAAGAGAGAGGCTGTGAGTGTGAGAGAGAGAGAGAG 2820
QY 2821 GCGGCGGCAAGGCTTATCCCTGTGAGAGAGAGGCTGTGAGTGTGAGAGAGAGAGAGAG 2880
DB 2821 GCGGCGGCAAGGCTTATCCCTGTGAGAGAGAGGCTGTGAGTGTGAGAGAGAGAGAGAG 2880
QY 2881 GCAAGGCACTATCCAGATGAGAGAGAGGCTGTGAGTGTGAGAGAGAGAGAGAGAGAG 2940
DB 2881 GCAAGGCACTATCCAGATGAGAGAGAGGCTGTGAGTGTGAGAGAGAGAGAGAGAGAG 2940
QY 2941 CCGCTTCAAGGCTGTGAG 3000
DB 2941 CCGCTTCAAGGCTGTGAG 3000
QY 3001 TCAAGGCTGTTTGTGATTTGAGAGTGAACAGGCTGTGAGAGAGAGAGAGAGAGAGAG 3060
DB 3001 TCAAGGCTGTTTGTGATTTGAGAGTGAACAGGCTGTGAGAGAGAGAGAGAGAGAGAG 3060
QY 3061 CAGAGTCTTCTGTCAG 3120
DB 3061 CAGAGTCTTCTGTCAG 3120
QY 3121 TCAAGAGTTTGAAG 3180
DB 3121 TCAAGAGTTTGAAG 3180
QY 3181 CTTGCTACTCATCTGTAAG 3240
DB 3181 CTTGCTACTCATCTGTAAG 3240
QY 3241 CCGGCTTGTGCTGTCAG 3300
DB 3241 CCGGCTTGTGCTGTCAG 3300
QY 3301 GATTCAG 3360
DB 3301 GATTCAG 3360
QY 3361 GCTGAGTGTGAG 3420
DB 3361 GCTGAGTGTGAG 3420
QY 3421 ACTGCTTGTGAG 3480
DB 3421 ACTGCTTGTGAG 3480
QY 3481 GAGCAG 3540
DB 3481 GAGCAG 3540
QY 3541 CACAGCAG 3600
DB 3541 CACAGCAG 3600
QY 3601 CATGTCAG 3660
DB 3601 CATGTCAG 3660
QY 3661 GAGTGTGAG 3720
DB 3661 GAGTGTGAG 3720
QY 3721 GGGCAG 3780
DB 3721 GGGCAG 3780
QY 3781 CCAGATTCGAGATTTGTTACAG 3840

Db 3781 CCAGATTGCGCAATTGTTCACCCCTGCGCCCTGCTCTTTGCTTCCACCCACCATCC 3840
Qy 3841 AGGTGAGACCTCTGAGAAAGACCTCTGGAGCTCTGGGAATTGAGTGCACAAAGTGTG 3900
Db 3841 AGGTGAGACCTCTGAGAAAGACCTCTGGAGCTCTGGGAATTGAGTGCACAAAGTGTG 3900
Qy 3901 CCTGTACACAGACGAGACCTCTGACCTGATGAGGAGGTCCCTGTGGGTCAATTGGGG 3960
Db 3901 CCTGTACACAGACGAGACCTCTGACCTGATGAGGAGGTCCCTGTGGGTCAATTGGGG 3960
Qy 3961 GAGTGTCTGGAGTAAATACTGAATATATGATTTTCACTTTGAAAAA 4015
Db 3961 GAGTGTCTGGAGTAAATACTGAATATATGATTTTCACTTTGAAAAA 4015
RESULT 5
AAD46821
ID AAD46821 standard; cDNA; 4015 BP.
XX
AC AAD46821;
XX
DT 27-JAN-2003 (first entry)
XX
DE Human telomerase reverse transcriptase (TERT) cDNA.
XX
KM Carbohydrate antigen, alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
KM transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
KM telomerase reverse transcriptase; gene; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "Human telomerase reverse transcriptase"
XX
PD MO200274948-A2.
XX
PF 26-SEP-2002.
XX
PR 21-MAR-2002; 2002W0-CA000378.
XX
PR 21-MAR-2001; 2001US-027781P.
XX
PA (GERO-) GERON CORP.
XX
PI Denning C, Clark AJ, Schiff JM;
XX
DR MPI: 2002-759895/82.
XX
DR P-PSDB; AAE29226.
XX
PT Mammalian cells, useful for producing animal tissues with carbohydrate
PT antigens that are compatible for transplantation into human patients.
XX
PS Disclosure; Page 33-34; 71pp; English.
XX
CC The invention relates to animal tissues with carbohydrate antigens that
CC are compatible for transplantation into human patients. The mammalian
CC cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
CC transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
CC fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
CC with carbohydrate antigens that are compatible for producing animal tissue
CC human patients. The present sequence is human telomerase reverse
CC transcriptase (TERT) cDNA used in the invention
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
Query Match 100.0%; Score 4015; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAGCGCTGCTGCTGCTGCGACGTGGAAAGCCCTGGCCCGGCAACCCCGCATGCC 60

Db 1 GCAGCGCTGCTGCTGCTGCGACGTGGAAAGCCCTGGCCCGGCAACCCCGCATGCC 60
Qy 61 GCGCGCTCCCGCTGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 GCGCGCTCCCGCTGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy 121 GCGCGTGGCAGCTTGTGTCGAGCGCTGAGGAGCCCGAGGAGCTGAGGAGCTGAGGAG 180
Db 121 GCGCGTGGCAGCTTGTGTCGAGCGCTGAGGAGCCCGAGGAGCTGAGGAGCTGAGGAG 180
Qy 181 GGAACCGGAGGCTTTCCGCGCGCTGAGGCGCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 181 GGAACCGGAGGCTTTCCGCGCGCTGAGGCGCAAGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Qy 241 AGCG 300
Db 241 AGCG 300
Qy 301 CGAGTGTGTCGAGAGGCTGTGTCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 301 CGAGTGTGTCGAGAGGCTGTGTCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Qy 361 GCTGTGTCGAGCGGAGCG 420
Db 361 GCTGTGTCGAGCGGAGCG 420
Qy 421 CCTGCCCAACAGCTGTGACCGAGCTGCTGAGGAGCGGAGGAGGAGGAGGAGGAGGAGG 480
Db 421 CCTGCCCAACAGCTGTGACCGAGCTGCTGAGGAGCGGAGGAGGAGGAGGAGGAGGAGG 480
Qy 481 CGCGTGGGCGAGCGAGTGTGTCGAGTGTGTCGAGTGTGTCGAGTGTGTCGAGTGTGTCG 540
Db 481 CGCGTGGGCGAGCGAGTGTGTCGAGTGTGTCGAGTGTGTCGAGTGTGTCGAGTGTGTCG 540
Qy 541 GCGTCCCAAGCTGCGCTGACAGAGTGTGCGGAGCGCGCGCTGTACACAGCTGAGCGCTG 600
Db 541 GCGTCCCAAGCTGCGCTGACAGAGTGTGCGGAGCGCGCGCTGTACACAGCTGAGCGCTG 600
Qy 601 TCAAGCCCG 660
Db 601 TCAAGCCCG 660
Qy 661 CTGGAACCACTAGCTGTGAGGAGGCGGAGGCTCCCGCTGAGGCTGCGAGCGCGCGGTCG 720
Db 661 CTGGAACCACTAGCTGTGAGGAGGCGGAGGCTCCCGCTGAGGCTGCGAGCGCGCGGTCG 720
Qy 721 GAGCGCGCGGCGCGAGTGTGCGAGCGGAGTGTGCGGTCGCGAGCGCGCGCGCGCGCG 780
Db 721 GAGCGCGCGGCGCGAGTGTGCGAGCGGAGTGTGCGGTCGCGAGCGCGCGCGCGCGCG 780
Qy 781 TCGCCCTGAGCGCGAGCGGAGCGCGCGCTGTGAGGAGGCTGCTGAGGCGCGCGCGCG 840
Db 781 TCGCCCTGAGCGCGAGCGGAGCGCGCGCTGTGAGGAGGCTGCTGAGGCGCGCGCGCG 840
Qy 841 GCGTGTGAGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGG 900
Db 841 GCGTGTGAGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGGAGTGTGCGG 900
Qy 901 CACTTTTGGAGGCTGCTGTGCGACGCGCGCACTTCCACCAATCGGTGGCGCGCA 960
Db 901 CACTTTTGGAGGCTGCTGTGCGACGCGCGCACTTCCACCAATCGGTGGCGCGCA 960
Qy 961 GCAACACGCGGCG 1020
Db 961 GCAACACGCGGCG 1020
Qy 1021 CCGGCTGTCGCGCGAGACCAAGCACTTCTCTACTCTGAGGAGCAAGAGAGAGTGTG 1080
Db 1021 CCGGCTGTCGCGCGAGACCAAGCACTTCTCTACTCTGAGGAGCAAGAGAGAGTGTG 1080
Qy 1081 GCGCTCTCTCTACTCTGAGTGTGAGGCGCGAGCTGAGGCTGAGGCTGAGGCTGAGG 1140
Db 1081 GCGCTCTCTCTACTCTGAGTGTGAGGCGCGAGCTGAGGCTGAGGCTGAGGCTGAGG 1140

Db 1081 GCCCTCTTCTACTGAGCTCTGAGGCCGACGCTGAGCGGCTTCGAGAGGCTCGTGA 1140
Qy 1141 GACCATCTTCTGAGGTTCCAGGCTTGATGCGAGGACTCCCGCAGGTTGCCCCCT 1200
Db 1141 GACCATCTTCTGAGGTTCCAGGCTTGATGCGAGGACTCCCGCAGGTTGCCCCCT 1200
Qy 1201 GCGCCAGCGCTACTGGAATGCGGCCCCCTGTTCTTGAGCTGCTTGAGAACAGCGCGA 1260
Db 1201 GCGCCAGCGCTACTGGAATGCGGCCCCCTGTTCTTGAGCTGCTTGAGAACAGCGCGA 1260
Qy 1261 GTCGCCCTACGAGGAGTGTCTCAAGACGACTCCGCTGCGAGCTGCGGTCAACCCAGC 1320
Db 1261 GTCGCCCTACGAGGAGTGTCTCAAGACGACTCCGCTGCGAGCTGCGGTCAACCCAGC 1320
Qy 1321 AGCGGCTGTGTGCTGCGGAGAAAGCCCGAGGCTCTGTGCGGCCCCCGAGAGAGGA 1380
Db 1321 AGCGGCTGTGTGCTGCGGAGAAAGCCCGAGGCTCTGTGCGGCCCCCGAGAGAGGA 1380
Qy 1381 CACAGACCCCGTCCGCTGAGCTGCTCCGCAAGCAGGAGCCCTGAGGTTGA 1440
Db 1381 CACAGACCCCGTCCGCTGAGCTGCTCCGCAAGCAGGAGCCCTGAGGTTGA 1440
Qy 1441 CGGCTTGTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Db 1441 CGGCTTGTGCGGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
Qy 1501 CAACGAAAGCGGCTTCTCTCAGAAACACCAAGAGTTATCTCTCTGAGGAAAGCATGCCA 1560
Db 1501 CAACGAAAGCGGCTTCTCTCAGAAACACCAAGAGTTATCTCTCTGAGGAAAGCATGCCA 1560
Qy 1561 GCTCTGCTGAGAGGCTGAGCTGAGAGATGAGGCTGAGGAGCTGAGGAGCTGAGGAG 1620
Db 1561 GCTCTGCTGAGAGGCTGAGCTGAGAGATGAGGCTGAGGAGCTGAGGAGCTGAGGAG 1620
Qy 1621 GAGCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db 1621 GAGCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Qy 1681 CAACTTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Db 1681 CAACTTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
Qy 1741 TGTCAAGGAGACAGCTTCAAAAGAAAGAGGCTCTTTTCTACCGAAAGTGTCTGAG 1800
Db 1741 TGTCAAGGAGACAGCTTCAAAAGAAAGAGGCTCTTTTCTACCGAAAGTGTCTGAG 1800
Qy 1801 CAACTTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Db 1801 CAACTTCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Qy 1861 GGAAGCAGAGGCTGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
Db 1861 GGAAGCAGAGGCTGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
Qy 1921 CTTGATCCCGCAAGCTGAGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1921 CTTGATCCCGCAAGCTGAGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Qy 1981 CAGAACTTCCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Db 1981 CAGAACTTCCCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Qy 2041 CAGAGTGTCTCAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100
Db 2041 CAGAGTGTCTCAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100
Qy 2101 CTTGACGATATCCAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2160
Db 2101 CTTGACGATATCCAGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2160
Qy 2161 GCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
Db 2161 GCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220

Qy 2221 GGAAGGCTCAAGAGGCTATGCGAGCATCATCAAAACCCAGAAACAGTACTGCTGCG 2280
Db 2221 GGAAGGCTCAAGAGGCTATGCGAGCATCATCAAAACCCAGAAACAGTACTGCTGCG 2280
Qy 2281 TCGATATCCGCTGCTCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Db 2281 TCGATATCCGCTGCTCAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
Qy 2341 GCTCTTCTACCTTGAAGACCTTCAGGCTTATGAGAGTTCGAGTTCGCTGCTGCTGCTGCT 2400
Db 2341 GCTCTTCTACCTTGAAGACCTTCAGGCTTATGAGAGTTCGAGTTCGCTGCTGCTGCTGCT 2400
Qy 2401 GACAGGCTGCTGAGGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Db 2401 GACAGGCTGCTGAGGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
Qy 2461 CAGTGGCTCTTCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
Db 2461 CAGTGGCTCTTCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
Qy 2521 CAGTGGCTCTTCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Db 2521 CAGTGGCTCTTCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580
Qy 2581 CAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Db 2581 CAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Qy 2641 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
Db 2641 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700
Qy 2701 CTTCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
Db 2701 CTTCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
Qy 2761 GACAGTGTGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
Db 2761 GACAGTGTGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
Qy 2821 GCGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
Db 2821 GCGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
Qy 2881 GCGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Db 2881 GCGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
Qy 2941 GCGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Db 2941 GCGGCTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Qy 3001 TCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Db 3001 TCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Qy 3061 CAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
Db 3061 CAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
Qy 3121 TCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
Db 3121 TCAAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
Qy 3181 CAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
Db 3181 CAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
Qy 3241 GCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Db 3241 GCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300


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Db      2881 GCAGAGCGACTACTCCAGCTATGCCGACCTCATCAGAGCGAGTCTCACCTTCAACCG 2940
Qy      2941 CGGCTTAAAGGCTGGAGAGAAATGCCCTCGAAATCTTTGGGGCTTGGCGGTGAAGTG 3000
Db      2941 CGGCTTAAAGGCTGGAGAGAAATGCCCTCGAAATCTTTGGGGCTTGGCGGTGAAGTG 3000
Qy      3001 TCACAGCTGTGTTTCGAGATTGTCAGAGTGAACAGCTCCAGAGCGGTGACCAACATCTA 3060
Db      3001 TCACAGCTGTGTTTCGAGATTGTCAGAGTGAACAGCTCCAGAGCGGTGACCAACATCTA 3060
Qy      3061 CAAGATCTCTCTGTCGAGCGGTACAGGTTTACGCGATGTGTGTCGACGCTCCATTTCA 3120
Db      3061 CAAGATCTCTCTGTCGAGCGGTACAGGTTTACGCGATGTGTGTCGACGCTCCATTTCA 3120
Qy      3121 TCAGAAATTTTGAAGAAACCCCACTTTTCTGGCGGTCTACTGTGACAGGCTCTCT 3180
Db      3121 TCAGAAATTTTGAAGAAACCCCACTTTTCTGGCGGTCTACTGTGACAGGCTCTCT 3180
Qy      3181 CTGCTACTCCATCTCGAAAGCCAAAGACGAGGATGTGCTGGGGGCGCAAGGGCGCGC 3240
Db      3181 CTGCTACTCCATCTCGAAAGCCAAAGACGAGGATGTGCTGGGGGCGCAAGGGCGCGC 3240
Qy      3241 CGGCGCTGTGCTTCCGAGCGCGTGCAGTGTGTGCGCAACAGGATTCCTGTCAAGCT 3300
Db      3241 CGGCGCTGTGCTTCCGAGCGCGTGCAGTGTGTGCGCAACAGGATTCCTGTCAAGCT 3300
Qy      3301 GACTTGAAACCGGTGTCACTTAAAGTCCACTCTCTGGGGTCACTCAGAGACGCCCAACGCA 3360
Db      3301 GACTTGAAACCGGTGTCACTTAAAGTCCACTCTCTGGGGTCACTCAGAGACGCCCAACGCA 3360
Qy      3361 GCTGAGTGGAAAGCTCCCGGGGACGAGCGTGACTGCTCCGAGAGCGGAGCCCGGC 3420
Db      3361 GCTGAGTGGAAAGCTCCCGGGGACGAGCGTGACTGCTCCGAGAGCGGAGCCCGGC 3420
Qy      3421 ACTGCGCTCAGACTTCAAGACCATCTGTGAGTGTGATGAGCCCGGCGCAAGCGAGCGCA 3480
Db      3421 ACTGCGCTCAGACTTCAAGACCATCTGTGAGTGTGATGAGCCCGGCGCAAGCGAGCGCA 3480
Qy      3481 GAGCGAACAACGAGCGCTCTGTCAAGCCCGGGTCTTACGTTCCAGAGGAGAGGGCGCGC 3540
Db      3481 GAGCGAACAACGAGCGCTCTGTCAAGCCCGGGTCTTACGTTCCAGAGGAGAGGGCGCGC 3540
Qy      3541 CACACCCAGGCGCGGACCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3600
Db      3541 CACACCCAGGCGCGGACCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3600
Qy      3601 CATGTCCGCGCTGAAAGCTGATGTGCGGCTGAGGCGCTGAGCGAGTGTCCAGCGAGGCT 3660
Db      3601 CATGTCCGCGCTGAAAGCTGATGTGCGGCTGAGGCGCTGAGCGAGTGTCCAGCGAGGCT 3660
Qy      3661 GAGTGTCCAGCAACCTGCGCTTCTCACTTCCCAAGGCTGGCGTGGCTTCCACCCCA 3720
Db      3661 GAGTGTCCAGCAACCTGCGCTTCTCACTTCCCAAGGCTGGCGTGGCTTCCACCCCA 3720
Qy      3721 GGGCGAGCTTTTCCACAGAGGCGCGCTTCCATCCGCCCATAGGAATGTGCATCC 3780
Db      3721 GGGCGAGCTTTTCCACAGAGGCGCGCTTCCATCCGCCCATAGGAATGTGCATCC 3780
Qy      3781 CCAGATTCGCGCATTTTCAACCCCTCGCCCTGCGCTTCTTGTGCTTCCACCCCAACATCC 3840
Db      3781 CCAGATTCGCGCATTTTCAACCCCTCGCCCTGCGCTTCTTGTGCTTCCACCCCAACATCC 3840
Qy      3841 AGGTGGAAGACCTTGAGAGAGACCTTGAGAGCTCTGGAAATTTGAGTGAACCAAGGTG 3900
Db      3841 AGGTGGAAGACCTTGAGAGAGACCTTGAGAGCTCTGGAAATTTGAGTGAACCAAGGTG 3900
Qy      3901 CCTGTACACAGGCGAGGACCTTGACCTGATGGGGGCTCTGGGGTCAATTTGGGG 3960
Db      3901 CCTGTACACAGGCGAGGACCTTGACCTGATGGGGGCTCTGGGGTCAATTTGGGG 3960
Qy      3961 GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGGAAAAA 4015
Db      3961 GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGGAAAAA 4015

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RESULT 7
ACCS7552
ID ACCS7552 standard; cDNA; 4015 BP.
XX
AC ACCS7552;
XX
DT 28-JUL-2003 (first entry)
XX
DE Human telomerase reverse transcriptase cDNA.
XX
KW Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
KW immunosuppressive; antifertility; fungicide; antiparasitic;
KW antiinflammatory; human; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH
FT Key Location/Qualifiers
FT CDS 56..3454
FT FT /*tag= a
FT FT /product= "TERT"
XX
PD WO2003034985-A2.
XX
PF 16-OCT-2002; 2002WO-US033146.
XX
PR 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX
XX (UNRP ) UNIV ROCHESTER.
XX
XX Rowley PT;
XX
XX MPI: 2003-403289/38.
XX
XX P-PSDB; ABR42063.
XX
XX
XX Novel nucleic acid encoding or comprising interfering RNAs which target
XX telomerase RNA, useful for inhibiting telomerase activity for treating
XX cancer, infertility and disorders of the immune system.
XX
XX Disclosure; Fig 3; 52pp; English.
XX
PS
XX
XX The present sequence is that of human telomerase reverse transcriptase
XX (TERT) cDNA. The invention relates to the discovery that double-stranded
XX interfering RNAs, such as short interfering RNAs (siRNA), which target
XX telomerase RNA or TERT mRNA are capable of inhibiting telomerase
XX activity. Inhibition of telomerase in cancer cells leads to telomere
XX shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
XX telomerase activity can also be used for treatment of infertility, for
XX contraception or sterilisation, for immunosuppression, for treatment of
XX yeast, parasite and fungal infections, and in antiinflammatory therapies.
XX As telomerase is active in a limited number of cell types, e.g. tumour
XX cells, germ-line cells, certain stem cells of the haematopoietic system, T
XX and B cells, sun-damaged skin, and proliferative cervix, most normal
XX cells are not affected by telomerase RNA interference therapy
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

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Query Match 100.0%; Score 4015; DB 8; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 GCGCGCTCCGCGTTCGAGCGCGTGGCGCTCCCTGTGCGAGCCACTACCGGAGTCT 120
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[illegible]

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Db	1201	GGCCCAAGCCTACTGGCAAAATCGGCGCCCTGTTTCTGGAAGCTGCTTGGAACCAACGGGCA	1260
QY	1261	GTGGCCCTTACGGGGGTGCTCTCAAGACGACCTGCCGCTGGAGCTGGGTCAACCCAGC	1320
Db	1261	GTGCCCCCTTACGGGGGTGCTCTTCAAGACGACCTGCCGCTGGAGCTGGGTCAACCCAGC	1320
QY	1321	AGCGGGTGTCTGTGCCCGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCCAGAGAGAGGA	1380
Db	1321	AGCGGGTGTGTGTGCCCGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCCAGAGAGAGGA	1380
QY	1381	CACAGACCCCCGTGCGCTGTGAGTGTCTCGCCAGCACAGCAGCCCTCGCAGGTGT	1440
Db	1381	CACAGACCCCCGTGCGCTGTGAGTGTCTTCCGACAGCACAGCAGCCCTCGCAGGTGT	1440
QY	1441	CGGCTTGTGCGGGGCTGTGCGCGGCGGTGTGGTCCCCAGGCTCTTGAGGCTCAAGCA	1500
Db	1441	CGGTTTGTGCGGGGCTGTGCGCGGCGGTGTGGTCCCCAGGCTCTTGAGGCTCAAGCA	1500
QY	1501	CAACGAACCGCGCTTCTCTAGGAACACAAAGAGTTCACTCCCTGGGGAACATGCGAA	1560
Db	1501	CAAGGAACCGCGCTTCTCTAGGAACACAAAGAGTTCACTCCCTGGGGAACATGCGAA	1560
QY	1561	GCTCTGCTCAGAGCTGACGTGAGAGATGAGCGTGGCGGACCTGCGTTGCTGCGAG	1620
Db	1561	GCTCTGCTCAGAGAGCTGACGTGAGAGATGAGCGTGGCGGACCTGCGTTGCTGCGAG	1620
QY	1621	GAGCCCAAGGGTGTGCTGTGTTCCGCGCCGAGACACCGTTCGCGTGAAGAGATCTGGC	1680
Db	1621	GAGCCCAAGGGTGTGCTGTGTTCCGCGCCGAGACACCGTTCGCGTGAAGAGATCTGGC	1680
QY	1681	CAAGTTCCTGACATGAGCTGATGATGTGTACGTGTGAGCTGCTAGGCTTTCTTTTA	1740
Db	1681	CAAGTTCCTGACATGAGCTGATGATGTGTACGTGTGAGCTGCTAGGCTTTCTTTTA	1740
QY	1741	TGTCAAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTGAGG	1800
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Db	1801	CAAGTTGCAAAAGCATTTGGAATCAGACAGCATTTGAAGAGGTGACGTGGGAGCTGTG	1860
QY	1861	GGAGACAGAGGTCAAGGACGATCGGGAAGCGAGCGCCCTGTGACGTTCAGACTCCG	1920
Db	1861	GGAGACAGAGGTCAAGGACGATCGGGAAGCGAGCGCCCTGTGACGTTCAGACTCCG	1920
QY	1921	CTTTCATCCCAAGCTGACGGGCTGCGGCGGATTTGTGAATGGAATCACTCTCGTGGAGC	1980
Db	1921	CTTTCATCCCAAGCTGACGGGCTGCGGCGGATTTGTGAATGGAATCACTCTCGTGGAGC	1980
QY	1981	CAGAAAGTTCCGACAGAGAAAAGGGCGGAGCTCTCACTCGAGGTTAAAGTCACTGT	2040
Db	1981	CAGAAAGTTCCGACAGAGAAAAGGGCGGAGCTCTCACTCGAGGTTAAAGTCACTGT	2040
QY	2041	CAGCGTGTCTCACTACAGACGGGCGCGCGGCGCTCCCTGGAGCGCTCTGTGCTGGG	2100
Db	2041	CAGCGTGTCTCACTACAGACGGGCGCGCGGCGCTCCCTGGAGCGCTCTGTGCTGGG	2100
QY	2101	CTTGAACGATATCAACAGGCGCTTGCGCACCTTGTGTGCTGTGCGGGCCAGAACCC	2160
Db	2101	CTTGAACGATATCAACAGGCGCTTGCGCACCTTGTGTGCTGTGCGGGCCAGAACCC	2160
QY	2161	GCGCGCTGAGCTGTACTTTGTCAAGTGAATGTACGGGCGGAGTACACCATCCGCCA	2220
Db	2161	GCGCGCTGAGCTGTACTTTGTCAAGTGAATGTACGGGCGGAGTACACCATCCGCCA	2220
QY	2221	GGACAGAGCTCAAGAGAGTCACTGCAGAGATCAACAAACCCAGAACAGTACTGCTGG	2280
Db	2221	GGACAGAGCTCAAGAGAGTCACTGCAGAGATCAACAAACCCAGAACAGTACTGCTGG	2280

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 RESULT 9
 ACC4482
 ID ACC4482 standard; DNA; 4015 BP.
 AC ACC4482;
 DT 29-AUG-2003 (first entry)
 DE Human telomerase reverse transcriptase gene.
 XX Gene; ds; human; telomerase reverse transcriptase; adipogenic capacity;
 KW primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
 KM anorectic; adiponectin; insulin.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 56..3454
 FT /tag= a
 FT /product= "telomerase reverse transcriptase"
 XX
 PN WO2003031640-A2.
 PD 17-APR-2003.
 PF 07-OCT-2002; 2002WO-US031635.
 XX 06-OCT-2001; 2001US-0327650P.
 PR 06-OCT-2001; 2001US-0327651P.
 XX (BOST-) BOSTON MEDICAL CENT CORP.
 PA Kirkland J, Tchkonja T;
 PI WPI; 2003-421278/39.
 DR P-PSDB; ABR58045.
 XX
 PT New primary preadipocyte strain expressing telomerase reverse
 PT transcriptase, useful in research applications, screening assays,
 PT clinical applications, and in the administration of therapeutic agents,
 PT particularly for obesity.
 XX
 PS Disclosure; Page 11-13; 53pp; English.
 CC The invention relates to the generation of primary preadipocyte cell
 CC strains that express telomerase reverse transcriptase (TERT- the
 CC catalytic subunit of telomerase), and maintain and/or enhance replicative
 CC potential and maintain adipogenic capacity of the cell. This sequence
 CC represents the gene encoding the TERT protein. The cell strain can be
 CC used in research to study all aspect of adipogenesis, especially in
 CC relation to researching treatments for e.g. obesity. The cell can also be
 CC used to identify adipogenesis modulators for use as therapeutic agents

CC such as hormones, growth factors, cytokines, enzymes, cholesterol binding
 CC proteins, cholesterol removing proteins or their combinations.
 CC Alternatively, the therapeutic agent may be an adipocytokine, preferably
 CC adiponectin, or insulin
 XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 4015; DB 8; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCAGGCTGCGCTCTGCTGCTGCGACGTGGAGACCTTGGCCCAATCCCGCATATGC 60
 DB 1 GCAGGCTGCGCTCTGCTGCTGCGACGTGGAGACCTTGGCCCAATCCCGCATATGC 60
 QY 61 GGGCGCTCCCGCTGCGCGACGCGTGGCTCCCTGTGCGACGCACTACCGGAGGTGCT 120
 DB 61 GGGCGCTCCCGCTGCGCGACGCGTGGCTCCCTGTGCGACGCACTACCGGAGGTGCT 120
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 DB 121 GCGCTGCGCACGTTCTGTGCGCGCTGCGGCGCCAGGAGCTTGTGCTGCAAGCGCG 180
 QY 181 GGAACCGCGCGCTTTCCGCGCGCTGCGCCAGTGCCTGTGTGCTGCTTGGAGCGC 240
 DB 181 GGAACCGCGCGCTTTCCGCGCGCTGCGCCAGTGCCTGTGTGCTGCTTGGAGCGC 240
 QY 241 AGGCG 300
 DB 241 AGGCG 300
 QY 301 CCGAGTGTCTGACAGAGGCTGTGCGAGCGCGCGCGCGAGAGAGTGTGCTTGGCTTGC 360
 DB 301 CCGAGTGTCTGACAGAGGCTGTGCGAGCGCGCGCGCGAGAGAGTGTGCTTGGCTTGC 360
 QY 361 GCTGTGAGCGGCG 420
 DB 361 GCTGTGAGCGGCG 420
 QY 421 CCTGCCAACAAGGTCACGACGACGACGACGACGACGACGACGACGACGACGACGAC 480
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Db 2521 CAAATCTTACGTCAGCTGCGAGGAGATCCCGAGGAGCTTCACTCTCTCAGAGCTGCTG 2580
Qy 2581 CAGGCTGCTTACGTCAGCTGCGAGGAGATCCCGAGGAGCTTCACTCTCTCAGAGCTGCTG 2640
Db 2581 CAGGCTGCTTACGTCAGCTGCGAGGAGATCCCGAGGAGCTTCACTCTCTCAGAGCTGCTG 2640
Qy 2641 GCTCTGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
Db 2641 GCTCTGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
Qy 2701 CTTCTCAGAGACCTTGTGCTGAGGTTCTCTGATGATGATGATGATGATGATGATGATGAT 2760
Db 2701 CTTCTCAGAGACCTTGTGCTGAGGTTCTCTGATGATGATGATGATGATGATGATGATGAT 2760
Qy 2761 GACAGTGTGAACTTCCCTGTGAAGAGAGAGGCGCTGGGTGAGAGGCTTTGTTGAT 2820
Db 2761 GACAGTGTGAACTTCCCTGTGAAGAGAGAGGCGCTGGGTGAGAGGCTTTGTTGAT 2820
Qy 2821 GCGGCGCCAGCGGCTATTCCTGCTGAGGCTGCTGATGATGATGATGATGATGATGATGAT 2880
Db 2821 GCGGCGCCAGCGGCTATTCCTGCTGAGGCTGCTGATGATGATGATGATGATGATGATGAT 2880
Qy 2881 GCAAGGCGACTACTCAGCTATGCGGAGCTTCAATCAGAGGAGGCTTCACTTCAACCG 2940
Db 2881 GCAAGGCGACTACTCAGCTATGCGGAGCTTCAATCAGAGGAGGCTTCACTTCAACCG 2940
Qy 2941 GCGCTTCAAGGCTGAGAGGAGATGAGTGCAGAACTTTTGGGGCTTGGCGGCTGAGG 3000
Db 2941 GCGCTTCAAGGCTGAGAGGAGATGAGTGCAGAACTTTTGGGGCTTGGCGGCTGAGG 3000
Qy 3001 TCACAGGCTGTTCTGATTTGAGATGAGAGGCTTCAAGAGGCTGAGAGGCTTCAACATCTA 3060
Db 3001 TCACAGGCTGTTCTGATTTGAGATGAGAGGCTTCAAGAGGCTGAGAGGCTTCAACATCTA 3060
Qy 3061 CAAAGTCTCTGCTGCTGAGGAGTACAGGTTTCAAGAGTGTGCTGAGCTCCCATTTCA 3120
Db 3061 CAAAGTCTCTGCTGCTGAGGAGTACAGGTTTCAAGAGTGTGCTGAGCTCCCATTTCA 3120

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QY 3121 TCAGAGATTGGAGAACCCCAATTTTCTGCGCGATCTCTGACACGGCTCCCT 3180
DB 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGATCTCTGACACGGCTCCCT 3180
QY 3181 CTGCTACTCCATCTCTGAAAGCAAGAACGAGGAGATGTGCTGGGGCCAGGGCCCGC 3240
DB 3181 CTGCTACTCCATCTCTGAAAGCAAGAACGAGGAGATGTGCTGGGGCCAGGGCCCGC 3240
QY 3241 CGGCGCTGCGCCCTCCGAGGCGCGTGCAGTGGCTGCACCAAGCAATTCCTGCTCAAGCT 3300
DB 3241 CGGCGCTGCGCCCTCCGAGGCGCGTGCAGTGGCTGCACCAAGCAATTCCTGCTCAAGCT 3300
QY 3301 GACTCGACACCGCTGCTCACTACGTGCGCACTCTGCGGCTCACTGAGACAGCCGAGACGA 3360
DB 3301 GACTCGACACCGCTGCTCACTACGTGCGCACTCTGCGGCTCACTGAGACAGCCGAGACGA 3360
QY 3361 GCTGAGTGGAGAGTCTCCGGGGAGACAGCTGATGCTGCTGAGGGCCGAGCCCAACCCGCG 3420
DB 3361 GCTGAGTGGAGAGTCTCCGGGGAGACAGCTGATGCTGCTGAGGGCCGAGCCCAACCCGCG 3420
QY 3421 ACTGCGCTGAGACTTCAAGACCAATCTGAGCTGATGAGCCACCCGCGCAGAGCGGCGGA 3480
DB 3421 ACTGCGCTGAGACTTCAAGACCAATCTGAGCTGATGAGCCACCCGCGCAGAGCGGCGGA 3480
QY 3481 GAGCAGACACCGAGCGCTGTGACAGCGCGGCTCTACGTCCAGAGGAGGAGGCGCGCC 3540
DB 3481 GAGCAGACACCGAGCGCTGTGACAGCGCGGCTCTACGTCCAGAGGAGGAGGCGCGCC 3540
QY 3541 CACACCCAGGCGCGGACCGCTGGAGTCTGAGGCTGAGAGTGTGGCCAGAGGCTG 3600
DB 3541 CACACCCAGGCGCGGACCGCTGGAGTCTGAGGCTGAGAGTGTGGCCAGAGGCTG 3600
QY 3601 CATGTCGGCTGAAAGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCAAGGAGCT 3660
DB 3601 CATGTCGGCTGAAAGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCAAGGAGCT 3660
QY 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGCGCTCCACCCCA 3720
DB 3661 GAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGCGCTCCACCCCA 3720
QY 3721 GGGCGACGCTTCTCTACACAGAGCGCGCTTCCACTCCCACTAGAGATAGTCCATCC 3780
DB 3721 GGGCGACGCTTCTCTACACAGAGCGCGCTTCCACTCCCACTAGAGATAGTCCATCC 3780
QY 3781 CCAGATTGCGCATGTTTCAACCCCTGCGCTGCGCTCTCTTGGCTCCACCCCACTCC 3840
DB 3781 CCAGATTGCGCATGTTTCAACCCCTGCGCTGCGCTCTCTTGGCTCCACCCCACTCC 3840
QY 3841 AGGTGAGACCTTGAGAGAGACCTTGAGAGCTTGAGATTTGAGTGCAGGATGTG 3900
DB 3841 AGGTGAGACCTTGAGAGAGACCTTGAGAGCTTGAGATTTGAGTGCAGGATGTG 3900
QY 3901 CCTCTGTACAGAGGAGAGACCTTGACACTGATGAGGGGCTCCGTGGGTCAAAATTTGGGG 3960
DB 3901 CCTCTGTACAGAGGAGAGACCTTGACACTGATGAGGGGCTCCGTGGGTCAAAATTTGGGG 3960
QY 3961 GAGGTGCTGTGGAGTAAATATGAAATATGATTTTCACTTTTGAAGAAAAA 4015
DB 3961 GAGGTGCTGTGGAGTAAATATGAAATATGATTTTCACTTTTGAAGAAAAA 4015

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RESULT 10

ACCS8039 standard; cDNA; 4015 BP.

ACCS8039;

11-AUG-2003 (first entry)

Human telomerase reverse transcriptase cDNA.

XX Telomerase reverse transcriptase; TERT; enzyme: RNA interference;
 KW Short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;

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KW Immunosuppressive; antifertility; fungicide; antiparasitic;
XX antinflammatory; human; gene therapy; gene; ss.
XX Homo sapiens.
OS
PH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "TERT"
PN MO2003035667-A2.
XX
XX 01-MAY-2003.
PD
PF 16-OCT-2002; 2002WO-US033065.
XX
XX 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX
XX (UYP) UNIV ROCHESTER.
PA
XX
XX Rowley PT;
PI
XX WPI; 2003-403336/38.
XX P-PSDB; ABR42384.
DR
XX Novel double-stranded short interfering RNA having sense and antisense
PT nucleic acids which are complementary to each other and to target nucleic
PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse
PT transcriptase.
XX
XX Disclosure; Fig 3A-B; 37pp; English.
PS
XX
XX The present sequence is that of human telomerase reverse transcriptase
CC (TERT) cDNA. The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
SQ

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Query Match 100.0%; Score 4015; DB 10; Length 4015;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCAGCGCTGCTGCTCTGCTGCGACGCTGGAGAGCCCTGGCCCGGACCCCGGATGCC 60
DB 1 GCAGCGCTGCTGCTCTGCTGCGACGCTGGAGAGCCCTGGCCCGGACCCCGGATGCC 60
QY 61 GCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 120
DB 61 GCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCAGGTGCT 120
QY 121 GCGGCTGCGCAGCTTGTGTGGGCGCTTGAGGAGCCCAAGGCTGGCGGCTGAGCGCG 180
DB 121 GCGGCTGCGCAGCTTGTGTGGGCGCTTGAGGAGCCCAAGGCTGGCGGCTGAGCGCG 180
QY 181 GAGCCGCGGCGCTTTCGCGCGCTGTGTGCGCAGTGTCTGTGTGTGCTCCCTGGGAGCG 240
DB 181 GAGCCGCGGCGCTTTCGCGCGCTGTGTGCGCAGTGTCTGTGTGTGCTCCCTGGGAGCG 240
QY 241 ACGGCGGCGCGCGCGCGCGCTCTTCCGCGCAGGTGTCTGTCTGAGAGAGTGTGGC 300
DB 241 ACGGCGGCGCGCGCGCGCGCTCTTCCGCGCAGGTGTCTGTCTGAGAGAGTGTGGC 300

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QY 301 CCGAGTGTGACAGAGGCTGTGCGAGCGCGGAGAAAGTGTGCTGGCTTCGCTTGGC 360
DB 301 CCGAGTGTGACAGAGGCTGTGCGAGCGCGGAGAAAGTGTGCTGGCTTCGCTTGGC 360
QY 361 GCTGTGTGAACGAGGAGCGCGGAGGAGCGCGGAGGAGCTTACCAACGAGTGTGAGCA 420
DB 361 GCTGTGTGAACGAGGAGCGCGGAGGAGCGCGGAGGAGCTTACCAACGAGTGTGAGCA 420
QY 421 CTTGCCCCAACAGGTGTACCGACACTGTGAGGAGAGCGGAGCGTGTGAGTGTGAG 480
DB 421 CTTGCCCCAACAGGTGTACCGACACTGTGAGGAGAGCGGAGCGTGTGAGTGTGAG 480
QY 481 CCGCGTGTGAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 540
DB 481 CCGCGTGTGAGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 540
QY 541 GAGCTCCAGCTGTGCTTACAGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 600
DB 541 GAGCTCCAGCTGTGCTTACAGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 600
QY 601 TTAGGCCCCGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 660
DB 601 TTAGGCCCCGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 660
QY 661 CTGGAACCATAGAGTGTGAGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 720
DB 661 CTGGAACCATAGAGTGTGAGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 720
QY 721 GAGGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 780
DB 721 GAGGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 780
QY 781 TGCCTCTGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 840
DB 781 TGCCTCTGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 840
QY 841 GCGTGTGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 900
DB 841 GCGTGTGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 900
QY 901 CACCTCTTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 960
DB 901 CACCTCTTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 960
QY 961 GACCAACGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 1020
DB 961 GACCAACGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 1020
QY 1021 CCGGAGTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1080
DB 1021 CCGGAGTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1080
QY 1081 GCGCTCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1140
DB 1081 GCGCTCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1140
QY 1141 GACCAATCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1200
DB 1141 GACCAATCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1200
QY 1201 GCGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260
DB 1201 GCGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1260
QY 1261 GTGCCCCCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1320
DB 1261 GTGCCCCCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1320
QY 1321 AGCCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1380
DB 1321 AGCCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1380

QY 1381 CACAGACCCCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1440
DB 1381 CACAGACCCCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1440
QY 1441 CCGCTTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1500
DB 1441 CCGCTTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1500
QY 1501 CAAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1560
DB 1501 CAAGGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1560
QY 1561 GCTCTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1620
DB 1561 GCTCTGTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1620
QY 1621 GAGCCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1680
DB 1621 GAGCCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1680
QY 1681 CAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1740
DB 1681 CAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1740
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QY 1861 GGAAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1920
DB 1861 GGAAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1920
QY 1921 CTTCAATCCCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1980
DB 1921 CTTCAATCCCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1980
QY 1981 CAGAAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2040
DB 1981 CAGAAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2040
QY 2041 CAGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2100
DB 2041 CAGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2100
QY 2101 CCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2160
DB 2101 CCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2160
QY 2161 GCGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2220
DB 2161 GCGGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2220
QY 2221 GGAAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2280
DB 2221 GGAAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2280
QY 2281 TGGGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2340
DB 2281 TGGGATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2340
QY 2341 CCGTCTTACTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2400
DB 2341 CCGTCTTACTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2400
QY 2401 GACCAAGCGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2460
DB 2401 GACCAAGCGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2460
QY 2461 CAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2520

Db 2461 CAGTGGCTCTTGAAGTCTTCTAAGCTTCAATGTGCAACAAGCCGTGCGATCAAGGG 2520
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 QY 2701 CTTCCTCAGAGACCTGTGCGAGGTGCTGAGTATGCTGTGCTGATGCTGAGTGA 2760
 Db 2701 CTTCCTCAGAGACCTGTGCGAGGTGCTGAGTATGCTGTGCTGATGCTGAGTGA 2760
 QY 2761 GACAGTGTGAATCTTCCCTGTAGAAAGACAGGCCCTGGGTGACCGGCTTTTGTGAGAT 2820
 Db 2761 GACAGTGTGAATCTTCCCTGTAGAAAGACAGGCCCTGGGTGACCGGCTTTTGTGAGAT 2820
 QY 2821 GCCGCGCCACGCGCTATTCCTCTGTGTGCGGCTGTGTGTGATACCCGACCTTGAGGT 2880
 Db 2821 GCCGCGCCACGCGCTATTCCTCTGTGTGCGGCTGTGTGTGATACCCGACCTTGAGGT 2880
 QY 2881 GCAGAGCGACTACTCCAGAGTATGCCGAGACCTCATCAGAGCCAGTCTCACTTCAACCG 2940
 Db 2881 GCAGAGCGACTACTCCAGAGTATGCCGAGACCTCATCAGAGCCAGTCTCACTTCAACCG 2940
 QY 2941 CGGCTTCAAGGCTGGAGAGAACATGCGTGCACAACTCTTGGGGTCTTGGCGCTGAAGTG 3000
 Db 2941 CGGCTTCAAGGCTGGAGAGAACATGCGTGCACAACTCTTGGGGTCTTGGCGCTGAAGTG 3000
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 Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGTACAAGGCTTCCCT 3180
 QY 3181 CTGCTACTCATCTCTGAAGCCAAAGAACGACGAGGATGTGCTGGGGGCCAAAGGCGCGC 3240
 Db 3181 CTGCTACTCATCTCTGAAGCCAAAGAACGACGAGGATGTGCTGGGGGCCAAAGGCGCGC 3240
 QY 3241 CGGCGCTCTGCGCTCCGAGGCGGAGTGTGCTGTGCAACAAGCTTCTGCTCAAGCT 3300
 Db 3241 CGGCGCTCTGCGCTCCGAGGCGGAGTGTGCTGTGCAACAAGCTTCTGCTCAAGCT 3300
 QY 3301 GACTCGACACCGTGTCACTTACGTGCCACTCTGGGGTCACTGAGCAAGCCGAGAGCA 3360
 Db 3301 GACTCGACACCGTGTCACTTACGTGCCACTCTGGGGTCACTGAGCAAGCCGAGAGCA 3360
 QY 3361 GCTGAGTCCGAAAGTCCCGGGGAGACGCTGACTGCTGAGAGCGGCAACCCGCGC 3420
 Db 3361 GCTGAGTCCGAAAGTCCCGGGGAGACGCTGACTGCTGAGAGCGGCAACCCGCGC 3420
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 Db 3421 ACTGCCCTCAGACTTCAAGACCATCTCTGAGCTGATGAGCCACCGCCACAGCGGCGCA 3480
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 Db 3481 GAGCAGACACACAGAGCCCTGTCAAGCGCGGCTTCAAGTCCAGAGAGAGAGGCGCGCC 3540
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 Db 3541 CACACCCAGGCGGACACCGCTGGAGTCTGAGGCTTGAAGTGTGCTTGGCCGAGGCTTG 3600

Db 3541 CACACCCAGGCGGACACCGCTGGAGTCTGAGGCTTGAAGTGTGCTTGGCCGAGGCTTG 3600
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 Db 3601 CATGTCCGGCTGAAGAGTGAAGTGTCCGGCTGAGGCTTGAAGAGTGTCCAGCAAGGCT 3660
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 Db 3901 CCTGTACACAGCGAGACCTTGCACCTGAGATGGGGTCCCTGTGGGTCAAAATTGGGG 3960
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 Db 3961 GAGTGTCTGTGGAGTAAATATGATATGATGTTTTCAGTTTGTGAAAAAA 4015

RESULT 11
 AD85223
 ID AD85223 standard; DNA; 4015 BP.
 XX
 AC AD85223;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Human telomerase reverse transcriptase DNA.
 XX
 KW telomerase catalytic activity;
 KW hydrogen peroxide-induced cellular senescence; proliferative disease;
 KW cancer; human; telomerase reverse transcriptase; ds; gene.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 2702..3454
 FT FT /tag= a
 FT FT /partial
 FT FT /product= "Telomerase reverse transcriptase"
 FT FT /note= "No start codon given"
 XX
 PN US2003225027-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 30-MAY-2003; 2003US-00449565.
 XX
 PR 31-MAY-2002; 2002US-0384806P.
 XX
 PA (HUAN/) HUANG J.
 PA (HUAN/) HUANG C.
 PA (LINM/) LIN M C M.
 PA (KUNG/) KUNG H.
 XX
 PI Huang JU, Huang C, Lin MCM, Kung H;
 XX
 WP1; 2004-089418/09.
 DR P-PSDB; AD85224.
 XX
 FT New human telomerase reverse transcriptase polypeptide, useful in

QY 1921 CTTCAATCCCAAGCCTGAGCGGCTGCGGCCGATTTGAACTATGACTAGCTGTGGAGC 1980
Db 1922 CTTCAATCCCAAGCCTGAGCGGCTGCGGCCGATTTGAACTATGACTAGCTGTGGAGC 1980
QY 1981 CAGAACTTCGCGAGAGAAAAGAGGCGCGAGCGTCACTCGAGGGGTAAAGCACTGTT 2040
Db 1981 CAGAACTTCGCGAGAGAAAAGAGGCGCGAGCGTCACTCGAGGGGTAAAGCACTGTT 2040
QY 2041 CAGCGTGTCAACTAGAGCGGCGCGCGGCCCTTCCTGCGGCTCTGTGCTGG 2100
Db 2041 CAGCGTGTCAACTAGAGCGGCGCGCGGCCCTTCCTGCGGCTCTGTGCTGG 2100
QY 2101 CTTGAGCATATTCACAGAGGCGCGCGCACTTCGTGCTGCTGCGAGGCGCGAGAGCC 2160
Db 2101 CTTGAGCATATTCACAGAGGCGCGCGCACTTCGTGCTGCTGCGAGGCGCGAGAGCC 2160
QY 2161 GCGGCTGAGCTGTACTTGTCAAGGTGATGACGAGGCGCGTACAGACATCCCGCA 2220
Db 2161 GCGGCTGAGCTGTACTTGTCAAGGTGATGACGAGGCGCGTACAGACATCCCGCA 2220
QY 2221 GGAAGGCTCAGAGAGGTGATGCGCAGCATCAAAACCCAGAGACGTACTGCGTGG 2280
Db 2221 GGAAGGCTCAGAGAGGTGATGCGCAGCATCAAAACCCAGAGACGTACTGCGTGG 2280
QY 2281 TCGGTATGCGGTGATCCAGAGGCGCGCGCACTGCGAGGCGCGTCAAGAGCA 2340
Db 2281 TCGGTATGCGGTGATCCAGAGGCGCGCGCACTGCGAGGCGCGTCAAGAGCA 2340
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Db 2341 CGTCTACCTTGAACAGACTCCAGCGGTATGCGACAGTGTGCGTCACTGAGAG 2400
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Db 2401 GACCAAGCGGCTGAGGATGCGGTGATGAGCAGAGTCTCTCTGATAGAGCGCAG 2460
QY 2461 CAGGCGCTTTCGAGCGTCTTCTCAAGCTCATGTGCAACGCGGCGCATCAGGCG 2520
Db 2461 CAGGCGCTTTCGAGCGTCTTCTCAAGCTCATGTGCAACGCGGCGCATCAGGCG 2520
QY 2521 CAGGCTTCAAGTCCAGAGGAGATCCCGCAGGCGCTCCATCTCTCCAGCGTCTG 2580
Db 2521 CAGGCTTCAAGTCCAGAGGAGATCCCGCAGGCGCTCCATCTCTCCAGCGTCTG 2580
QY 2581 CAGGCTTGTCTACGCGCAATGAGAAACAAGCTGTTGCGGAGATTCGCGGAGCGGCT 2640
Db 2581 CAGGCTTGTCTACGCGCAATGAGAAACAAGCTGTTGCGGAGATTCGCGGAGCGGCT 2640
QY 2641 GCTCTGCGTTTGGTGTGATGTTCTTGTGTGAGCACTCACTCAACCCAGCGAGAAC 2700
Db 2641 GCTCTGCGTTTGGTGTGATGTTCTTGTGTGAGCACTCACTCAACCCAGCGAGAAC 2700
QY 2701 CTTCTCAGAGACCTGTGTCGAGGTGTCCTGAGTATGCTGCTGCTGTAATCTTGGAA 2760
Db 2701 CTTCTCAGAGACCTGTGTCGAGGTGTCCTGAGTATGCTGCTGCTGTAATCTTGGAA 2760
QY 2761 GACAGTGTGAATCTTCTGTGAAAGACAGAGGCGCTGAGTGTGCTGCTGAT 2820
Db 2761 GACAGTGTGAATCTTCTGTGAAAGACAGAGGCGCTGAGTGTGCTGCTGAT 2820
QY 2821 GCGGCGCCAGCGCTATTTCCCTGTGTGAGGCTCTGCTGTGATACCGGAGCCGTGAGGT 2880
Db 2821 GCGGCGCCAGCGCTATTTCCCTGTGTGAGGCTCTGCTGTGATACCGGAGCCGTGAGGT 2880
QY 2881 GCAGAGGCACTACTCAGACTATGCCGAGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2940
Db 2881 GCAGAGGCACTACTCAGACTATGCCGAGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2940
QY 2941 CCGGCTTCAAGGCTGAGAGAAACATGCGTCCGAACTCTTGGGGGTCTTGGGGCTGAAGTG 3000
Db 2941 CCGGCTTCAAGGCTGAGAGAAACATGCGTCCGAACTCTTGGGGGTCTTGGGGCTGAAGTG 3000

QY 3001 TCACAGCTGTGTTGATTTGAGTGGAGTGAACAGGCTCCAGAGCGGTGTCACCAACATCTA 3060
Db 3001 TCACAGCTGTGTTGATTTGAGTGGAGTGAACAGGCTCCAGAGCGGTGTCACCAACATCTA 3060
QY 3061 CAAGATCTCTGCTGCAAGCGGTACAGGTTTCAAGCATGTGTGCTGCAAGTCTTCA 3120
Db 3061 CAAGATCTCTGCTGCAAGCGGTACAGGTTTCAAGCATGTGTGCTGCAAGTCTTCA 3120
QY 3121 TCAGAGATTTGAGAGAACCCCACTTTTCTGCGGCTCATCTCTGACAGGCGCTCCCT 3180
Db 3121 TCAGAGATTTGAGAGAACCCCACTTTTCTGCGGCTCATCTCTGACAGGCGCTCCCT 3180
QY 3181 CTGCTACTCTCACTCTGAAGAGCAAGAGATGTCGTGAGGAGCAAGGCGCGC 3240
Db 3181 CTGCTACTCTCACTCTGAAGAGCAAGAGATGTCGTGAGGAGCAAGGCGCGC 3240
QY 3241 CCGGCTCTGCTGCTGCAAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Db 3241 CCGGCTCTGCTGCTGCAAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
QY 3301 GACTGACACCGGTGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
Db 3301 GACTGACACCGGTGACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
QY 3361 GCTGAGTGGAGAGCTCCGCGGAGCAGAGCTGCTGCTGAGGCGCGAGCCAGCCGCGC 3420
Db 3361 GCTGAGTGGAGAGCTCCGCGGAGCAGAGCTGCTGCTGAGGCGCGAGCCAGCCGCGC 3420
QY 3421 ACTGCTCTGAGCTTCAAGAGCCATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
Db 3421 ACTGCTCTGAGCTTCAAGAGCCATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
QY 3481 GAGCAGACACGAGAGCGCTGTCAGCGCGGCTTACGTCACGAGGAGGAGGAGGCGCGC 3540
Db 3481 GAGCAGACACGAGAGCGCTGTCAGCGCGGCTTACGTCACGAGGAGGAGGAGGCGCGC 3540
QY 3541 CACACCCAGGCGCGCAGCGCTGAGTGTGAGGCGCTGAGTGTGAGTGTGAGTGTGAGTGTG 3600
Db 3541 CACACCCAGGCGCGCAGCGCTGAGTGTGAGGCGCTGAGTGTGAGTGTGAGTGTGAGTGTG 3600
QY 3601 CATGTCCGCTGAGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3660
Db 3601 CATGTCCGCTGAGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 3660
QY 3661 GAGTGTCCAGACACCTGCGGCTTCACTTCCCAAGGCTGCGCTGCGCTGCGCTGCGCTGCGCT 3720
Db 3661 GAGTGTCCAGACACCTGCGGCTTCACTTCCCAAGGCTGCGCTGCGCTGCGCTGCGCTGCGCT 3720
QY 3721 GGGCCAGCTTTTCTTCAACAGAGGCGGCTTCACTTCCCAAGTATGTCATTC 3780
Db 3721 GGGCCAGCTTTTCTTCAACAGAGGCGGCTTCACTTCCCAAGTATGTCATTC 3780
QY 3781 CCAGATTCGCAATGTTTCAACCTGCGGCTGCGCTTCTGCTTCAACCCCAACATTC 3840
Db 3781 CCAGATTCGCAATGTTTCAACCTGCGGCTGCGCTTCTGCTTCAACCCCAACATTC 3840
QY 3841 AGGTGAGAGACCTGAGAGAGACCTTGGAGCTCTGAGATTTGAGTGTGCAAAAGGTGTG 3900
Db 3841 AGGTGAGAGACCTGAGAGAGACCTTGGAGCTCTGAGATTTGAGTGTGCAAAAGGTGTG 3900
QY 3901 CCCTGTACACAGCGAGAGACCTTGCATCTGATGAGGAGTCCCTGTGAGTCAAAATTTGGGG 3960
Db 3901 CCCTGTACACAGCGAGAGACCTTGCATCTGATGAGGAGTCCCTGTGAGTCAAAATTTGGGG 3960
QY 3961 GAGTGTCTGAGAGAGTAAATTAATGATTTTCAAGTTTGAAGTGTG 4015
Db 3961 GAGTGTCTGAGAGAGTAAATTAATGATTTTCAAGTTTGAAGTGTG 4015

RESULT 12
AD182171 standard: cDNA, 4015 BP.
ID AD182171
XX

AC	AD182171;	
AD	22-APR-2004 (first entry)	
XX		
DE	Human cDNA encoding telomerase reverse transcriptase.	
XX		
KW	Human; ss; gene; embryonic stem cell; pluripotent stem cell;	
XX	abnormal cell growth; malignancy; differentiation.	
OS	Homo sapiens.	
XX		
PN	US2003224411-A1.	
XX		
PD	04-DEC-2003.	
XX		
PF	13-MAR-2003; 2003US-00388578.	
XX		
PR	13-MAR-2003; 2003US-00388578.	
XX		
PA	(STAN/) STANTON L W.	
PA	(BRAN/) BRANDENBERGER R.	
PA	(GOLD/) GOLD J D.	
PA	(IRVI/) IRVING J M.	
PA	(MAND/) MANDALAM R.	
PA	(MOKM/) MOK M.	
PA	(SHEL/) SHELTON D.	
XX		
PI	Statton LW, Brandenberger R, Gold JD, Irving JM, Mandalam R;	
PI	Mok M, Shelton D;	
DR	WPI, 2004-119701/12.	
XX	P-PSDB; AD182172.	
XX		
PT	Assessing culture of undifferentiated primate pluripotent stem cells by	
PT	detecting expression of markers e.g., Zic family member 3, other than	
PT	human telomerase reverse transcriptase/occamer binding transcription	
PT	factor.	
XX		
PS	Claim 1; SEQ ID NO 1; 106bp; English.	
XX		
XX		
CC	The invention relates to assessing a culture of undifferentiated primate	
CC	pluripotent stem cells (pPS, e.g. embryonic stem cells), involving	
CC	detecting expression of markers (MR1) e.g. Zic family member 3 (ZIC3), as	
CC	given in specification, other than human telomerase reverse transcriptase	
CC	(hTERT) or occamer binding transcription factor (Ocf)3/4, or a marker	
CC	(MR2) such as criplo or podocalyxin-like protein and hTERT and/or Ocf3/4	
CC	or second marker chosen from (MR2). Also included are maintaining (M2)	
CC	pPS cells in a pluripotent state (involves causing them to express one of	
CC	the following markers (MR3) at a higher level, FOXO1A, ZIC3, hypohelical	
CC	protein Flt20582, Forkhead box H1 (FOXH1), Zinc finger protein, Hsdl,	
CC	KRAE-zinc finger protein SZF1-1 or zinc finger protein of cerebellum	
CC	ZIC3, or any other marker (MR4) chosen from PHD protein Jade-1 (Jade-1),	
CC	knpkel-like zinc finger protein (ZNF300), etc., as given in the	
CC	specification), causing pPS cells to differentiate into a particular	
CC	tissue type by causing them to express one of the markers chosen from	
CC	(MR3) or (MR4) (or markers chosen from GATA binding protein 3 (GATA3),	
CC	core promoter element binding protein (COPEB), etc., as given in the	
CC	specification), maintaining pPS cells in a pluripotent state (involves	
CC	culturing pPS cells or their progeny in the presence of a normally	
CC	secreted protein that is encoded by a gene that down-regulated upon	
CC	differentiation of human embryonic stem (hES) cells, chosen from	
CC	Fib1illin 3 gene, Lefty B gene, ZIC3 gene, EphA1 gene, etc., as given in	
CC	the specification), causing pPS cells to differentiate (involves	
CC	culturing pPS cells or their progeny in the presence of a normally	
CC	secreted protein that is encoded by a gene that up-regulated upon	
CC	differentiation of hES cells, chosen from P311 protein gene, Tax	
CC	interaction protein 1 gene, KIA0853 protein gene, Keratin 19 (KRT 19)	
CC	gene, etc., as given in the specification), causing an encoding sequence	
CC	to be preferentially expressed in undifferentiated pPS cells, causing an	
CC	encoding sequence to be preferentially expressed in differentiated cells,	
CC	sorting (M4) differentiated cells from less differentiated cells	
CC	(involves separating cells expressing a surface marker chosen from any	
CC	one of MRI from cells not expressing the marker), causing pPS cells to	

CC proliferate without differentiation, identifying genes that are up or
CC down regulated during differentiation of pps cells, and a kit (II) for
CC assessing a culture of pps cells by M1. The method, (M1) is useful for
CC assessing culture of undifferentiated primate pluripotent stem cells and
CC for assessing the growth characteristics of a cell population. The cell
CC population has been obtained by culturing cells from human blastocyst or
CC from a human patient suspected of having a clinical condition related to
CC abnormal cell growth. The method further involves determining whether the
CC cell population is pluripotent from the marker expression and assessing
CC whether the patient has a malignancy from the marker expression. The
CC present sequence is a cDNA whose expression is down regulated in
CC pluripotent stem cells.

SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match	100.0%;	Score 4015;	DB 12;	Length 4015;
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2006 200604 02mmataaccy      22000: 00: 0/
Matches 4015; Conservative    0; Indels    0; Gaps    0;

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OY		1	GCAGGCGCTGCTCCGTGCGGCAAGTGGAAAGCCCTGGCCCCGGGCAACCCCGGGATGCG	60
Db		1	GCAGCGCTGCTCTGTCTGGCAGCTGGAAAGCCCTGGCCCCGGGCAACCCCGGGATGCG	60
OY		61	GGCGGCTCCCGCTGGCGGAGGCGTGGCGCTCCCTGTGGCGAGCCATTACCGGAGTGGCT	120
Db		61	GGCGGCTCCCGCTGGCGGAGGCGTGGCGCTCCCTGTGGCGAGCCATTACCGGAGTGGCT	120
OY		121	GCCGCTGGGCAAGTTGCTGGCGGCGCTTGGGAGCCCGAGGCTGGCGCTGGTGCAGCGCG	180
Db		121	GCCGCTGGGCAAGTTGCTGGCGGCGCTTGGGAGCCCGAGGCTGGCGCTGGTGGAGCGG	180
OY		181	GGAGCCGGGCGGCTTTCCGCGGCGTGGTGGCCCAATGGTCTGGTGGTGGGCGCTGGAGGCG	240
Db		181	GGAGCCGGGCGGCTTTCCGCGGCGTGGTGGCCCAATGGTCTGGTGGTGGGCGCTGGAGGCG	240
OY		241	ACGGCGGCCCCCGCGCGCCCCCTCTCTTCCGCGCAGGTGTCCTGGCTGAAGAGCTGGTGGC	300
Db		241	ACGGCGGCCCCCGCGCGCCCCCTCTCTTCCGCGCAGGTGTCCTGGCTGAAGAGCTGGTGGC	300
OY		301	CCGAGTGTGCAGAGGCTGTGGCGAGCGCGCGCAGAGAAGCTGTGGCGTTCCGCTTGGC	360
Db		301	CCGAGTGTGCAGAGGCTGTGGCGAGCGCGCGCAGAGAAGCTGTGGCGTTCCGCTTGGC	360
OY		361	GCTGCTGAGCGGGGCCCGCGGGGGCCCCCGGAGGCTTTCACACACAGCTGGCGAGCTTA	420
Db		361	GCTGCTGAGCGGGGCCCGCGGGGGCCCCCGGAGGCTTTCACACACAGCTGGCGAGCTTA	420
OY		421	CCCTGCCCAACCGGTGACCGACCTGGCGGGAGCGGGGCGTGGGGGCTGGCTGGCG	480
Db		421	CCCTGCCCAACCGGTGACCGACCTGGCGGGAGCGGGGCGTGGGGGCTGGCTGGCG	480
OY		481	CCGGTGGGCGACGACGTCGTGGTTTCACTTGTGGACGCTGGCGCGCTTGTGTGGT	540
Db		481	CCGGTGGGCGACGACGTCGTGGTTTCACTTGTGGACGCTGGCGCGCTTGTGTGGT	540
OY		541	GCGTCCCAAGCTGGCGCTTACCAAGTGTGGGCGCGCGCTGTACCAAGCTCGGCGCTGGCAC	600
Db		541	GCGTCCCAAGCTGGCGCTTACCAAGTGTGGGCGCGCGCGCTGTACCAAGCTCGGCGCTGGCAC	600
OY		601	TCAAGCCCGGCCCCCGGCGACACGCTTAATGGACCCCGAAGGGGTGTGGGATTCGAACGGGCG	660
Db		601	TCAAGCCCGGCCCCCGGCGACACGCTTAATGGACCCCGAAGGGGTGTGGGATTCGAACGGGCG	660
OY		661	CTGGAACCATATGAGCTCAGGAGGAGCGGGGATCCCTTGGGCTTGGCAGCCCCGGGTGGAG	720
Db		661	CTGGAACCATATGAGCTCAGGAGGAGCGGGGATCCCTTGGGCTTGGCAGCCCCGGGTGGAG	720
OY		721	GAGGCGCGGGGCGAGTGCAGCCGAAAGTCTTGGCTTCCCAAGAGGCGCCAGGCGTGGCGC	780
Db		721	GAGGCGCGGGGCGAGTGCAGCCGAAAGTCTTGGCTTCCCAAGAGGCGCCAGGCGTGGCGC	780
OY		781	TGCCCCCTGAGCCGGAAGCGGAGGCCCGTTTGGGCAAGGCTCTGGGCGCACTCGGGCAAGAC	840

Db 781 TGCCCTGAGCCGAGGAGGAGCCGCTTGGGACAGGGTCTTGAGGCCACCCGGGACAGAC 840
QY 841 GCGTGAACGAGACCGGTGTTTCTGTGTGTGTCACTTGACAGACCCGCGAAGAAC 900
Db 841 GCGTGAACGAGACCGGTGTTTCTGTGTGTGTCACTTGACAGACCCGCGAAGAAC 900
QY 901 CACCTCTTTGAGAGGTGCGCTCTCTGACAGCGCCCACTCCCACTCCATCCGTGGGCGCA 960
Db 901 CACCTCTTTGAGAGGTGCGCTCTCTGACAGCGCCCACTCCCACTCCATCCGTGGGCGCA 960
QY 961 GCAACAAGCGGGGCCCCCATCCATCCATCGCGGCCACACGTCCTGGGACACGCTTGTC 1020
Db 961 GCAACAAGCGGGGCCCCCATCCATCCATCGCGGCCACACGTCCTGGGACACGCTTGTC 1020
QY 1021 CCGGGGTGATGCGGAGACCAAGACCTTCTCTCTGAGGAGCAAGAGAGAGCGTGG 1080
Db 1021 CCGGGGTGATGCGGAGACCAAGACCTTCTCTCTGAGGAGCAAGAGAGAGCGTGG 1080
QY 1081 GCGCTCTTCTCTACTGAGCTCTGTAGGCCAGCCTGACCTGAGCGCTTGAGGCTGTGGA 1140
Db 1081 GCGCTCTTCTCTACTGAGCTCTGTAGGCCAGCCTGACCTGAGCGCTTGAGGCTGTGGA 1140
QY 1141 GACCATCTTTCTGAGGTTCAGAGCCCTGAGATGCGAGGACCTCCCGACAGTTCGCGCT 1200
Db 1141 GACCATCTTTCTGAGGTTCAGAGCCCTGAGATGCGAGGACCTCCCGACAGTTCGCGCT 1200
QY 1201 GCGCCAGCGCTACTGAGCAATGAGGCGCCCTGTTTCTGAGAGCTGTTGGAGAACAGCGCA 1260
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QY 1441 CCGGCTTGTGCGGAGCGCTGCGCGCGCGGTGTGTGCGCGCGGTGTGTGCGCGCGGTGTG 1500
Db 1441 CCGGCTTGTGCGGAGCGCTGCGCGCGCGGTGTGTGCGCGCGGTGTGTGCGCGCGGTGTG 1500
QY 1501 CAAAGCAAGCGCGCTTCTCTCAAGAACACCAAGAGTTCATCTCCCTGGGAGAGATGCGCA 1560
Db 1501 CAAAGCAAGCGCGCTTCTCTCAAGAACACCAAGAGTTCATCTCCCTGGGAGAGATGCGCA 1560
QY 1561 GCTCTGCTGACAGAGCTGAGTGAAGATGAGAGTGCAGGAGCTGAGCGCTTGGCTGCGCAG 1620
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QY 1621 GAGCCCAAGGGGTGTGCTGTTCGCGCGCAGAGACCGTCTGAGAGAGATCTTGTC 1680
Db 1621 GAGCCCAAGGGGTGTGCTGTTCGCGCGCAGAGACCGTCTGAGAGAGATCTTGTC 1680
QY 1681 CAAAGTCTCTGACAGCTGAGTGAAGTGTGATGCTGTGAGCTGTCAAGCTTCTTTTGA 1740
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QY 1741 TGTACAGGAGACCAAGTTCAAAAGACAGAGCTTCTTACCGAGAGAGTGTCTGAG 1800
Db 1741 TGTACAGGAGACCAAGTTCAAAAGACAGAGCTTCTTCTTACCGAGAGAGTGTCTGAG 1800
QY 1801 CAAAGTTCAGAGATTCAGATTCAGACAGCACTTGAAGAGGTGAGTGTGGGAGCTGTC 1860
Db 1801 CAAAGTTCAGAGATTCAGATTCAGACAGCACTTGAAGAGGTGAGTGTGGGAGCTGTC 1860
QY 1861 GGAAGCAGAGGTGAGGAGATGCGGAGAGCCAGGCGCGCTGTGACGTCAGACTCCG 1920
Db 1861 GGAAGCAGAGGTGAGGAGATGCGGAGAGCCAGGCGCGCTGTGACGTCAGACTCCG 1920

QY 1921 CTTCAATCCCAAGGCTGACAGGCTGCGGCGAATGTGAAATGAGACTAGCTGTGGAGC 1980
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QY 1981 CAGAAAGTTCGAGAGAAAGAGGCGCAGAGCTTCACTTGAAGGTGAAGCACTGT 2040
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Db 2461 CAGTGGCTCTTCAAGAGTCTTCTCACTGAGCTTCAATGTCACACAGCGCTGCGATCAGGG 2520
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Qy 181 GGAACCCGGCGGCTTTCGCGCGCGCTGTGTGGCCAGTGTGCTGTGTGTGCGCCCTTGGAGCG 240
Db 188 GGAACCCGGCGGCTTTCGCGCGCGCTGTGTGGCCAGTGTGCTGTGTGTGCGCCCTTGGAGCG 247
Qy 241 AGGGCCGCCCCCGCGCGCGCTTTCGCGCGCGCTGTGTGGCCAGTGTGCTGTGTGTGCGCG 300
Db 248 AGGGCCGCCCCCGCGCGCGCTTTCGCGCGCGCTGTGTGGCCAGTGTGCTGTGTGTGCGCG 307
Qy 301 CCGAGTGTGTGAGGGGTGTGTGCGCGCGCGCGCGAGAAAGTGTGTGCTTTCGCGCTTTCGCG 360
Db 308 CCGAGTGTGTGAGGGGTGTGTGCGCGCGCGCGAGAAAGTGTGTGCTTTCGCGCTTTCGCG 367
Qy 361 GCTGTGTGAGCGGGGCCCGCGGGGGCCCCCGAGGCTTTCACACACAGCTGTGGAGCTA 420
Db 368 GCTGTGTGAGCGGGGCCCGCGGGGGCCCCCGAGGCTTTCACACACAGCTGTGGAGCTA 427
Qy 421 CTTGTCCCAACAGGTGTACCGACGCTGTGGGGGAGCGGGGCGTGGGGGCTGTGTGCG 480
Db 428 CTTGTCCCAACAGGTGTACCGACGCTGTGGGGGAGCGGGGCGTGGGGGCTGTGTGCG 487
Qy 481 CCGGCTGGGCGACGAGCTGTGTGTACCTGTGTGCGACGCTGTGGGCGCTTTCGTGTGTGT 540
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Qy 541 GCGTCCAGCTGTGTGTACAGAGTGTGTGGGGCGCGCTGTGTACAGCTGTGGCGCTGTGCAC 600
Db 548 GCGTCCAGCTGTGTGTACAGAGTGTGTGGGGCGCGCTGTGTACAGCTGTGGCGCTGTGCAC 607
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Db 608 TCAAGGCGGGGGCCCCCGCGCACAGCTGTGTGACCCCCGAAAGGCTGTGGAGTGTGCAAGCGG 667
Qy 661 CTGGAACCATATAGGCTCAAGGAGGCGGGGCTCCCTGTGGGCTGTGCACGCCCGGGGTGTGAG 720
Db 668 CTGGAACCATATAGGCTCAAGGAGGCGGGGCTCCCTGTGGGCTGTGCACGCCCGGGGTGTGAG 727
Qy 721 GAGGCGCGGGGGGAGTGTGTCCAGCGGAAGTGTGCGGTGTGCCAAGAGGCGCGAGCGTGTG 780
Db 728 GAGGCGCGGGGGGAGTGTGTCCAGCGGAAGTGTGCGGTGTGCCAAGAGGCGCGAGCGTGTG 787
Qy 781 TGGCCCTGAGCGGAGCGAGCGCGCGCTGTGGGCGAGGGGTCTGTGGGCCACCCCGGGCGAGAC 840
Db 788 TGGCCCTGAGCGGAGCGAGCGCGCGCTGTGGGCGAGGGGTCTGTGGGCCACCCCGGGCGAGAC 847
Qy 841 GCGTGAACCGAGTGTACCGT 900
Db 848 GCGTGAACCGAGT 907
Qy 901 CAGCTCTTTTGAAGGGT 960
Db 908 CAGCTCTTTTGAAGGGT 967
Qy 961 GCAACACGCGGGGCCCGCCCATTCACATCGGGGCCACACAGTCCCTGTGGGACACGCTTGTTC 1020
Db 968 GCAACACGCGGGGCCCGCCCATTCACATCGGGGCCACACAGTCCCTGTGGGACACGCTTGTTC 1027
Qy 1021 CCGGCTGTGACCGGAGACCAAGCATTCCTTACTCTCAGGCGACCAAGAGCAGTGTGCG 1080
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Db 1088 GCGCTCTCTTCTATCTATAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1147
Qy 1141 GACCATCTTTTGTGGTTCAGAGCCCTGAGTGTGCAAGGAGCTCCCGCGAGGTTGCCCGGCT 1200
Db 1148 GACCATCTTTTGTGGTTCAGAGCCCTGAGTGTGCAAGGAGCTCCCGCGAGGTTGCCCGGCT 1207
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Db 1208 GCGCCAGCGCTATGTGCAAAATGTGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1267

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Qy 1321 AGCGGT 1380
Db 1328 AGCGGT 1387
Qy 1381 CACAGACCCCCGCTGT 1440
Db 1388 CACAGACCCCCGCTGT 1447
Qy 1441 CCGCTTGTGTGGGGGCTGT 1500
Db 1448 CCGCTTGTGTGGGGGCTGT 1507
Qy 1501 CAAAGAACCGCGCTTCTCAGGAACACCAAGAAATTCATCTCTGTGGGAAACATGCCAA 1560
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Qy 1561 GCTTGT 1620
Db 1568 GCTTGT 1627
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Db 1628 GAGCCAGGGGTTGT 1687
Qy 1681 CAAAGTCTGT 1740
Db 1688 CAAAGTCTGT 1747
Qy 1741 TGTCAAGAGACCAAGTTTCAAAAAGACAGGCTTTTCTTCAACGGAAGAGTGTGTGTGTGT 1800
Db 1748 TGTCAAGAGACCAAGTTTCAAAAAGACAGGCTTTTCTTCAACGGAAGAGTGTGTGTGTGT 1807
Qy 1801 CAAAGT 1860
Db 1808 CAAAGT 1867
Qy 1861 GGAAGCAGAGGT 1920
Db 1868 GGAAGCAGAGGT 1927
Qy 1921 CTTCAATCCCAAGGCTGT 1980
Db 1928 CTTCAATCCCAAGGCTGT 1987
Qy 1981 CAGAACGTTTCCGACAGAAAAGAGGGCCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
Db 1988 CAGAACGTTTCCGACAGAAAAGAGGGCCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2047
Qy 2041 CAGGCTGT 2100
Db 2048 CAGGCTGT 2107
Qy 2101 CTTGAGCATATTCACAGGGGCTGT 2160
Db 2108 CTTGAGCATATTCACAGGGGCTGT 2167
Qy 2161 GCGGCTGT 2220
Db 2168 GCGGCTGT 2227
Qy 2221 GGAAGAGGT 2280
Db 2228 GGAAGAGGT 2287
Qy 2281 TCGGTATGCGGT 2340
Db 2288 TCGGTATGCGGT 2347

2341 CGTCTCACTTGAAGACCTTCAGCCGTAATGCGACAGTTTCGTGCTCACTTCGAGA 2400
2348 CGTCTCACTTGAAGACCTTCAGCCGTAATGCGACAGTTTCGTGCTCACTTCGAGA 2407
2401 GACCAAGCCGCTGAGGAGATGCGTGTCTATCGAGCAGAGCTTCCTCTGAATGAGGCCAG 2460
2408 GACCAAGCCGCTGAGGAGATGCGTGTCTATCGAGCAGAGCTTCCTCTGAATGAGGCCAG 2467
2461 CAGTGGCCCTTTCAGAGTCTTCCTACGCTTCATGTCGACCAAGCCGTCGATCAGAGGG 2520
2468 CAGTGGCCCTTTCAGAGTCTTCCTACGCTTCATGTCGACCAAGCCGTCGATCAGAGGG 2527
2521 CAGTCTCACTGCAAGTGCAGAGGATCCCGAGGCTTCATCTCTCCAGCCTGCTCTG 2580
2528 CAGTCTCACTGCAAGTGCAGAGGATCCCGAGGCTTCATCTCTCCAGCCTGCTCTG 2587
2581 CAGCCTGTCTACGCGGACATGAGAACAGCTGTTTCGCGGAGATTCGCGGAGCGGCT 2640
2588 CAGCCTGTCTACGCGGACATGAGAACAGCTGTTTCGCGGAGATTCGCGGAGCGGCT 2647
2641 GCTCCTGGTTTGGTGAATGATTTCTGTGGTGAACCTCACTCAACCCAGCGGAAAC 2700
2648 GCTCCTGGTTTGGTGAATGATTTCTGTGGTGAACCTCACTCAACCCAGCGGAAAC 2707
2701 CTTCTCAAGAACCTGTCGAGTGTCCCTGAGTATGCTGCTGAGTGAACCTTGCGGA 2760
2708 CTTCTCAAGAACCTGTCGAGTGTCCCTGAGTATGCTGCTGAGTGAACCTTGCGGA 2767
2761 GACAGTGTGAACCTTCCCTGTAAGAACAGAGCCCTGAGTGCACGCGCTTTTGTTCAGAT 2820
2768 GACAGTGTGAACCTTCCCTGTAAGAACAGAGCCCTGAGTGCACGCGCTTTTGTTCAGAT 2827
2821 GCGGCGCCCAAGCCGCTATTCCTGTCGAGGCGCTGCTGCTGAGTATCCCGAACCTCGAGGT 2880
2828 GCGGCGCCCAAGCCGCTATTCCTGTCGAGGCGCTGCTGCTGAGTATCCCGAACCTCGAGGT 2887
2881 GCAGAGCGCATCTACCTCAGCTATGCCCAGACCTTCATCAGAGCAGTCTCACTTCAACCG 2940
2888 GCAGAGCGCATCTACCTCAGCTATGCCCAGACCTTCATCAGAGCAGTCTCACTTCAACCG 2947
2941 CCGCTTCAAGGCTGAGGAGACATGCTGCGAACTCTTTGGGAGCTTTCGCGCTGAAGTG 3000
2948 CCGCTTCAAGGCTGAGGAGACATGCTGCGAACTCTTTGGGAGCTTTCGCGCTGAAGTG 3007
3001 TCACAGCCGCTTTCAGATTTTCAGAGTGAACAGCCCTCCAGAGAGTGTGACCAACATCTA 3060
3008 TCACAGCCGCTTTCAGATTTTCAGAGTGAACAGCCCTCCAGAGAGTGTGACCAACATCTA 3067
3061 CAAAGTCCCTCTGTCGACAGCGTACAGTTCACGATGTGTGCTGACAGTCCCATTTCA 3120
3068 CAAAGTCCCTCTGTCGACAGCGTACAGTTCACGATGTGTGCTGACAGTCCCATTTCA 3127
3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGTCACTCTGACACGCGCTCCCT 3180
3128 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGTCACTCTGACACGCGCTCCCT 3187
3181 CTGCTACTTCATCTCGAAGAACCCCAAGAACCCAGAGATGTGTGCTGAGGCGCAAGGCGCGC 3240
3188 CTGCTACTTCATCTCGAAGAACCCCAAGAACCCAGAGATGTGTGCTGAGGCGCAAGGCGCGC 3247
3241 CCGGCTCTGCGCTCCGAGAGCGGTGACATGCTGTCGACCAAGCATTCCTGCTCAAGCT 3300
3248 CCGGCTCTGCGCTCCGAGAGCGGTGACATGCTGTCGACCAAGCATTCCTGCTCAAGCT 3307
3301 GACTGACACCGTGTCACTACCTGCTCACTCTGCGGTCACTCAGGACAGCCAGCGCA 3360
3308 GACTGACACCGTGTCACTACCTGCTCACTCTGCGGTCACTCAGGACAGCCAGCGCA 3367
3361 GGTGAGTGGAGAGCTCCCGGGAGACGCTGACTGCTCTGAGGCGCGAGCCACCCGCGC 3420
3368 GGTGAGTGGAGAGCTCCCGGGAGACGCTGACTGCTCTGAGGCGCGAGCCACCCGCGC 3427
3421 ACTGCCCTCAGACTTCAAGACCATCTGAGATGATGGCCACCGGCCACAGCCAGGCCGA 3480

3428 ACTGCCCTCAGACTTCAAGACCATCTGAGATGAGCCACCGGCCACAGCCAGGCCGA 3487
3481 GAGCAGACACACAGAGCCCTGTCACGCGGCTCAACGTCACAGGAGGAGGAGGCGGC 3540
3488 GAGCAGACACACAGAGCCCTGTCACGCGGCTCAACGTCACAGGAGGAGGAGGCGGC 3547
3541 CACACCCAGGCGCCGAGCTGAGAGTCTGAGGAGCTGAGTGAATGTTTGCCGAGGCTG 3600
3548 CACACCCAGGCGCCGAGCTGAGAGTCTGAGGAGCTGAGTGAATGTTTGCCGAGGCTG 3607
3601 CATGTCCGCTGAAGCTGAGTGTCCGCTGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 3660
3608 CATGTCCGCTGAAGCTGAGTGTCCGCTGAGGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 3667
3661 GAGTGTCCAGACACACCTCCGCTTCACTTCCCAACAGGCTGAGGCTGAGGCTGAGGCT 3720
3668 GAGTGTCCAGACACACCTCCGCTTCACTTCCCAACAGGCTGAGGCTGAGGCTGAGGCT 3727
3721 GGGCAGCTTTTCTCAACAGAGCCGCTTCACTTCCCAACAGGCTGAGGCTGAGGCTGAGGCT 3780
3728 GGGCAGCTTTTCTCAACAGAGCCGCTTCACTTCCCAACAGGCTGAGGCTGAGGCTGAGGCT 3787
3781 CCAAGTTCGCAATGTTTCAACCCCTGCGCTTCTGCTTTCACCCCTCAGATCC 3840
3788 CCAAGTTCGCAATGTTTCAACCCCTGCGCTTCTGCTTTCACCCCTCAGATCC 3847
3841 AGGTGAGACCTTGAAGAGACCTTGGAGCTCTGGAAATTTGGAGTACCAAGTGTG 3900
3848 AGGTGAGACCTTGAAGAGACCTTGGAGCTCTGGAAATTTGGAGTACCAAGTGTG 3907
3901 CCTGTACACAGGCGAGGACCTGACCTGATGAGGAGGCTCCTGAGGCTCAATTTGGGG 3960
3908 CCTGTACACAGGCGAGGACCTGACCTGATGAGGAGGCTCCTGAGGCTCAATTTGGGG 3967
3961 GAGGTGCTGTGGAGTAAATATCTGAATATGAGTTTTCAGTTTGAAGAAAA 4015
3968 GAGGTGCTGTGGAGTAAATATCTGAATATGAGTTTTCAGTTTGAAGAAAA 4022

RESULT 14
ABL53711
ID ABL53711 standard; cDNA; 4070 BP.
XX
AC ABL53711;
XX
DT 17-JUN-2002 (first entry)
XX
DE Human telomerase catalytic subunit hTERT cDNA.
XX
KW hTERT; telomerase; reverse transcriptase; immortalisation; human;
XX
KW vaccine; enzyme; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200216555-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-GB003726.
XX
PR 17-AUG-2000; 2000GB-00020246.
XX
PR 17-AUG-2000; 2000US-0225734P.
XX
PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX
PI Jones CJ, Kipling DG, Wilkinson G, Mcsharry B, Skinner JW;
XX
XX WPI; 2002-315462/35.
XX
XX Novel hTERT-immortalized cell line (human telomerase reverse
XX
XX transcriptase) useful for human vaccine production and preparation of
XX
XX antigen, such as a virus or virus-derived agent.

1821 CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGAGCTGTC 1880
1861 GGAACAGAGGTCACGACGATTCGGGAATCCAGAGCCCGCCCTGCTGACCTTCCAGACTCCG 1920
1881 GGAACAGAGGTCACGACGATTCGGGAATCCAGAGCCCGCCCTGCTGACCTTCCAGACTCCG 1940
1921 CTTCAATCCCAAGACCTGACGAGGCTGGGCGCGAATTTGGAACATGAGACTAGTGGTGGAGC 1980
1941 CTTCAATCCCAAGACCTGACGAGGCTGGGCGCGAATTTGGAACATGAGACTAGTGGTGGAGC 2000
1981 CAGAACTTTCCGACAGAAAGAGAGGCGCGACGCTCTACCTTCGAGGGTGAAGGCACTGTT 2040
2001 CAGAACTTTCCGACAGAAAGAGAGGCGCGACGCTCTACCTTCGAGGGTGAAGGCACTGTT 2060
2041 CAGCGTGTCTCACTACGAGCGGGCGCGGCGCCCGGCTCTGAGGGGCTCTGTGTGTGG 2100
2061 CAGCGTGTCTCACTACGAGCGGGCGCGGCGCCCGGCTCTGAGGGGCTCTGTGTGTGG 2120
2101 CCTGACGATATTCACAGAGGCTGGGCGCACTTCGTGCTGCGTGTGCGGAGCCAGAGCC 2160
2121 CTTGACGATATTCACAGAGGCTGGGCGCACTTCGTGCTGCGTGTGCGGAGCCAGAGCC 2180
2161 GCGGCTGTGAGCTGTACTTTGTCAAGGTGATGACGAGCGCGGTACGACACCATCCCA 2220
2181 GCGGCTGTGAGCTGTACTTTGTCAAGGTGATGACGAGCGCGGTACGACACCATCCCA 2240
2221 GGAACAGGCTCAGGAGGATCATGCGCCAGCATCATCAACCCAGAAACAGTACTGCTGTGG 2280
2241 GGAACAGGCTCAGGAGGATCATGCGCCAGCATCATCAACCCAGAAACAGTACTGCTGTGG 2300
2281 TCGGATATGCGTGTGTCAGAAAGGCGCCAGTGGGCGACGTCCGCAAGGCTTCAAGAGCA 2340
2301 TCGGATATGCGTGTGTCAGAAAGGCGCCAGTGGGCGACGTCCGCAAGGCTTCAAGAGCA 2360
2341 CGTCTTACCTTGAACAGACCTCCAGCGGTGATCATGACAGATTCGTGTGTGCTCACTGAGGA 2400
2361 CGTCTTACCTTGAACAGACCTCCAGCGGTGATCATGACAGATTCGTGTGTGCTCACTGAGGA 2420
2401 GACCAAGCCGCTGAGGAGATGCGGTGATCATGACAGATTCGTGTGTGCTCACTGAGGA 2460
2421 GACCAAGCCGCTGAGGAGATGCGGTGATCATGACAGATTCGTGTGTGCTCACTGAGGA 2480
2461 CAGTGGCTCTTTCAGAGCTCTTCTCACTGATGTCACACAGCGCGTGGAGCATAGGGG 2520
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2521 CAGTCTTACCTTGAACAGACCTCCAGCGGTGATCATGACAGATTCGTGTGTGCTCACTGAGGA 2580
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2641 GCTCCGCTGAGTGTGATGATTTCTTGTGTGACACCTCACCTCAGCCAGCGAAAC 2700
2661 GCTCCGCTGAGTGTGATGATTTCTTGTGTGACACCTCACCTCAGCCAGCGAAAC 2720
2701 CTTCTCAGAGACCTTGTGAGGTGTCCTGAGTATGCTGTGAGTGAATCTTGCGGA 2760
2721 CTTCTCAGAGACCTTGTGAGGTGTCCTGAGTATGCTGTGAGTGAATCTTGCGGA 2780
2761 GACAGTGTGAGTGAATCTTCTGTGAGAACAGAGGCTCGGGTGAACGAGCTTTTGTAGAT 2820
2781 GACAGTGTGAGTGAATCTTCTGTGAGAACAGAGGCTCGGGTGAACGAGCTTTTGTAGAT 2840
2821 GCGGCGCCAGGCGCTATTCCTGCTGTGAGGCTGTGCTGTGATACCGGAGCTTGAGGT 2880
2841 GCGGCGCCAGGCGCTATTCCTGCTGTGAGGCTGTGCTGTGATACCGGAGCTTGAGGT 2900
2881 GCGAGCGCATCTACCTGAGCTATGCGGAGCTTCATCAGAGCGAGTCTCACTTCAACCG 2940
2901 GCGAGCGCATCTACCTGAGCTATGCGGAGCTTCATCAGAGCGAGTCTCACTTCAACCG 2960

2941 CCGCTTCAAGGCTGGAGAGATGCGTTCGCAAACTTTTGGGGTCTTCCGCTGAAGTG 3000
2961 CCGCTTCAAGGCTGGAGAGATGCGTTCGCAAACTTTTGGGGTCTTCCGCTGAAGTG 3020
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3121 TCAGAGGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGTGACAGGCGCTCT 3180
3141 TCAGAGGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGTGACAGGCGCTCT 3200
3181 CTGTACTTCCATCTGAAAGCCAGAAACGACAGGATGTGCTGTGGGGCCAGGGCGCGC 3240
3201 CTGTACTTCCATCTGAAAGCCAGAAACGACAGGATGTGCTGTGGGGCCAGGGCGCGC 3260
3241 CCGGCTCTGCGCTCCGAGGCGGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3300
3261 CCGGCTCTGCGCTCCGAGGCGGTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3320
3301 GACTGACACCGGTGTCACTGATGATCTGAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 3360
3321 GACTGACACCGGTGTCACTGATGATCTGAGGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 3380
3361 GCTGAGTGGAGGCTCCCGGGAGCAGCGCTGACTGTGAGGCGCGAGCCAGCCCGG 3420
3381 GCTGAGTGGAGGCTCCCGGGAGCAGCGCTGACTGTGAGGCGCGAGCCAGCCCGG 3440
3421 ACTGCGCTTGAACCTTCAAGACCATCTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGT 3480
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3561 CACACCCAGGCGCGACCGCTGGAGTGTGAGGCGTGTGAGTGTGTGTGTGTGTGTGTGTGT 3620
3601 CATGTCCGCTGAAGGCTGAGTGTGCGGCTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGT 3660
3621 CATGTCCGCTGAAGGCTGAGTGTGCGGCTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGT 3680
3661 GAGTGTCCAGCACACCTGCGCTTCACTTCCCAAGGCTGGGCTCGGCTTCAACCCA 3720
3681 GAGTGTCCAGCACACCTGCGCTTCACTTCCCAAGGCTGGGCTCGGCTTCAACCCA 3740
3721 GGGCCAGCTTTTCTCAGAGGAGGCGCGCTTCACTTCCCAATGAGTAATGTCCATCC 3780
3741 GGGCCAGCTTTTCTCAGAGGAGGCGCGCTTCACTTCCCAATGAGTAATGTCCATCC 3800
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3801 CCAATTTCCCATTTGTTCAACCTTGCCTGCTTCTTGTGCTTCAACCCCACTATCC 3860
3841 AGGTGAGACCGCTGAGAAAGAACCTTGGAGGCTGTGGAAATTTGAGTGAACAAAGGTGTG 3900
3861 AGGTGAGACCGCTGAGAAAGAACCTTGGAGGCTGTGGAAATTTGAGTGAACAAAGGTGTG 3920
3901 CCTGTACACAGGCGAGACCTTGCACCTGATGTGGAGTCTCTGTGTGTCAAAATTTGGGG 3960
3921 CCTGTACACAGGCGAGACCTTGCACCTGATGTGGAGTCTCTGTGTGTCAAAATTTGGGG 3980
3961 GAGTGTCTGTGGAGTGAATTAATGAAATTAAGATTTTCACTTTTGAAGAAAAA 4015
3981 GAGTGTCTGTGGAGTGAATTAATGAAATTAAGATTTTCACTTTTGAAGAAAAA 4035

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RESULT 15
AAZ08150
ID AAZ08150 standard; cDNA; 4015 BP.
XX
AC AAZ08150;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human telomerase reverse transcriptase cDNA.
XX
KW Human telomerase reverse transcriptase; hTERT; telomerase; hEST2;
KW catalytic protein component; cell proliferative capacity;
KW cell immortality; neoplastic phenotype; diagnostic application;
KW prognostic application; telomerase related condition; cancer;
KW therapeutic agent; telomerase expression; telomerase activity; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /*tag= a
FT /product= "Human telomerase reverse transcriptase"
FT /transl_except= (pos:1877..1879, aa:Gln)
XX
XX MO9950279-A1.
XX 07-OCT-1999.
XX
XX 31-MAR-1999; 99MO-US007160.
XX
XX 31-MAR-1998; 98US-00052919.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB,
XX Andrews WH;
XX WPI; 1999-610834/52.
XX P-PSDB; AAY28881.
XX
XX Antisense polynucleotides for human telomerase reverse transcriptase used
XX for diagnosing or treating cancer.
XX
XX Claim 1; Fig 1; 31pp; English.
XX
XX The present sequence encodes for human telomerase reverse transcriptase
XX (hTERT). This is the catalytic protein component of telomerase and is also
XX referred to as hEST2. This correlates with cell proliferative capacity,
XX cell immortality, and the development of a neoplastic phenotype. Human
XX TRT antisense oligonucleotides are useful for diagnostic or prognostic
XX applications to telomerase related conditions, including cancer. They are
XX also useful as therapeutic agents, for inhibition of telomerase
XX expression and activity
XX
XX Sequence 4015 BP; 663 A; 1364 C; 1274 G; 714 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 4013.4; DB 2; Length 4015;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 4014; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GCAGCGCTGCTCTCTCTGCGACGTTGGAGAGCCCTGAGCCCGGCCAGATGCC 60
XX DB 1 GCAGCGCTGCTCTCTCTGCGACGTTGGAGAGCCCTGAGCCCGGCCAGATGCC 60
XX QY 61 GCGCGCTCCCGCGTCCGAGCGGTGGCTCCCTGCTGCGACGACCTACCGGAGGTGCT 120
XX DB 61 GCGCGCTCCCGCGTCCGAGCGGTGGCTCCCTGCTGCGACGACCTACCGGAGGTGCT 120
XX QY 121 GCGCGTGGCCAGCTTCTGTCGCGCGCTGAGGCGCCAGGCGCTGAGCGCGCG 180
XX DB 121 GCGCGTGGCCAGCTTCTGTCGCGCGCTGAGGCGCCAGGCGCTGAGCGCGCG 180
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QY 181 GGAACCCGCGGCTTTCCGCGCGTGGTGGCCCAAGTCTGTGTGCTGCTCCCTGGAGCC 240
DB 181 GGAACCCGCGGCTTTCCGCGCGTGGTGGCCCAAGTCTGTGTGCTGCTCCCTGGAGCC 240
QY 241 ACAGCGCCCGCCCGCGCCCTCTCTTCCGCGAGGTCTCTGCTTGAAGAGAGTGGTGC 300
DB 241 ACAGCGCCCGCCCGCGCCCTCTCTTCCGCGAGGTCTCTGCTTGAAGAGAGTGGTGC 300
QY 301 CCGAGTCTGCGAGAGGCTGTGAGAGCGCGCGCGGAGAAAGTGTGCTTGGCTTGGC 360
DB 301 CCGAGTCTGCGAGAGGCTGTGAGAGCGCGCGCGGAGAAAGTGTGCTTGGCTTGGC 360
QY 361 GCTGCTGAGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB 361 GCTGCTGAGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 421 CCTGCCCAACAGGTGACCGAGCGCACTGCGGCGGAGCGGCGGCGGCTGCTGCG 480
DB 421 CCTGCCCAACAGGTGACCGAGCGCACTGCGGCGGAGCGGCGGCGGCTGCTGCG 480
QY 481 CCGCGTGGCGGAGCGAGTGTCTGTTCACTGCTGGAGCGCTGCGGCTTTGTGCTGCT 540
DB 481 CCGCGTGGCGGAGCGAGTGTCTGTTCACTGCTGGAGCGCTGCGGCTTTGTGCTGCT 540
QY 541 GGCTCCCAAGCTGCGCTTACAGAGTGGCGGCGCGCGCGCTGTCACAGCTCGGCGCG 600
DB 541 GGCTCCCAAGCTGCGCTTACAGAGTGGCGGCGCGCGCGCTGTCACAGCTCGGCGCG 600
QY 601 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 601 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 661 CTGGAACCATTAACCTGCGAGGAGAGCGCGGCGTCCCTCTGCGGCTGCGAGCGCGG 720
DB 661 CTGGAACCATTAACCTGCGAGGAGAGCGCGGCGTCCCTCTGCGGCTGCGAGCGCGG 720
QY 721 GAGGCGCGGCGGCGAGTGCAGCGCAAGTCTGCGCGTGTGCGCAAGAGCGCGCGCG 780
DB 721 GAGGCGCGGCGGCGAGTGCAGCGCAAGTCTGCGCGTGTGCGCAAGAGCGCGCGCG 780
QY 781 TCCCTCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
DB 781 TCCCTCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 841 GCGTGAACGAGTGAACGAGTGTCTGTGTGTGTGTCACCTGCGAGACCGCGCGAGAGC 900
DB 841 GCGTGAACGAGTGAACGAGTGTCTGTGTGTGTGTCACCTGCGAGACCGCGCGAGAGC 900
QY 901 CACCTCTTTTGAAGGAGTGTCTCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
DB 901 CACCTCTTTTGAAGGAGTGTCTCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 961 GACACACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
DB 961 GACACACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 1021 CCGGTTAGCGCGGAGCGAGCACTTCTCTACTCTCTCAGGCGAGAGAGAGCGAGTGC 1080
DB 1021 CCGGTTAGCGCGGAGCGAGCACTTCTCTACTCTCTCAGGCGAGAGAGAGCGAGTGC 1080
QY 1081 GCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
DB 1081 GCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
QY 1141 GACCATCTTTTCTGAGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
DB 1141 GACCATCTTTTCTGAGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
QY 1201 GCGCCAGGCGCTACTGCGAAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
DB 1201 GCGCCAGGCGCTACTGCGAAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
```

QY 1261 GTGCCCCCTACGGGGGTGCTCTCCAGAACGCACTGCCGTGCGAGCTGCGGTCACCCCAGC 1320
Db 1261 GTGCCCCCTACGGGGGTGCTCTCCAGAACGCACTGCCGTGCGAGCTGCGGTCACCCCAGC 1320
QY 1321 AGCCGGGTCTGTGCTCCGGGAGAGAGCCCAAGGGCTCTGTGCGGGCCCCCGAGAGAGAGA 1380
Db 1321 AGCCGGGTCTGTGCTCCGGGAGAGAGCCCAAGGGCTCTGTGCGGGCCCCCGAGAGAGAGA 1380
QY 1381 CACAGAACCCCGGTGCGCTGTGTCAGCTGTCTCCGACAGCAGACAGCCCCCTGCGAGGTGA 1440
Db 1381 CACAGAACCCCGGTGCGCTGTGTCAGCTGTCTCCGACAGCAGACAGCCCCCTGCGAGGTGA 1440
QY 1441 CGGCTTCGTGCGGGGCTGCTGCTGCGCGCGGTGTCGCCAGGCTCTGTGGGCTCCAGGCA 1500
Db 1441 CGGCTTCGTGCGGGGCTGCTGCTGCGCGCGGTGTCGCCAGGCTCTGTGGGCTCCAGGCA 1500
QY 1501 CAACGAAAGCGCGCTTCTCAGAGAACCAAGAAATTATCTCTCTGCGGAGACATGCGCA 1560
Db 1501 CAACGAAAGCGCGCTTCTCAGAGAACCAAGAAATTATCTCTCTGCGGAGACATGCGCA 1560
QY 1561 GCTCTGCGTGCAGAGAGCTGACGTTGGAAGATGAGCGTGCAGGCACTGCGCTTGGCTGGCAG 1620
Db 1561 GCTCTGCGTGCAGAGAGCTGACGTTGGAAGATGAGCGTGCAGGCACTGCGCTTGGCTGGCAG 1620
QY 1621 GAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGACCGTCTGCTGAGAGAAATCTTGAC 1680
Db 1621 GAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGACCGTCTGCTGAGAGAAATCTTGAC 1680
QY 1681 CAAGTTCCTGCACTGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
Db 1681 CAAGTTCCTGCACTGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 1741 TGTCTCAGAGAACCAAGTTTCAAAAAGAGGCTCTTTTCTACCCGGAAGATGTCGAG 1800
Db 1741 TGTCTCAGAGAACCAAGTTTCAAAAAGAGGCTCTTTTCTACCCGGAAGATGTCGAG 1800
QY 1801 CAAGTTCGAAAGCATTTGGAATCAGACAGCATTTGAAGAGGTCGAGCTCGGAGGCTGTC 1860
Db 1801 CAAGTTCGAAAGCATTTGGAATCAGACAGCATTTGAAGAGGTCGAGCTCGGAGGCTGTC 1860
QY 1861 GGAAGCAGAGGTCAGGCGAGCATCGGAGAGCCAGGCGCGCTGCTGACGTCAGACTCGG 1920
Db 1861 GGAAGCAGAGGTCAGGCGAGCATCGGAGAGCCAGGCGCGCTGCTGACGTCAGACTCGG 1920
QY 1921 CTTTATCCCAAGAGCTGACGCGCTGCGGCGCATTTGGAACATGACATTAAGTCTGAGAC 1980
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QY 1981 CAGAAAGTTCCGAGAGAAAGAGGCGAGGCGTCACTCGAGGGGTGAAGCACTGTT 2040
Db 1981 CAGAAAGTTCCGAGAGAAAGAGGCGAGGCGTCACTCGAGGGGTGAAGCACTGTT 2040
QY 2041 CAGCGTGTCAACTACAGAGCGGGCGCGCGCGCTCTGAGGCGCTCTGTGTGTCGAG 2100
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Db 2101 CCTGGAAGATATCAGAGGCGCTGCGCACCTTCTGTGCTGCTGTGCGGGCCAGAGACC 2160
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QY 2281 TCGGTATGCTGTGTCTCAAGAGGCGCGCATGAGGCACTGCGGAGGCTTCAAGAGCA 2340
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
FAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
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Morin, Gregg B.
Harley, Calvin
Andrews, William H.
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NUMBER OF SEQUENCES: 225
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
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FILING DATE: <Unknown>
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APPLICATION NUMBER: US 08/844,419
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FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
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Query Match 100.0%; Score 4015; DB 14; Length 4015;
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US-10-044-539-1
; Sequence 1, Application US/10044539
; Publication No. US20030100033A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru

Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
City: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
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TYPE: nucleic acid
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QY 2881 GGAAGGCGATCTCAGCTAGTACCGGAGCTCCATCAGAGCACTGACCTTCAACG 2940
Db 2881 GGAAGGCGATCTCAGCTAGTACCGGAGCTCCATCAGAGCACTGACCTTCAACG 2940
QY 2941 CGGCTTCAAGGCTGGAGAGATGAGTGTGCAAACTTTTGGGGTCTTGGCTGAAATG 3000
Db 2941 CGGCTTCAAGGCTGGAGAGATGAGTGTGCAAACTTTTGGGGTCTTGGCTGAAATG 3000
QY 3001 TCAAGCTGTTTCTGAGATTTGAGGTGAACAGCTTCCAGCGTGTGCAACATCTA 3060
Db 3001 TCAAGCTGTTTCTGAGATTTGAGGTGAACAGCTTCCAGCGTGTGCAACATCTA 3060
QY 3061 CAAAGTCCCTGCTGAGGCGGTACAGGTTTACGAGTGTGTGCACTCCATTGA 3120
Db 3061 CAAAGTCCCTGCTGAGGCGGTACAGGTTTACGAGTGTGTGCACTCCATTGA 3120
QY 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGCTATCTGACAGGCTCCCT 3180
Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGCTATCTGACAGGCTCCCT 3180
QY 3181 CTGCTACTCATCTGAAAGCCCAAGAACGAGGATGTGCTGGGAGCCAGGCGCTC 3240
Db 3181 CTGCTACTCATCTGAAAGCCCAAGAACGAGGATGTGCTGGGAGCCAGGCGCTC 3240
QY 3241 CGGCTCTGCGCTTCCGAGGCGGTGAGTGTGTGACCAAGACATTCCTCTCAAGT 3300
Db 3241 CGGCTCTGCGCTTCCGAGGCGGTGAGTGTGTGACCAAGACATTCCTCTCAAGT 3300
QY 3301 GACTGAGACGCTGTCACTTACGTGCACTCTGAGGAGTCACTCAAGACAGCCAGCGA 3360
Db 3301 GACTGAGACGCTGTGTCACTTACGTGCACTCTGAGGAGTCACTCAAGACAGCGA 3360
QY 3361 GCTGAGTGGAAAGCTCCGCGGAGCAAGCTGACTGCTCCGAGGCGGCAACCCGCG 3420
Db 3361 GCTGAGTGGAAAGCTCCGCGGAGCAAGCTGACTGCTCCGAGGCGGCAACCCGCG 3420

Db	361	GCCTGTGGACGGGGGCCCCGGGGGGCCCCCGAAGCCTTCAACACACAGCTGGCCAGCTA	420
Qy	421	CCTGCGCAACAACGATGACCGAACGCACTTGCGGGGGAGACGGGGCGTGGGGCTGCTGGC	480
Db	421	CCTGCCCAACACGGTGAACGACGCACTCGGGGGGAGCGGGCGTGGGGGCTGCTGGC	480
Qy	481	CCGCTGGGGCCACACGCTGCTGGTTCACTGTGGCAACGCTGGCGCTCTTTGTGCTGGT	540
Db	481	CCGCTGGGGCCACACGCTGCTGGTTCACTGTGGCAACGCTGGCGCTCTTTGTGCTGGT	540
Qy	541	GGCTCCACAGCTGCGCTCAACAGGTGTGGGGCGCGCTGTACAGAGCTGGCGCTGCAC	600
Db	541	GGCTCCACAGCTGCGCTCAACAGGTGTGGGGCGCGCTGTGTACAGAGCTGGCGCTGCAC	600
Qy	601	TCAGGCGCGGCCCCCGCCACAACGCTAGTGAACCCGGAAGCGCTTGGAGTGCAGCGGC	660
Db	601	TCAGGCGCGGCCCCCGCCACAACGCTAGTGAACCCGGAAGCGCTTGGAGTGCAGCGGC	660
Qy	661	CTGGAACCATAGCTGACAGAGAGCGGGGGTCCCCCTGGAGCTTCGACGCCGGGTGGAG	720
Db	661	CTGGAACCATAGCTGACAGAGAGCGGGGGTCCCCCTGGAGCTTCGACGCCGGGTGGAG	720
Qy	721	GAGGCGCGGGGGCAGTGTGACGCCGAAGCTGCGCTGTGGCCAAAGAGCCAGACGTGGCGC	780
Db	721	GAGGCGCGGGGGCAGTGTGACGCCGAAGCTGCGCTGTGGCCAAAGAGCCAGACGTGGCGC	780
Qy	781	TGCCCCCTAGCGGAGCGGACGCGCCGTTGGGACAGGGATCTTGGGCCACCCGGGACAGAC	840
Db	781	TGCCCCCTAGCGGAGCGGACGCGCCGTTGGGACAGGGATCTTGGGCCACCCGGGACAGAC	840
Qy	841	GCGTGGACCGAGTGAACCGTGGTTTCTGTGTGTGTCACTGACAGACCCGCGGAAGAGC	900
Db	841	GCGTGGACCGAGTGAACCGTGGTTTCTGTGTGTGTCACTGACAGACCCGCGGAAGAGC	900
Qy	901	CACCTCTTTGAGAGGGTGGGCTCTGCGAGACGGGCACCTCCACCATCCGAGGGCCGCA	960
Db	901	CACCTCTTTGAGAGGGTGGGCTCTGCGAGACGGGCACCTCCACCATCCGAGGGCCGCA	960
Qy	961	GCACCACGCGGGCCCCCATCCACATCCGCGGCACACAGTCCCTGGAGCAAGCCTTGTCC	1020
Db	961	GCACCACGCGGGCCCCCATCCACATCCGCGGCACACAGTCCCTGGAGCAAGCCTTGTCC	1020
Qy	1021	CCCGGTGTAACGCCGAGACCAAGCATTCTCTACTCTCAGAGCAAGAGACGCTGCG	1080
Db	1021	CCCGGTGTAACGCCGAGACCAAGCATTCTCTACTCTCAGAGCAAGAGACGCTGCG	1080
Qy	1081	GGCCTCTTCTCTACTCACTCACTGAGGCCCAAGCTGACCTGACCTGGAGAGCTCTGGA	1140
Db	1081	GGCCTCTTCTCTACTCACTCACTGAGGCCCAAGCTGACCTGACCTGGAGAGCTCTGGA	1140
Qy	1141	GACCATCTTTCTGGGTTTCAAGGACCTCTGAGGCCACGCTGTAGTGGCGCTCGAGAGCTGGA	1200
Db	1141	GACCATCTTTCTGGGTTTCAAGGACCTCTGAGGCCACGCTGTAGTGGCGCTCGAGAGCTGGA	1200
Qy	1201	GGCCAGCGCTACTGGCAAAATGGGCGCCCTGTTCTGAGAGCTGTGGGAACCAAGCGCA	1260
Db	1201	GGCCAGCGCTACTGGCAAAATGGGCGCCCTGTTCTGAGAGCTGTGGGAACCAAGCGCA	1260
Qy	1261	GTGCCCCCTACCGGGGTCTCTTCMAAGCACTGCGCCGCTGGAGGTGGGTATCCCAAGC	1320
Db	1261	GTGCCCCCTACCGGGGTCTCTTCMAAGCACTGCGCCGCTGGAGGTGGGTATCCCAAGC	1320
Qy	1321	AGCCGGTGTCTGTGCGCGGAGAAACCCCAAGGACTCTGTGGCGGGCCCCCGAGAGAGAGA	1380
Db	1321	AGCCGGTGTCTGTGCGCGGAGAAACCCCAAGGACTCTGTGGCGGGCCCCCGAGAGAGAGA	1380
Qy	1381	CACAGACCCCGTGCCTGTGTGACACTCTCGCCAGCAACAGACCCCTGTGACAGTGT	1440
Db	1381	CACAGACCCCGTGCCTGTGTGACACTCTCGCCAGCAACAGACCCCTGTGACAGTGT	1440
Qy	1441	CGGCTTCTGTGCGGGCTGTGCTGCGCGGCTGTGTGCCCCCAGAGCTCTTGGAGCTCAAGCA	1500
Db	1441	CGGCTTCTGTGCGGGCTGTGCTGCGCGGCTGTGTGCCCCCAGAGCTCTTGGAGCTCAAGCA	1500

QY	1501	CAAGGAAGCCGCTTCTCTCAGAGAACACCAAGAAATTATCTTCCTGGGGAAGCATGCCAA	1568
Db	1501	CAAGGAACGCCGCTTCTCTCAGAGAACACCAAGAAATTATCTTCCTGGGGAAGCATGCCAA	1568
QY	1561	GCTCTCGCTGAGAGAGCTGACGTGGGAAGATGAGGCTCGGGACTGCGCTTGAGTGGCGAG	1620
Db	1561	GCTCTCGCTGAGAGAGCTGACGTGGGAAGATGAGGCTCGGGACTGCGCTTGAGTGGCGAG	1620
QY	1621	GAGCCCAAGGGGTTGAGCTGTGTTCGGCCGCAGAGCAACGCTGCTGCTGAGAGATCTGGC	1680
Db	1621	GAGCCCAAGGGGTTGAGCTGTGTTCGGCCGCAGAGCAACGCTGCTGCTGAGAGATCTGGC	1680
QY	1681	CAAGTTCCTGACATCGGCTGATGAGTGTGTATGCTGTGAGCTGCTCAGAGCTTTCTTTTA	1740
Db	1681	CAAGTTCCTGACATCGGCTGATGAGTGTGTATGCTGTGAGCTGCTCAGAGCTTTCTTTTA	1740
QY	1741	TGTCAACGAGACACAGTTTCAAAAAGAACAGGCTCTTTTCTTACCAGGAAGATGTCTGAG	1800
Db	1741	TGTCAACGAGACACAGTTTCAAAAAGAACAGGCTCTTTTCTTACCAGGAAGATGTCTGAG	1800
QY	1801	CAAGTTCGAAAGCAATTGGAAATCACAACAGCATTTGAAAGGGTGTGACGTGCGGGAGCTGTC	1860
Db	1801	CAAGTTCGAAAGCAATTGGAAATCACAACAGCATTTGAAAGGGTGTGACGTGCGGGAGCTGTC	1860
QY	1861	GGAAGCAGAGAGTCAAGGCGAGCATCCGGGAAAGCCAGGCCCGCTCTGCTGACGTCCAGACTTCG	1920
Db	1861	GGAAGCAGAGAGTCAAGGCGAGCATCCGGGAAAGCCAGGCCCGCTCTGCTGACGTCCAGACTTCG	1920
QY	1921	CTTCAATCCCAAGCCTTGAACGGGCTGCGGCGCATTTGTGACATGGAATTAAGTCTGTGGAGAC	1980
Db	1921	CTTCAATCCCAAGGCTTGAACGGGCTGCGGCGCATTTGTGACATGGAATTAAGTCTGTGGAGAC	1980
QY	1981	CAGAACGTTCCGCGAGAGAAAGAGGGCCGACGCTCACTCACTCGAAGGGTGAAGGCACTGTT	2040
Db	1981	CAGAACGTTCCGCGAGAGAAAGAGGGCCGACGCTCACTCACTCGAAGGGTGAAGGCACTGTT	2040
QY	2041	CAGCGTGTCTAACTACAGACGGGAGCGCGGCGCCCGGCTCTCTGAGCGCTTGTGTGCTGGG	2100
Db	2041	CAGCGTGTCTAACTACAGACGGGAGCGCGGCGCCCGGCTCTCTGAGCGCTTGTGTGCTGGG	2100
QY	2101	CCTGGAAGCATATCCACAAGGCGCTGGCGCACCTTGTGTGTGTGTGTGGCGGCGCCAGAGACCC	2160
Db	2101	CCTGGAAGCATATCCACAAGGCGCTGGCGCACCTTGTGTGTGTGTGTGGCGGCGCCAGAGACCC	2160
QY	2161	GCCGCGTAGCTGTAACCTTGTCAAGGTGTGATGTACCGGCGCGCTGACGACACATTCGCCCA	2220
Db	2161	GCCGCGTAGCTGTAACCTTGTCAAGGTGTGATGTACCGGCGCGCTGACGACACATTCGCCCA	2220
QY	2221	GGAAGAGCTTCAACGAGAGTCAATCGCCAGCATATCAAAACCCAGAACAGATGCTGTGTGCG	2280
Db	2221	GGAAGAGCTTCAACGAGAGTCAATCGCCAGCATATCAAAACCCAGAACAGATGCTGTGTGCG	2280
QY	2281	TGCGATATCCGTGTGTGCAAGAGCGCGCCATGAGGCAAGTTCGCGAAGGCTTCAAGAGGCA	2340
Db	2281	TGCGATATCCGTGTGTGCAAGAGCGCGCCATGAGGCAAGTTCGCGAAGGCTTCAAGAGGCA	2340
QY	2341	CGTCTCTACCTTTCAGACAGACTCTCAGCCGTACATGCGACAGTTCGTGTGCTCACTGACAGA	2400
Db	2341	CGTCTCTACCTTTCAGACAGACTCTCAGCCGTACATGCGACAGTTCGTGTGCTCACTGACAGA	2400
QY	2401	GACCAAGCCCGCTGAGAGGATGCGCGGTGTATGAGAGAGAGCTTCCTCTGAATGAGGCCAG	2460
Db	2401	GACCAAGCCCGCTGAGAGGATGCGCGGTGTATGAGAGAGAGCTTCCTCTGAATGAGGCCAG	2460
QY	2461	CAGTGTGCTTCTTCAGACGTCTTCTTAAGCTTTCATGTGCAACACGCGCTGTGCGCATCAAGGG	2520
Db	2461	CAGTGTGCTTCTTCAGACGTCTTCTTAAGCTTTCATGTGCAACACGCGCTGTGCGCATCAAGGG	2520
QY	2521	CAAGTCTCAAGCTCAAGTGTCCAGAGGGATATCCGCGAAGGCTCATCTCTTCACAGCTGTCTG	2580
Db	2521	CAAGTCTCAAGCTCAAGTGTCCAGAGGGATATCCGCGAAGGCTCATCTCTTCACAGCTGTCTG	2580

QY 2581 CAGCTGCTAGTACGAGCATGAGAAACAGCTGTTTCCGGGGATTCGGGGGAGCGGGCT 2640
 DB 2581 CAGCTGCTAGTACGAGCATGAGAAACAGCTGTTTCCGGGGATTCGGGGGAGCGGGCT 2640
 QY 2641 GCTCCTGCTGTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAACCAACCGGAAAC 2700
 DB 2641 GCTCCTGCTGTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAACCAACCGGAAAC 2700
 QY 2701 CTTCCTCAGAGCCCTGGTCCGAGGTGTCCTGAGTATGAGTGTGCTGCTGTGAATCTTGGGAA 2760
 DB 2701 CTTCCTCAGAGCCCTGGTCCGAGGTGTCCTGAGTATGAGTGTGCTGCTGTGAATCTTGGGAA 2760
 QY 2761 GACAGTGTGAATCTTCCCTGTAGAAAGACAGGCCCTGGTGGACAGGCTTTTGTTCAGAT 2820
 DB 2761 GACAGTGTGAATCTTCCCTGTAGAAAGACAGGCCCTGGTGGACAGGCTTTTGTTCAGAT 2820
 QY 2821 GCGGGCCACGCGCTATTTCCCTGTGTGCGGCTGTCTGTGATACCCGAACTTGTTCAGAT 2880
 DB 2821 GCGGGCCACGCGCTATTTCCCTGTGTGCGGCTGTCTGTGATACCCGAACTTGTTCAGAT 2880
 QY 2881 GCAAGAGCACTACTCAGCTATGCGCGGACCTCCATCAGAGCCAGCTTCAACCG 2940
 DB 2881 GCAAGAGCACTACTCAGCTATGCGCGGACCTCCATCAGAGCCAGCTTCAACCG 2940
 QY 2941 CGGCTTCAAGGCTGGAGAGAAACATGCTGCAAACTTTTGGGGTCTTGGGGCTGAAGTG 3000
 DB 2941 CGGCTTCAAGGCTGGAGAGAAACATGCTGCAAACTTTTGGGGTCTTGGGGCTGAAGTG 3000
 QY 3001 TCACAGCTGTTTCTGATTTGACAGGTGAAACAGCTTCAACAGGTGTGACCAACATCTA 3060
 DB 3001 TCACAGCTGTTTCTGATTTGACAGGTGAAACAGCTTCAACAGGTGTGACCAACATCTA 3060
 QY 3061 CAAGATCTCTGCTGACGAGCGTACAGGTTTCAAGCATGTGTGCTGAGCTCCCATTTCA 3120
 DB 3061 CAAGATCTCTGCTGACGAGCGTACAGGTTTCAAGCATGTGTGCTGAGCTCCCATTTCA 3120
 QY 3121 TCAGCAAGTTTGAAGAAACCCCAATTTTCTGCGGCTCATCTTGACAGGCTCCCT 3180
 DB 3121 TCAGCAAGTTTGAAGAAACCCCAATTTTCTGCGGCTCATCTTGACAGGCTCCCT 3180
 QY 3181 CTGCTACTCATCTCTGAAAGCAAGAACGAGGAGATGCTGAGGGGCGCAAGGCGCCG 3240
 DB 3181 CTGCTACTCATCTCTGAAAGCAAGAACGAGGAGATGCTGAGGGGCGCAAGGCGCCG 3240
 QY 3241 CGGCGCTCTGCGCTCCGAGGCGGTGACAGTGTGTGCAACCAAGCTTCTGCTCAAGCT 3300
 DB 3241 CGGCGCTCTGCGCTCCGAGGCGGTGACAGTGTGTGCAACCAAGCTTCTGCTCAAGCT 3300
 QY 3301 GACTCGACACCGGTGACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
 DB 3301 GACTCGACACCGGTGACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
 QY 3361 GCTGAGTCCGAAAGCTCCGAGGAGACGAGCTGACCTGCTGAGAGGAGGAGGAGGAGGAGG 3420
 DB 3361 GCTGAGTCCGAAAGCTCCGAGGAGACGAGCTGACCTGCTGAGAGGAGGAGGAGGAGGAGG 3420
 QY 3421 ACTGCGCTCAGATTTGAAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
 DB 3421 ACTGCGCTCAGATTTGAAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
 QY 3481 GAGCAGACACACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
 DB 3481 GAGCAGACACACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
 QY 3541 CACACCCAGGCGCGACCGCTGAGAGTCTGAGGCTGAGTGTGTTTGGCGAGGCGTG 3600
 DB 3541 CACACCCAGGCGCGACCGCTGAGAGTCTGAGGCTGAGTGTGTTTGGCGAGGCGTG 3600
 QY 3601 CATGTCCGCTGAAGGCTAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
 DB 3601 CATGTCCGCTGAAGGCTAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
 QY 3661 GAGTGTCCAGACACCTGCGCTTTCATCTTCCCAAGGCTGGCGCTGCGCTTCAACCCCA 3720

DB 3661 GAGTGTCCAGACACCTGCGCTTTCATCTTCCCAAGGCTGGCGCTGCGCTTCAACCCCA 3720
 QY 3721 GGGCCAGCTTTTCTCAGCAGAGAGCCGGCTTCACTCCCAATGAAATGTCCATCC 3780
 DB 3721 GGGCCAGCTTTTCTCAGCAGAGAGCCGGCTTCACTCCCAATGAAATGTCCATCC 3780
 QY 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
 DB 3781 CCAGATTCCGCAATTTTCAACCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
 QY 3841 AGGTGAGACCCCTGAGAGAGACCTTGGAGCTTGGGAATTTGAGTGAACCAAGGTG 3900
 DB 3841 AGGTGAGACCCCTGAGAGAGACCTTGGAGCTTGGGAATTTGAGTGAACCAAGGTG 3900
 QY 3901 CCTGTACACAGGCGAGACCTTGCACCTGATGAGGAGTCCCTGTGGTCAAAATTGGGG 3960
 DB 3901 CCTGTACACAGGCGAGACCTTGCACCTGATGAGGAGTCCCTGTGGTCAAAATTGGGG 3960
 QY 3961 GAGTGTCTGGAGTAAATCTGAATATGAGTTTTCAGTTTGAAGAAAA 4015
 DB 3961 GAGTGTCTGGAGTAAATCTGAATATGAGTTTTCAGTTTGAAGAAAA 4015

RESULT 13
 US-10-388-578-1
 ; Sequence 1, Application US/10388578
 ; Publication No. US2003022441A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation
 ; APPLICANT: Stanton, Lawrence
 ; APPLICANT: Ralph, Brandenberger
 ; APPLICANT: Joseph, Gold D.
 ; APPLICANT: John, Irving
 ; APPLICANT: Mandalam, Ramkumar
 ; APPLICANT: Mok, Michael
 ; APPLICANT: Shelton, Dawne
 ; TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of Human Embryonic Stem Cells
 ; FILE REFERENCE: 135/001
 ; CURRENT APPLICATION NUMBER: US/10/388,578
 ; CURRENT FILING DATE: 2003-03-13
 ; NUMBER OF SEQ ID NOS: 139
 ; SOFTWARE: Custom
 ; SEQ ID NO 1
 ; LENGTH: 4015
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (56)..(3454)
 ; OTHER INFORMATION:
 US-10-388-578-1

Query Match 100.0%; Score 4015; DB 15; Length 4015;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4015; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 DB 1 GAGGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 QY 61 GCGCGCTCCCGCTGCGAGCGAGCGTGGCTCCCTGCTGCGAGCACTACCGAGGAGTCT 120
 DB 61 GCGCGCTCCCGCTGCGAGCGAGCGTGGCTCCCTGCTGCGAGCACTACCGAGGAGTCT 120
 QY 121 GCGCGTGGCCAGCTTCTGCTGCGAGCGCTGCGAGCGCCCAAGGCTGCGGCTGTGTGACCGCG 180
 DB 121 GCGCGTGGCCAGCTTCTGCTGCGAGCGCTGCGAGCGCCCAAGGCTGCGGCTGTGTGACCGCG 180
 QY 181 GAGCCCGGCGCTTTCCGCGCGCTGTGTGTGAGCCCAATGCTGTGTGTGCTGCTTGGAGCGC 240
 DB 181 GAGCCCGGCGCTTTCCGCGCGCTGTGTGTGAGCCCAATGCTGTGTGTGCTGCTTGGAGCGC 240

241 AGGCGGCGCCCGGCGCCCTCTCTCCGCGAGGTCCTGCTGAAGAGCTGTGCG 300
241 AGGCGGCGCCCGGCGCCCTCTCTCCGCGAGGTCCTGCTGAAGAGCTGTGCG 300
Qy 301 CCGAGTGTGCAAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGTGCGCTTGTGCGC 360
Db 301 CCGAGTGTGCAAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGTGCGCTTGTGCGC 360
Qy 361 GGTGCTGGAACGGGGGCGCGGGGGGCGCGAGGCTTACACACAGGCTGCGACGTA 420
Db 361 GGTGCTGGAACGGGGGCGCGGGGGGCGCGAGGCTTACACACAGGCTGCGACGTA 420
Qy 421 CTGCGCCAAACAGGTCGAGCGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCG 480
Db 421 CTGCGCCAAACAGGTCGAGCGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCG 480
Qy 481 CCGCGTGGGCGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 CCGCGTGGGCGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 541 GCGTCCCAAGCTGCGCTTACAGAGTGTGCGGGCGCGGCTGTACAGCTGCGGCTGCG 600
Db 541 GCGTCCCAAGCTGCGCTTACAGAGTGTGCGGGCGCGGCTGTACAGCTGCGGCTGCG 600
Qy 601 TCAGGCGCGGCGCGCGCGCACAGCTAGTGAACCGCGAAGCGCTGCGGAGTGAAGCG 660
Db 601 TCAGGCGCGGCGCGCGCGCACAGCTAGTGAACCGCGAAGCGCTGCGGAGTGAAGCG 660
Qy 661 CTGGAACCAATAGCGTTCAGAGAGGCGCGGGTCCCTGTGGGCTGCGACCGCGGGTGCAG 720
Db 661 CTGGAACCAATAGCGTTCAGAGAGGCGCGGGTCCCTGTGGGCTGCGACCGCGGGTGCAG 720
Qy 721 GAGGCGCGGGGCGAGTGTGCGAGCGCGAAGTGTGCGGTCGCGAAGAGCGCGAGCGCG 780
Db 721 GAGGCGCGGGGCGAGTGTGCGAGCGCGAAGTGTGCGGTCGCGAAGAGCGCGAGCGCG 780
Qy 781 TGCCCTGAGCGGAGCGAGCGCGGTTGAGGAGGGGCTGTGGGCGCGCGCGAGCGAG 840
Db 781 TGCCCTGAGCGGAGCGAGCGCGGTTGAGGAGGGGCTGTGGGCGCGCGCGAGCGAG 840
Qy 841 GCGTGAACCGAGTGAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 841 GCGTGAACCGAGTGAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Qy 901 CACTCTTTTGAAGGTGCGCTCTCTGCGACGCGCGCACTCCACCACTCCGTGGGCGCGCA 960
Db 901 CACTCTTTTGAAGGTGCGCTCTCTGCGACGCGCGCACTCCACCACTCCGTGGGCGCGCA 960
Qy 961 GAGCAACGCGGGGCGCGCGCGCATGCGAGCGCGCAACAGCTCCCTGGGAGCAAGCTGTGCG 1020
Db 961 GAGCAACGCGGGGCGCGCGCGCATGCGAGCGCGCAACAGCTCCCTGGGAGCAAGCTGTGCG 1020
Qy 1021 CCGGCTGTAGCGCGAGCAAGCACTTCTCTACTCTCTGAGCGAGCAAGAGAGCTGCG 1080
Db 1021 CCGGCTGTAGCGCGAGCAAGCACTTCTCTACTCTCTGAGCGAGCAAGAGAGCTGCG 1080
Qy 1081 GCGCTCTCTTCTACTAGCTCTTGAAGCGCGAGCTGAGCTGCGAGCTGCGAGCTGCGAG 1140
Db 1081 GCGCTCTCTTCTACTAGCTCTTGAAGCGCGAGCTGAGCTGCGAGCTGCGAGCTGCGAG 1140
Qy 1141 GAGCAATCTTCTGAGGTCGAGAGCGCGTGAAGCGAGGAGCTCCCGAGAGGTGCGCGCGCT 1200
Db 1141 GAGCAATCTTCTGAGGTCGAGAGCGCGTGAAGCGAGGAGCTCCCGAGAGGTGCGCGCGCT 1200
Qy 1201 GCGCCAGCGCTACTGCGCAATGCGGCGCGCTGTTCTGAGAGCTGTTGAGAGCAACGCGCA 1260
Db 1201 GCGCCAGCGCTACTGCGCAATGCGGCGCGCTGTTCTGAGAGCTGTTGAGAGCAACGCGCA 1260
Qy 1261 GTGCGCCCTAGCGGGGTGCTCTCAAGAGAGGAGCTGCGCGCTGCGAGCTGCGGCTCAAGCG 1320
Db 1261 GTGCGCCCTAGCGGGGTGCTCTCAAGAGAGGAGCTGCGCGCTGCGAGCTGCGGCTCAAGCG 1320

Qy 1321 AGCGGCTGTGTGCGCGGAGAGAGCGCCAGAGGCTGTGTGCGGCGCGCGAGAGAGGA 1380
Db 1321 AGCGGCTGTGTGCGCGGAGAGAGCGCCAGAGGCTGTGTGCGGCGCGCGAGAGAGGA 1380
Qy 1381 CACAGACCCCGGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
Db 1381 CACAGACCCCGGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
Qy 1441 CCGCTTGTGCGGGGCTGCGCTGCGCGCGGCTGCGCGCGGCTGCGCGGCTGCGAGGA 1500
Db 1441 CCGCTTGTGCGGGGCTGCGCTGCGCGCGGCTGCGCGCGGCTGCGCGGCTGCGAGGA 1500
Qy 1501 CAACGAGCGCGCTTCTCTAGAGAACCAAGAGATTCTCTCTGCGGAGCATGCCAA 1560
Db 1501 CAACGAGCGCGCTTCTCTAGAGAACCAAGAGATTCTCTCTGCGGAGCATGCCAA 1560
Qy 1561 GCTTGTGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGGGAGCTGCGCTGCGCGAG 1620
Db 1561 GCTTGTGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGGGAGCTGCGCTGCGCGAG 1620
Qy 1621 GAGCCAGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db 1621 GAGCCAGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Qy 1681 CAAGTTCCTGCACTGCTGATGAGTGTGACGTGCTGCAAGCTGCTTCTTTT 1740
Db 1681 CAAGTTCCTGCACTGCTGATGAGTGTGACGTGCTGCAAGCTGCTTCTTTT 1740
Qy 1741 TGTCAAGAGAACAGCTTCAAAAGAGAGCTCTTTTCTACCGGAGAGTGTGTGAG 1800
Db 1741 TGTCAAGAGAACAGCTTCAAAAGAGAGCTCTTTTCTACCGGAGAGTGTGTGAG 1800
Qy 1801 CAAGTTCCTGCACTGCTGATGAGTGTGACGTGCTGCAAGCTGCTTCTTTT 1860
Db 1801 CAAGTTCCTGCACTGCTGATGAGTGTGACGTGCTGCAAGCTGCTTCTTTT 1860
Qy 1861 GGAAGCAGAGGTCAGGAGCACTGCGAAGCGCGCGCGCTGCTGCAAGCTGCG 1920
Db 1861 GGAAGCAGAGGTCAGGAGCACTGCGAAGCGCGCGCGCTGCTGCAAGCTGCG 1920
Qy 1921 GTTCAATCCCAAGCTGAGCGGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 1980
Db 1921 GTTCAATCCCAAGCTGAGCGGCTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 1980
Qy 1981 CAGAGCTTCCGCAAGAGAAAGAGGCGCGAGGCTGCTGAGAGGTCGAGAGGCTG 2040
Db 1981 CAGAGCTTCCGCAAGAGAAAGAGGCGCGAGGCTGCTGAGAGGTCGAGAGGCTG 2040
Qy 2041 CAGCGTCTCACTAGAGCGGCGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 2100
Db 2041 CAGCGTCTCACTAGAGCGGCGCGCGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCG 2100
Qy 2101 CTTGAGCAGATATCAAGAGGCTGCGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Db 2101 CTTGAGCAGATATCAAGAGGCTGCGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Qy 2161 GCGCGTGTGCTGTCTTGTCAAGTGTGAGTGTGAGCGGCGGTCGAGACCATCCCGCA 2220
Db 2161 GCGCGTGTGCTGTCTTGTCAAGTGTGAGTGTGAGCGGCGGTCGAGACCATCCCGCA 2220
Qy 2221 GAGCAGGCTCAGGAGGTCATGCGCAGCATCAAAACCCAGAAACAGTACTGCTGCG 2280
Db 2221 GAGCAGGCTCAGGAGGTCATGCGCAGCATCAAAACCCAGAAACAGTACTGCTGCG 2280
Qy 2281 TCGGTATGCTGTGTGTCAGAGAGCGCGCGCATGCGAGCGCTTCAAGAGCA 2340
Db 2281 TCGGTATGCTGTGTGTCAGAGAGCGCGCGCATGCGAGCGCTTCAAGAGCA 2340
Qy 2341 GGTCTCTACTCTTGAAGAGCTTCAAGCGCGCATGCGAGCAAGTGTGCGCTCACTGAGGA 2400
Db 2341 GGTCTCTACTCTTGAAGAGCTTCAAGCGCGCATGCGAGCAAGTGTGCGCTCACTGAGGA 2400
Qy 2401 GAGCAGCGCGCTGAGGAGTGCCTGTCTATGAGAGAGAGCTCTCTGATGAGCGAG 2460

[illegible]

Db	1201	GGCCCCGGCTACTGGCAAAATGCGGCCCTCTTTCTTGAGCTGCTGGAAACACGGCGCA	1260
QY	1261	GTGCCCCCTACCGGGGTGCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGATCACCCAGC	1320
Db	1261	GTGCCCCCTACGGGGGTGCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGATCACCCAGC	1320
QY	1321	AGCGGTGTCTGTGCTCCGGGAGANGCCCGAGGGCTCTGTGGCGGCCCTCCGAGAGAGAGA	1380
Db	1321	AGCGGTGTCTGTGCTCCGGGAGANGCCCGAGGGCTCTGTGGCGGCCCTCCGAGAGAGAGA	1380
QY	1381	CACAGACCCCGGTGGCCCTGAGAGAGCTGTCGCGCAGACAGCAGCCCTTGAGAGTGA	1440
Db	1381	CACAGACCCCGGTGGCCCTGAGAGAGCTGTCGCGCAGACAGCAGCCCTTGAGAGTGA	1440
QY	1441	CGGCTTCTGTCGGGGCTTGCCCTGCGCCCGGCTTGTTGCCCTCTGGGGCTCCAGGCA	1500
Db	1441	CGGCTTCTGTCGGGGCTTGCCCTGCGCCCGGCTTGTTGCCCTCTGGGGCTCCAGGCA	1500
QY	1501	CAACGAACGCGCGTCTCTCAAGAAACACCAAGAGTTCACTCCCTGGGGAAAGCATGCCAA	1560
Db	1501	CAACGAACGCGCGTCTCTCAAGAAACACCAAGAGTTCACTCCCTGGGGAAAGCATGCCAA	1560
QY	1561	GCTCTCGCTGAGAGAGCTGACGTGAAAGTAGAGGTGCGGGACATGCGCTTGGGCTGCGAG	1620
Db	1561	GCTCTCGCTGAGAGAGCTGACGTGAAAGTAGAGGTGCGGGACATGCGCTTGGGCTGCGAG	1620
QY	1621	GAGCCCAAGGGGTTTGGATCTGTGTTCCGGGCGGACAGACACCGTGTGCTGAGAGATCTGCGC	1680
Db	1621	GAGCCCAAGGGGTTTGGATCTGTGTTCCGGGCGGACAGACACCGTGTGCTGAGAGATCTGCGC	1680
QY	1681	CAAGTCTCTGACATGAGCTGATGAGTGTGTATGTCGTGCACTGCTCAAGTCTTTCCTTTA	1740
Db	1681	CAAGTCTCTGACATGAGCTGATGAGTGTGTATGTCGTGCACTGCTCAAGTCTTTCCTTTA	1740
QY	1741	TGTCAACGGAGACACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGATGTCTGAG	1800
Db	1741	TGTCAACGGAGACACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGATGTCTGAG	1800
QY	1801	CAAGTGTGAAGACATTGGAAATCAAGACAGCATTTGAAGAGGTGACAGCTGCGGAGCTGTC	1860
Db	1801	CAAGTGTGAAGACATTGGAAATCAAGACAGCATTTGAAGAGGTGACAGCTGCGGAGCTGTC	1860
QY	1861	GGAAGCAGAGGTCAAGGACATCGGGAAGCCAGGCCCGGCTCTGTGAAGTCCAGACTTCG	1920
Db	1861	GGAAGCAGAGGTCAAGGACATCGGGAAGCCAGGCCCGGCTCTGTGAAGTCCAGACTTCG	1920
QY	1921	CTTCAATCCCCAAGCTTGAACGGGCTGCGGCCGATTTGTGAACATGGAATTAAGTCTGTGGAGC	1980
Db	1921	CTTCAATCCCCAAGCTTGAACGGGCTGCGGCCGATTTGTGAACATGGAATTAAGTCTGTGGAGC	1980
QY	1981	CAGAAAGTTCGCGAGAGAAAAGAGGGGCGAGCGTCTCAACTCGAGGGGTGAAGGACATGTT	2040
Db	1981	CAGAAAGTTCGCGAGAGAAAAGAGGGGCGAGCGTCTCAACTCGAGGGGTGAAGGACATGTT	2040
QY	2041	CAGCGTGTCAAATCAACGACGCGGGCGCGCGCCCGGCTCTCTGGAGCGCTCTGTGCTGG	2100
Db	2041	CAGCGTGTCAAATCAACGACGCGGGCGCGCGCCCGGCTCTCTGGAGCGCTCTGTGCTGG	2100
QY	2101	CCTGAGCATATTCACAGGGGCTTGCGGCACTTGTGTGCTGTGCTGTGGGGCTCCAGAACCC	2160
Db	2101	CCTGAGCATATTCACAGGGGCTTGCGGCACTTGTGTGCTGTGCTGTGGGGCTCCAGAACCC	2160
QY	2161	GCCGCTGAGCTGATCTTGTCAAGGTGGAATGTAACGGGGCGGTAGACACATCTCCCA	2220
Db	2161	GCCGCTGAGCTGATCTTGTCAAGGTGGAATGTAACGGGGCGGTAGACACATCTCCCA	2220
QY	2221	GGACAGGCTCAACGAGGTCAATGCGACAGATCATCAAAACCCAGAACAGATTAAGTCTGCG	2280
Db	2221	GGACAGGCTCAACGAGGTCAATGCGACAGATCATCAAAACCCAGAACAGATTAAGTCTGCG	2280
QY	2281	TGCGTATGCTGCTCCAGAAAGCGCGCCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2340
Db	2281	TGCGTATGCTGCTCCAGAAAGCGCGCCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2340

D	b	1	GCAGGCGTGCCTGCTGCGCAGCTGGGAAAGCCTTGGACCCCGGCAACCCCGCATGCC	60
O	y	61	GGGGCTCCCCGCTCCGAGCCGATGCGCTCTCCCTGCTGCGACCACTACCGAGAGTCT	120
D	b	61	GGCGCTCTCCCGCTCCGAGCCGTGCGCTCTCTGCTGCGCACCACTACCGAGAGTCT	120
O	y	121	GGCGGTGGCCACGTTCCGTGCGCGGCTGGGGGCCCAAGGACTGGCGGCTGGTGAACCGG	180
D	b	121	GGCGGTGGCCACGTTCCGTGCGCGGCTGGGGGCCCAAGGACTGGCGGCTGGTGAACCGG	180
O	y	181	GAACCCGCGAGCTTCCGCGGCGCTGGTGAACCAAGTGCCTGGTGTGCTGGGCCCTGGAGCG	240
D	b	181	GAACCCGCGAGCTTCCGCGGCGCTGGTGAACCAAGTGCCTGGTGTGCTGGGCCCTGGAGCG	240
O	y	241	ACGGCGGCCCCCGCGGCGCCCTCTCTTCGCGCAGGTGTCTTGCTGAAGAGTGTGGC	300
D	b	241	ACGGCGGCCCCCGCGGCGCCCTCTCTTCGCGCAGGTGTCTTGCTGAAGAGTGTGGC	300
O	y	301	CCGAGTGTGCAAGAGGCTGTGTGAGCGCGGCGCCAAAGACGTGCTGGCTTCGGCTTGGC	360
D	b	301	CCGAGTGTGCAAGAGGCTGTGTGAGCGCGGCGCCAAAGACGTGCTGGCTTCGGCTTGGC	360
O	y	361	GCTGTGAGACGGGAGGCGCGGGGGGGCCCCCGAGGACTTCAACACAGGTGGCGAGCTA	420
D	b	361	GCTGTGAGACGGGAGGCGCGGGGGGGCCCCCGAGGACTTCAACACAGGTGGCGAGCTA	420
O	y	421	CCTGCGCCAAACGGTGAACGACACTGCGGGGAGACGGGGCGTGGGGGCTGCTGCTCG	480
D	b	421	CCTGCGCCAAACGGTGAACGACACTGCGGGGAGACGGGGCGTGGGGGCTGCTGCTCG	480
O	y	481	CCGCGTGGGCGACACAGTGTGTGGTTCACTGTGACAGCTGCGGCTCTTTGTGTGGT	540
D	b	481	CCGCGTGGGCGACACAGTGTGTGGTTCACTGTGACAGCTGCGGCTCTTTGTGTGGT	540
O	y	541	GGCTCCCAAGCTGCGGCTACAGGTGTGGGGGCGCGCTGTACACAGCTCGGCGGTGCAC	600
D	b	541	GGCTCCCAAGCTGCGGCTACAGGTGTGGGGGCGCGCTGTACACAGCTCGGCGGTGCAC	600
O	y	601	TCAGGCGCGGCCCCCGCCACACGCTAGTGTGACCCCGAAGAGGCTGTGGATGCAACGGGC	660
D	b	601	TCAGGCGCGGCCCCCGCCACACGCTAGTGTGACCCCGAAGAGGCTGTGGATGCAACGGGC	660
O	y	661	CTGGAACTATAGCTGACGAGGAGGCGGGGGTCCCTCGGGGCTGCCAGCCCCGGGTGCAG	720
D	b	661	CTGGAACTATAGCTGACGAGGAGGCGGGGGTCCCTCGGGGCTGCCAGCCCCGGGTGCAG	720
O	y	721	GAGGCGCGGGGCGAGTGCACGCGCAAGTCTGCGCTGTGGCCCAAGAGGCCCAAGCGTGGGC	780
D	b	721	GAGGCGCGGGGCGAGTGCACGCGCAAGTCTGCGCTGTGGCCCAAGAGGCCCAAGCGTGGGC	780
O	y	781	TGCCCTTAGCGGAGCGGACGCGCCGTTGGGCGAGGGGTCTGTGGCCACCCGGGCGAGAC	840
D	b	781	TGCCCTTAGCGGAGCGGACGCGCCGTTGGGCGAGGGGTCTGTGGCCACCCGGGCGAGAC	840
O	y	841	GCGTGAACGAGTGAACGCTGGTTCTGTGTGGTGTCACTGCGCAGACCAGCCGCGAAGAGC	900
D	b	841	GCGTGAACGAGTGAACGCTGGTTCTGTGTGGTGTCACTGCGCAGACCAGCCGCGAAGAGC	900
O	y	901	CACTCTTTTGAAGGGTGTGCTCTGTGACACGCGCACTTCCCAACCATCCGTGGGCGCGCA	960
D	b	901	CACTCTTTTGAAGGGTGTGCTCTGTGACACGCGCACTTCCCAACCATCCGTGGGCGCGCA	960
O	y	961	GCACCAACGCGGGCCCCCATTCACATCCGCGGCAACAGTCCCTTGGGACAGCCTTGTCC	1020
D	b	961	GCACCAACGCGGGCCCCCATTCACATCCGCGGCAACAGTCCCTTGGGACAGCCTTGTCC	1020
O	y	1021	CCCGGTGTACGCGGAGACCAAGCACTTCTCTTACTCTCAAGCGCAAGAGAGCACTGCG	1080
D	b	1021	CCCGGTGTACGCGGAGACCAAGCACTTCTCTTACTCTCAAGCGCAAGAGAGCACTGCG	1080
O	y	1081	GGCTCTCTTCTTCACTCACTCACTGTGAGGCCCAAGCTGACTGGCGTGGAGAGCTGTGGA	1140
D	b	1081	GGCTCTCTTCTTCACTCACTCACTGTGAGGCCCAAGCTGACTGGCGTGGAGAGCTGTGGA	1140

QY	1141	GACCACTCTTTTGTGGGTTCCAGGCGCTTGATATGCCAGGACATCCCGCAGAGTTGCCCGGCT	1200
Db	1141	GACCATCTTTCTGTGGGTTCCAGGCGCTTGATATGCCAGGACATCCCGCAGAGTTGCCCGGCT	1200
QY	1201	GCCCCAGCGCTACTGGGAAATATGCGGCGCTGTTTCTGAGCTGCTTGAGAAACACGCGCA	1260
Db	1201	GCCCCAGCGCTACTGGCAATATGCGGCGCTGTTTCTGAGCTGCTTGAGAAACACGCGCA	1260
QY	1261	GTGCCCTTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTCGGTCAACCCAGC	1320
Db	1261	GTGCCCTTACGGGGTGCTCCTCAAGAGCGCACTGCCGCTGAGACTCGGTCAACCCAGC	1320
QY	1321	AGCCGCTGTCTGTGCTCCCGGAGANCCCAAGGCTCTGTGCGCGGCCCCGAGAGAGGA	1380
Db	1321	AGCCGCTGTCTGTGCTCCCGGAGAGCCCAAGGCTCTGTGCGCGGCCCCGAGAGAGGA	1380
QY	1381	CACAGACCCCCGTGGCGCTGTGTCAGCTGTCCGACACAGACAGCCCTTGCGCAGGTGA	1440
Db	1381	CACAGACCCCCGTGGCTGTGTCAGCTGTCCGACACAGACAGCCCTTGCGCAGGTGA	1440
QY	1441	CGGCTCTGTGCGGGCTGTGCTGCGCGCGAGTGTGCTCCCGCAGGCGCTTGAGGCTCAAGCA	1500
Db	1441	CGGCTCTGTGCGGGCTGTGCTGCGCGCGAGTGTGCTCCCGCAGGCGCTTGAGGCTCAAGCA	1500
QY	1501	CAACGAACCGCGCTTCTCAGAGAACACCAAGAGTTGATCTCCCTGCGGAGAGATGCCAA	1560
Db	1501	CAACGAACCGCGCTTCTCAGAGAAACCAAGAGTTGATCTCCCTGCGGAGAGATGCCAA	1560
QY	1561	GCTCTCGCTGAGAGACTGACGTGTGAAGTATGAGGTGTGCGGACTGTGGCTGCGAG	1620
Db	1561	GCTCTCGCTGAGAGACTGACGTGTGAAGTATGAGGTGTGCGGACTGTGGCTGCGAG	1620
QY	1621	GAGCCCAAGGGGTTGGCTGTGTTCGCGCGCAGAGACACCGTCTGCTGATGAGAGATCTGAC	1680
Db	1621	GAGCCCAAGGGGTTGGCTGTGTTCGCGCGCAGAGACACCGTCTGCTGATGAGAGATCTGAC	1680
QY	1681	CAAGTCTTCGCACTGAGCTGATGAGTGTGTACGTGTGAGCTGCTCAGGTTCTTTCTTTA	1740
Db	1681	CAAGTCTTCGCACTGAGCTGATGAGTGTGTACGTGTGAGCTGCTCAGGTTCTTTCTTTA	1740
QY	1741	TGTCAACGAGACCAACGTTTCAAAGAAACAGGCTCTTTTCTACCGGAAGTGTCTTGAG	1800
Db	1741	TGTCAACGAGACCAACGTTTCAAAGAAACAGGCTCTTTTCTACCGGAAGTGTCTTGAG	1800
QY	1801	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGAGCTGCGGAGCTGTC	1860
Db	1801	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGAGCTGCGGAGCTGTC	1860
QY	1861	GGAAGCAGAGGTCAAGGAGCATCGGAGAAAGCAGGCGCGCCTGTGTCAGTCTCAACTCCG	1920
Db	1861	GGAAGCAGAGGTCAAGGAGCATCGGAGAAAGCAGGCGCGCCTGTGTCAGTCTCAACTCCG	1920
QY	1921	CTTCATCCCAAGCTTGAACGGGCTGTGCGGCGGATTTGTAACATGGACTTACGTCGGAGC	1980
Db	1921	CTTCATCCCAAGCTTGAACGGGCTGTGCGGCGGATTTGTAACATGGACTTACGTCGGAGC	1980
QY	1981	CAGAAACGTTCCGCAAGAAAAAAGAGGGCGAGCGCTCACTCCAGAGGTTGAAGGACATGTT	2040
Db	1981	CAGAAACGTTCCGCAAGAAAAAAGAGGGCGAGCGCTCACTCCAGAGGTTGAAGGACATGTT	2040
QY	2041	CAGGCTGTCAACTACAGAGCGGAGCGGCGCGGCTCTCTGTGGGCGCTCTGTGTGCTGGG	2100
Db	2041	CAGGCTGTCAACTACAGAGCGGAGCGGCGCGGCTCTCTGTGGGCGCTCTGTGTGCTGGG	2100
QY	2101	CTTGAACGATATCCACAGGCGCTGCGCCACCTTGCTGTGCTGTGTGCGGCGCCAGAGACC	2160
Db	2101	CTTGAACGATATCCACAGGCGCTGCGCCACCTTGCTGTGCTGTGTGCGGCGCCAGAGACC	2160
QY	2161	GCGGCTGTGATCTTTGTCAAGGTGTGATGTGACGGGCGCGTACACACATCTCCCA	2220
Db	2161	GCGGCTGTGATCTTTGTCAAGGTGTGATGTGACGGGCGCGTACACACATCTCCCA	2220

QY 2221 GGACAGGCTCAAGAGTATCGCCAGCATCATCAAAACCCAGAAACAGTCTGCGG 2280
 Db 2221 GGACAGGCTCAAGAGTATCGCCAGCATCATCAAAACCCAGAAACAGTCTGCGG 2280
 QY 2281 TCGGATATCCGCTGCTCAAGAAAGCCGATGAGGACGTCGCAAGGCTTTCAAGAGCA 2340
 Db 2281 TCGGATATCCGCTGCTCAAGAAAGCCGATGAGGACGTCGCAAGGCTTTCAAGAGCA 2340
 QY 2341 CGTCTCACTTGAAGAGCTCCAGCCGATATCATGAGACAGTTCGTCGCTCACTGAGGA 2400
 Db 2341 CGTCTCACTTGAAGAGCTCCAGCCGATATCATGAGACAGTTCGTCGCTCACTGAGGA 2400
 QY 2401 GACCAAGCCGCTGAAGAGATGCGCTGATCATGAGACAGTCTCTCCGTAATGAGGCGAG 2460
 Db 2401 GACCAAGCCGCTGAAGAGATGCGCTGATCATGAGACAGTCTCTCCGTAATGAGGCGAG 2460
 QY 2461 CAGTGGGCTCTTCAAGCTCTTCTCAAGCTTATGTCACCAAGCCGTCGATCAGAGG 2520
 Db 2461 CAGTGGGCTCTTCAAGCTCTTCTCAAGCTTATGTCACCAAGCCGTCGATCAGAGG 2520
 QY 2521 CAACTCTCAAGCTCCAGTGGCCAGGAGATCCGCAAGGCTCACTCTCCAGGCTCTG 2580
 Db 2521 CAACTCTCAAGCTCCAGTGGCCAGGAGATCCGCAAGGCTCACTCTCCAGGCTCTG 2580
 QY 2581 CAGCTCTGCTCAAGGCAATGAGAAACAAGCTGTTGCGGAGATTCGCGGAGCGGCT 2640
 Db 2581 CAGCTCTGCTCAAGGCAATGAGAAACAAGCTGTTGCGGAGATTCGCGGAGCGGCT 2640
 QY 2641 GCTCTGCTGCTGAGTATGATTTCTGTTGTTGAGACCTCACTCAAGCCAGGAAAC 2700
 Db 2641 GCTCTGCTGCTGAGTATGATTTCTGTTGTTGAGACCTCACTCAAGCCAGGAAAC 2700
 QY 2701 CTTCCTCAGAACCTTGCTGAGGATGCTCCGTAATGAGTCTGCGGAGTCTTGGGAA 2760
 Db 2701 CTTCCTCAGAACCTTGCTGAGGATGCTCCGTAATGAGTCTGCGGAGTCTTGGGAA 2760
 QY 2761 GACAGTGTAACTTCCCTGTAGAAAGAGAGCCCTGAGTGGCAAGGCTTTGTAGAT 2820
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 QY 2881 GCGAGGCTATCTCCAGCTATGCTCCGAGCTCATCAGAGCAGTCTCACTTCAACCG 2940
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 QY 3121 TCAGCAAGTTTGAAGAACCCCACTTTTCCGCGGCTCATCTGACACAGGCTCCCT 3180
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 QY 3301 GACTGACACCGTGTCACTAGTGCCTCTGAGGCTCATCAGAGACAGCCACAGCGA 3360

Db 3301 GACTGACACCGTGTCACTAGTGCCTCTGAGGCTCATCAGAGACAGCCACAGCGA 3360
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 Db 3421 ACTGCTCTGAGCTTCAAGACCAATCTGATGATGAGCCAGCCGACAGCCAGCCGA 3480
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 Db 3541 CACACCCAGGCGCGACCGCTGAGTCTGAGGAGCTGAGTGTGTTGGCGAGGCGCTG 3600
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 Db 3601 CATGCTCGGCTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGAGTGTCCAGCCAGGCT 3660
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 QY 3781 CCAGATGCGCAATGTTTCAACCTGCGCTGCGCTGCTTGTGCTTCCACCCACATCC 3840
 Db 3781 CCAGATGCGCAATGTTTCAACCTGCGCTGCGCTGCTTGTGCTTCCACCCACATCC 3840
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 Db 3901 CCTGTACACAGGCGAGGACCTTGCACCTGATGAGGAGTCCCTGAGGCTCAAAATGGGGG 3960
 QY 3961 GAGTGTCTGTGAGTAAATATGAAATATGAGTGTGAGTGTGAGTGTGAGTGTG 4015
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